

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 24, 2004, 23:54:27 ; Search time 1832.72 Seconds
(without alignments)
16460.143 Million cell updates/sec

Title: US-10-051-835-14
Perfect score: 696
Sequence: 1 taaatatctgataggcagt.....ttttgaaaatatataaaat 696

Scoring table: IDENTITY NUC
Gapop 10.0 / Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	GenEmbl.*
1:	gb_ba.*
2:	gb_hcg.*
3:	gb_in.*
4:	gb_om.*
5:	gb_ov.*
6:	gb_pat.*
7:	gb_ph.*
8:	gb_pl.*
9:	gb_pr.*
10:	gb_ro.*
11:	gb_sts.*
12:	gb_sy.*
13:	gb_un.*
14:	gb_vi.*
15:	em_ba.*
16:	em_fun.*
17:	em_hum.*
18:	em_in.*
19:	em_mu.*
20:	em_om.*
21:	em_or.*
22:	em_ov.*
23:	em_pat.*
24:	em_ph.*
25:	em_pl.*
26:	em_ro.*
27:	em_sts.*
28:	em_un.*
29:	em_vi.*
30:	em_htg_hum.*
31:	em_htg_inv.*
32:	em_htg_other.*
33:	em_htg_mus.*
34:	em_htg_pln.*
35:	em_htg_rdt.*
36:	em_htg_mam.*
37:	em_htg_vrt.*
38:	em_sy.*
39:	em_htgo_hum.*
40:	em_htgo_mus.*
41:	em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	681.8	98.0	110000	2	AC112773_1	Continuation (2 of
2	681.8	98.0	156043	2	AC013631	AC013631 Homo sapi
3	681.8	98.0	160301	2	AC130417	AC130417 Homo sapi
4	681.8	98.0	178147	2	AC020694	AC020694 Homo sapi
5	681.8	98.0	191246	9	AC068769	AC068769 Homo sapi
6	681.8	98.0	192420	2	AC129804	AC129804 Homo sapi
7	89	12.8	7218	6	I66494	I66494 Sequence 14
8	50	7.5	134210	9	AC005052	AC005052 Homo sapi
9	50	7.2	72968	2	AC115957	AC115957 Mus muscu
10	49.8	7.2	221659	2	AC128582	AC128582 Rattus no
11	49.8	7.2	263081	2	AC115498	AC115498 Rattus no
12	47.6	6.8	128262	9	AL138681	AL138681 Human DNA
13	47.2	6.8	143577	9	AC013828	AC013828 Homo sapi
14	47.2	6.8	149059	9	AC027779	AC027779 Homo sapi
15	47.2	6.8	155185	2	AC074374	AC074374 Homo sapi
16	47.2	6.8	181755	2	AC026996	AC026996 Homo sapi
17	46.8	6.7	225182	2	AC107742	AC107742 Mus muscu
18	46.2	6.6	143501	2	AC125113	AC125113 Mus muscu
19	45.8	6.6	221782	2	AC111765	AC111765 Rattus no
20	45.2	6.5	168576	2	AC120150	AC120150 Mus muscu
21	45.2	6.5	216517	10	AL20415	AL20415 Mus muscu
22	45.2	6.5	248577	2	AC107771	AL845494 Mouse DNA
23	45.2	6.5	73450	2	AC137580	AC137580 Homo sapi
24	45	6.5	149041	9	AC044782	AC044782 Homo sapi
25	45	6.5	179391	9	AC012558	AC012558 Homo sapi
26	45	6.5	179789	9	AC069543	AC069543 Homo sapi
27	45	6.5	202050	2	AC060229	AC060229 Homo sapi
28	44.8	6.4	9415	6	AX345197	AX345197 Sequence
29	44.6	6.4	11391	1	AE011280	AE011280 Leptospir
30	44.6	6.4	86734	2	AC144956	AC144956 Silurana
31	44.4	6.4	143722	10	AL731792	AL731792 Mouse DNA
32	44.4	6.4	74784	9	AL359823	AL359823 Human DNA
33	44.2	6.4	92487	10	BX511247	BX511247 Mouse DNA
34	44.2	6.4	110000	2	BX572080_2	Continuation (3 of
35	44.2	6.4	165358	2	AC009020	AC009020 Homo sapi
36	44.2	6.4	186187	9	AC007464	AC007464 Homo sapi
37	44.2	6.4	187101	9	AL589862	AL589862 Human DNA
38	44.2	6.4	201381	10	AL845491	AL845491 Mouse DNA
39	44.2	6.4	211410	2	BX813319	BX813319 Mus muscu
40	44.2	6.3	863	11	CNS06EVQ	AL395628 T7 end of
41	44	6.3	2000	6	AX655393	AX655393 Sequence
42	43.8	6.3	110000	2	BX323883_0	BX323883 Danio rer
43	43.8	6.3	110000	2	BX470178_1	Continuation (2 of
44	43.8	6.3	152617	2	BX005387	Continuation (2 of
45	43.8	6.3	152617	2	BX005387	Continuation (2 of

ALIGNMENTS

RESULT 1
AC112773_1
WPCOMMENT
Sequence split into 4 fragments LOCUS AC112773 Accession AC112773
Fragment Name Begin End
AC112773_0 1 110000
AC112773_1 100001 210000
AC112773_2 200001 310000
AC112773_3 300001 352840
Continuation (2 of 4) of AC112773 from base 100001 (AC112773 Homo sapiens chromosome 3)
Query Match 98.0%; Score 681.8; DB 2; Length 110000;
Best Local Similarity 99.6%; Pred. No. 2.1e-157;
Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

[illegible]

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160301)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-oman,F.R., Allen,C.,
Alsbrooks,S.L., Amaral, H.C., Are,J.R., Ayala,M., Banks,T.,
Barbier,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhaý,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Delanwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisai,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorall,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karleson,B., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lien,C., Liu,J., Liu,W., Louieged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojucan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonake,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umami,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,X., Wu,Y., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 160301)
Worley,K.C.
Direct Submission
Submitted (10-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 160301)
Worley,K.C.
Direct Submission
Submitted (08-JAN-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
-----
Center project name: HCUJ
Center clone name: RP11-12L14
----- Summary Statistics
Chemistry: Dye-primer Body: Infinity% of reads
Chemistry: Dye-terminator Big Dye: Infinity% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 147684 bases at least Q40
Consensus quality: 152184 bases at least Q30

Consensus quality: 154364 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 3125: contig of 3125 bp in length
* 3225: gap of unknown length
* 3226: contig of 3460 bp in length
* 6685: gap of unknown length
* 6786: contig of 2672 bp in length
* 9458: gap of unknown length
* 9557: gap of unknown length
* 13397: contig of 3839 bp in length
* 13496: gap of unknown length
* 13497: contig of 3385 bp in length
* 16881: gap of unknown length
* 16882: contig of 6865 bp in length
* 16982: gap of unknown length
* 23847: contig of 5320 bp in length
* 23947: gap of unknown length
* 29267: contig of 9559 bp in length
* 29366: gap of unknown length
* 38926: contig of 11243 bp in length
* 39025: gap of unknown length
* 50268: contig of 10488 bp in length
* 50368: gap of unknown length
* 50289: contig of 8831 bp in length
* 60857: gap of unknown length
* 60956: contig of 10488 bp in length
* 69787: gap of unknown length
* 69788: contig of 10990 bp in length
* 69888: gap of unknown length
* 80877: contig of 16722 bp in length
* 80978: gap of unknown length
* 97793: gap of unknown length
* 115578: contig of 17777 bp in length
* 115676: gap of unknown length
* 115677: contig of 44625 bp in length.
* 115677: Location/Qualifiers
* 1. 160301
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /chromosome="3"
* /clone="RP11-12L14"
*
ORIGIN
Query Match 98.0%; Score 681.8; DB 2; Length 160301;
Best Local Similarity 99.6%; Pred. No. 2e-157;
Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1 TAAATATCTGATAGGAGGTTAGAAATTTGAGTTTGGAAACACAGGAGAGGCTTTGATG 60
Db 58278 TAAATATCAATAGGAGGTTAGAAATTTGAGTTTGGAAACACAGGAGAGGCTTTGATG 58337
Qy 61 CGGATACAGCTTCGAGACATCATGCTGAGCAGTAAATGAGATGATTTCAGGAAAGAGT 120
Db 58338 CGGATACAGCTTCGAGACATCATGCTGAGCAGTAAATGAGATGATTTCAGGAAAGAGT 58397
Qy 121 ATAACTGGGAAGAGGACAGAGGACAGGCTCAAGGAAACATATTTCAGGAGTGGGTAGAAA 180
Db 58398 ATAACTGGGAAGAGGACAGAGGACAGGCTCAAGGAAACATATTTCAGGAGTGGGTAGAAA 58457
Qy 181 AACAGAGAGTATGACACAGAGTGGAGGATTTAGCAGTGACCTTTGAGAGTACATCT 240
Db 58458 AACAGAGAGTATGACACAGAGTGGAGGATTTAGCAGTGACCTTTGAGAGTACATCT 58517
Qy 241 CTAGAGTGGTATGTGTAGAGCCAGATTTTCAGATCAGAACCATCAAGCATTTTGGGGGT 300
Db 58518 CTAGAGTGGTATGTGTAGAGCCAGATTTTCAGATCAGAACCATCAAGCATTTTGGGGGT 58577
```


* 38031	44862: contig of 5832 bp in length
* 44862	gap of 100 bp
* 44962	52959: contig of 7997 bp in length
* 52960	53059: gap of 100 bp
* 53060	.61323: contig of 8264 bp in length
* 61323	61424: gap of 100 bp
* 61424	72880: contig of 11457 bp in length
* 72881	72980: gap of 100 bp
* 72981	87502: contig of 14522 bp in length
* 87502	87602: gap of 100 bp
* 87602	104472: contig of 16870 bp in length
* 104472	104572: gap of 100 bp
* 104572	121407: contig of 16835 bp in length
* 121408	121507: gap of 100 bp
* 121508	139979: contig of 18472 bp in length
* 139980	140079: gap of 100 bp
* 140080	160274: contig of 20195 bp in length
* 160275	160374: gap of 100 bp
* 160375	178147: contig of 17773 bp in length.

FEATURES
source

Location/Qualifiers
1. .178147
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3"
/clone="RP11-63N15"
/Clone_lib="RPC1-11 Human Male BAC"

misc_feature
1. .1341
/notes="assembly_fragment"
1442..2032
/notes="assembly_fragment"
3033..4701
/notes="assembly_fragment"
4802..6902
/notes="assembly_fragment"
7003..9887
/notes="assembly_fragment"
9988..12646
/notes="assembly_fragment"
12747..17627
/notes="assembly_fragment"
17728..19438
/notes="assembly_fragment
clone_end:SP6
vector_side:right"
misc_feature
19539..23850
/notes="assembly_fragment"
23951..30298
/notes="assembly_fragment"
30399..37930
/notes="assembly_fragment"
38031..44862
/notes="assembly_fragment"
44963..52959
/notes="assembly_fragment
clone_end:T7
vector_side:right"
misc_feature
53060..61323
/notes="assembly_fragment"
61424..72880
/notes="assembly_fragment"
72981..87502
/notes="assembly_fragment"
87603..104472
/notes="assembly_fragment"
104573..121407
/notes="assembly_fragment"
121508..139979
/notes="assembly_fragment"
140080..160274
/notes="assembly_fragment"
160375..178147

repeat_region	/rpt_family="AluSc"	6966..7235	DB 9; Length 191246;
STS	/rpt_family="L1MB6"	6966..7235	Best Local Similarity 99.6%; Pred. No. 2e-157;
STS	/standard_name="SHGC-77593"	6966..7235	Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
repeat_region	/standard_name="SHGC-77593"	6966..7235	
repeat_region	/complement(7972..8142)	6966..7235	
repeat_region	/rpt_family="AluSc"	6966..7235	
repeat_region	/complement(8448..8518)	6966..7235	
repeat_region	/rpt_family="AluSc"	6966..7235	
repeat_region	/complement(8570..8860)	6966..7235	
repeat_region	/rpt_family="AluSc"	6966..7235	
repeat_region	/complement(8954..9004)	6966..7235	
repeat_region	/rpt_family="MER58A"	6966..7235	
repeat_region	/rpt_family="L1PA16"	6966..7235	
repeat_region	/complement(9467..9722)	6966..7235	
repeat_region	/rpt_family="AluSc"	6966..7235	
repeat_region	/complement(10245..10245)	6966..7235	
repeat_region	/rpt_family="L1PA16"	6966..7235	
repeat_region	/complement(10372..10520)	6966..7235	
repeat_region	/rpt_family="MIR"	6966..7235	
repeat_region	/complement(10587..10928)	6966..7235	
repeat_region	/rpt_family="L1MB2"	6966..7235	
repeat_region	/complement(11233..11233)	6966..7235	
repeat_region	/rpt_family="AluSc"	6966..7235	
repeat_region	/complement(11244..11548)	6966..7235	
repeat_region	/rpt_family="AluSc"	6966..7235	
repeat_region	/complement(11549..11721)	6966..7235	
repeat_region	/rpt_family="L1MB2"	6966..7235	
repeat_region	/complement(11737..11943)	6966..7235	
repeat_region	/rpt_family="AluSc"	6966..7235	
repeat_region	/complement(12728..12819)	6966..7235	
repeat_region	/rpt_family="L1M4"	6966..7235	
Query Match	98.0%; Score 681.8; DB 9; Length 191246;		
Best Local Similarity	99.6%; Pred. No. 2e-157;		
Matches 694;	Conservative 0; Mismatches 2; Indels 1; Gaps 1;		
QY	1 TAAATATCTGATAGGCGATTAGAAATTTGAGTTTGGAAACACAGGAGAGAGCGTTTGATG 60		
DB	119700 TAAATATCAATAGGCGATTAGAAATTTGAGTTTGGAAACACAGGAGAGAGCGTTTGATG 119759		
QY	61 CGGATACAGCTTGGAGACATCAGTCTGACGAGTAAATGAGATGATTCAGGAAAGACT 120		
DB	119760 CGGATACAGCTTGGAGACATCAGTCTGACGAGTAAATGAGATGATTCAGGAAAGACT 119819		
QY	121 ATAACTGGGAAGAGGACAGAGGACAGGCTCAAGGACATATTTAAGGCTGGGTAGAAA 180		
DB	119820 ATAACTGGGAAGAGGACAGAGGACAGGCTCAAGGACATATTTAAGGCTGGGTAGAAA 119879		
QY	181 AACAGAGAGTATGAACAAGAGTGGAGAGATTTAGCAGTGGCTTTCAGAGTACATCT 240		
DB	119880 AACAGAGAGTATGAACAAGAGTGGAGAGATTTAGCAGTGGCTTTCAGAGTACATCT 119939		
QY	241 CTAGAGTGTATGTGTAGAGCCAGATTTTTCAGCATCAGAACCATCAGATTTTGGGGGT 300		
DB	119940 CTAGAGTGTATGTGTAGAGCCAGATTTTTCAGCATCAGAACCATCAGATTTTGGGGGT 119999		
QY	301 GGAAGGAAAAGGAGCCATGATCAAAAGGTTGGGAAAAGGCTTTTGGGAGGTGGCGATG 360		
DB	120000 GGAAGGAAAAGGAGCCATGATCAAAAGGTTGGGAAAAGGCTTTTGGGAGGTGGCGATG 120059		
QY	361 TGGGTAGGAGTAGGCTCCGGTTAGATATCATGATGAAGAAGGTGAGCAGCCAT 420		
DB	120060 TGGGTAGGAGTAGGCTCCGGTTAGATATCATGATGAAGAAGGTGAGCAGCCAT 120119		
QY	421 TTCCTTTACACAGAAATAACAGATTTTCCCGAGCTCTTAACCAAGAAAGAAACCAAGTTTGG 480		


```
repeat_region      /rpt_family="L2"
repeat_region      /rpt_family="Alu"
repeat_region      /rpt_family="L2"
repeat_region      /rpt_family="L2"
repeat_region      /rpt_family="MER1_type"
repeat_region      11200..11309
repeat_region      /rpt_family="L2"
repeat_region      11310..11544
repeat_region      /rpt_family="Alu"
repeat_region      11545..11610
repeat_region      /rpt_family="L2"
repeat_region      11860..12166
repeat_region      /rpt_family="Alu"
repeat_region      12126..12175
repeat_region      /note="similar to EST AI025436 (NID:g3241049) ow27h07.sl"
repeat_region      12178..12228
repeat_region      /rpt_family="L1"
repeat_region      12405..12520
repeat_region      /rpt_family="L1"
repeat_region      12712..13008
repeat_region      /rpt_family="Alu"
repeat_region      13009..13315
repeat_region      /rpt_family="Alu"
repeat_region      13603..13850
repeat_region      /rpt_family="ERVL"
repeat_region      13851..14147
repeat_region      /rpt_family="Alu"
repeat_region      14148..14222
repeat_region      /rpt_family="ERVL"
repeat_region      14223..14526
repeat_region      /rpt_family="Alu"
repeat_region      14527..14713
repeat_region      /rpt_family="ERVL"
repeat_region      14815..15244
repeat_region      /rpt_family="L2"
repeat_region      15245..15566
repeat_region      /rpt_family="Alu"
repeat_region      15567..16446
repeat_region      /rpt_family="L2"
repeat_region      16447..16580
repeat_region      /rpt_family="Alu"
repeat_region      16581..16866
repeat_region      /rpt_family="L2"
repeat_region      16867..17178
repeat_region      /rpt_family="Alu"
repeat_region      17179..17251
repeat_region      /rpt_family="L2"
repeat_region      17255..17390
repeat_region      /rpt_family="MER1_type"
repeat_region      17872..18165
repeat_region      /rpt_family="Alu"
repeat_region      18239..18532
repeat_region      /rpt_family="Alu"
repeat_region      18540..18841
repeat_region      /rpt_family="Alu"
repeat_region      18631..18876
repeat_region      /note="similar to EST AW867673 (NID:g8001829)"
repeat_region      19286..19570
repeat_region      /rpt_family="L2"
repeat_region      19885..20185
repeat_region      /rpt_family="Alu"
repeat_region      21149..21446
repeat_region      /rpt_family="Alu"
repeat_region      21559..21803
repeat_region      /rpt_family="Alu"
repeat_region      21835..21951
repeat_region      /rpt_family="L1"
repeat_region      21979..22286
repeat_region      /rpt_family="Alu"
repeat_region      23260..23565
repeat_region      /rpt_family="Alu"

repeat_region      23568..23864
misc_feature        /rpt_family="Alu"
misc_feature        23875..23924
misc_feature        /note="similar to EST AI735654 (NID:g5057178) at19b08.x1"
misc_feature        23875..23924
misc_feature        /note="similar to EST AW619972 (NID:g7326156)"
misc_feature        23878..23926

Query Match       7.5%; Score 52; DB 9; Length 134210;
Best Local Similarity 47.2%; Pred. No. 0.024;
Matches 189; Conservative 0; Mismatches 210; Indels 1; Gaps 1;

QY 14 AGCGATTGAGAAATTTGAGTTTGGAAACACAGAGAGAGCCTTTGATGGGTATACAGACTT 73
Db 112683 AGGGAGGGAAGAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG-GGA 112625

QY 74 GGAAGACATCAGTCTGTCAGCAGTAAATGAGATGATTCAGGAAAGAGTATAAATCTGGGAAG 133
Db 112624 GAAAGAGAAAAGGAGGAGGAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 112565

QY 134 AGGACAGAGCAGCAGCTCAAGGAACATATTTAAGACCTGGGTAGAAAACAAGAGAGTAT 193
Db 112564 AAAAGGGAGGAGGAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAATAA 112505

QY 194 GAACAGAGTGAGGAGATTTATTAGCAGTCACCTTTGAGAGTACATCTCTAGAGTGTATG 253
Db 112504 GGAAGAGGAAGGAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGG 112445

QY 254 TGTAGAGCCAGATTTTTCAGCATCAGAACCATCAAGCATTTTGGGGGTGGAAGGAAGGA 313
Db 112444 GAGGAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 112385

QY 314 GCCTGATCAAAAGGTGGGGAAGAGGCTTTTGGAGGTGCGAGTGTGGGTAGGGAGTA 373
Db 112384 GAAAAGAGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 112325

QY 374 GGGCTCCGTTAGATACATGATGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA 413
Db 112324 GGAATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 112285

RESULT 9
AC115957 72968 bp DNA linear HTG 15-JAN-2003
LOCUS Mus musculus clone RP24-63E7, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC115957
ACCESSION AC115957
VERSION HTG; HTGS PHASE0.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 72968)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP24-63E7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 72968)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,L.,
Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
```

REFERENCE
JOURNAL

AUTHORS

TITLE
JOURNAL

COMMENT

Center code: W1BR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24947
Center clone name: 63_E_7

NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 954: contig of 954 bp in length
* 955 1054: gap of 100 bp
* 1055 2005: contig of 951 bp in length
* 2006 2105: gap of 100 bp
* 2106 3071: contig of 966 bp in length
* 3072 3171: gap of 100 bp
* 3172 4124: contig of 953 bp in length
* 4125 4224: gap of 100 bp
* 4225 5207: contig of 983 bp in length
* 5208 5307: gap of 100 bp
* 5308 6303: contig of 996 bp in length
* 6304 6403: gap of 100 bp
* 6404 7338: contig of 935 bp in length
* 7339 7439: gap of 100 bp
* 7439 8432: contig of 994 bp in length
* 8433 8532: gap of 100 bp
* 8533 9498: contig of 966 bp in length
* 9499 9598: gap of 100 bp

Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Topham, K., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travis, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 72968)

Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Gial, J. S., Dodge, S.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,
Matthews, C., McCarthy, M., Meldrum, J., Meneau, L., Mihova, T.,
Ming, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,
Travis, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (15-JAN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 15, 2003 this sequence version replaced gi:25046528.
All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24947
Center clone name: 63_E_7

NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 954: contig of 954 bp in length
* 955 1054: gap of 100 bp
* 1055 2005: contig of 951 bp in length
* 2006 2105: gap of 100 bp
* 2106 3071: contig of 966 bp in length
* 3072 3171: gap of 100 bp
* 3172 4124: contig of 953 bp in length
* 4125 4224: gap of 100 bp
* 4225 5207: contig of 983 bp in length
* 5208 5307: gap of 100 bp
* 5308 6303: contig of 996 bp in length
* 6304 6403: gap of 100 bp
* 6404 7338: contig of 935 bp in length
* 7339 7439: gap of 100 bp
* 7439 8432: contig of 994 bp in length
* 8433 8532: gap of 100 bp
* 8533 9498: contig of 966 bp in length
* 9499 9598: gap of 100 bp

10583: contig of 985 bp in length
10683: gap of 100 bp
11674: contig of 964 bp in length
11747: gap of 100 bp
12706: contig of 959 bp in length
12806: gap of 100 bp
13774: contig of 968 bp in length
13874: gap of 100 bp
14815: contig of 941 bp in length
14915: gap of 100 bp
15904: contig of 989 bp in length
16004: gap of 100 bp
16959: contig of 955 bp in length
17053: gap of 100 bp
18023: contig of 964 bp in length
18123: gap of 100 bp
19118: contig of 995 bp in length
19218: gap of 100 bp
20307: contig of 989 bp in length
20307: gap of 100 bp
21297: contig of 990 bp in length
21397: gap of 100 bp
22329: contig of 932 bp in length
22429: gap of 100 bp
23445: contig of 1016 bp in length
23445: gap of 100 bp
24478: contig of 933 bp in length
24578: gap of 100 bp
25554: contig of 976 bp in length
25654: gap of 100 bp
26555: contig of 1002 bp in length
26756: gap of 100 bp
27171: contig of 961 bp in length
27171: gap of 100 bp
28792: contig of 975 bp in length
28892: gap of 100 bp
29863: contig of 971 bp in length
29863: gap of 100 bp
30953: contig of 990 bp in length
31053: gap of 100 bp
32032: contig of 979 bp in length
32132: gap of 100 bp
32132: contig of 992 bp in length
32132: gap of 100 bp
32224: gap of 100 bp
34237: contig of 1013 bp in length
34337: gap of 100 bp
35339: contig of 1002 bp in length
35439: gap of 100 bp
35449: contig of 1010 bp in length
35449: gap of 100 bp
35539: contig of 990 bp in length
37639: gap of 100 bp
38621: contig of 982 bp in length
38721: gap of 100 bp
39706: contig of 985 bp in length
39806: gap of 100 bp
40789: contig of 983 bp in length
40889: gap of 100 bp
41795: contig of 906 bp in length
41895: gap of 100 bp
42907: contig of 1012 bp in length
43007: gap of 100 bp
44017: contig of 1010 bp in length
44117: gap of 100 bp
44094: contig of 977 bp in length
45194: gap of 100 bp
46189: contig of 995 bp in length
46289: gap of 100 bp
47263: contig of 974 bp in length
47363: gap of 100 bp
48338: contig of 975 bp in length
48438: gap of 100 bp
49412: contig of 974 bp in length

		7.2%;	Score 50;	DB 2;	Length 72968;
Query Match					
Best Local Similarity		38.4%;	Pred. No. 0.076;		
Matches 214;	Conservative	0;	Mismatches 343;	Indels	1; Gaps 1;
49413	*	49512: gap of 100 bp			
49513	*	50510: contig of 998 bp in length			
50511	*	50610: gap of 100 bp			
50611	*	51587: contig of 977 bp in length			
51588	*	51687: gap of 100 bp			
51688	*	52675: contig of 988 bp in length			
52676	*	52775: gap of 100 bp			
52776	*	53789: contig of 1014 bp in length			
53790	*	53889: gap of 100 bp			
53890	*	54867: contig of 978 bp in length			
54868	*	54967: gap of 100 bp			
54968	*	55943: contig of 976 bp in length			
55944	*	56043: gap of 100 bp			
56044	*	56918: contig of 875 bp in length			
56919	*	57018: gap of 100 bp			
57019	*	58000: contig of 982 bp in length			
58001	*	58100: gap of 100 bp			
58101	*	59077: contig of 977 bp in length			
59078	*	59177: gap of 100 bp			
59178	*	60134: contig of 957 bp in length			
60135	*	60234: gap of 100 bp			
60235	*	61221: contig of 987 bp in length			
61222	*	61321: gap of 100 bp			
61322	*	62283: contig of 962 bp in length			
Query Match					
Best Local Similarity 38.4%; Pred. No. 0.076; Length 72968;					
Matches 214; Conservative 0; Mismatches 343; Indels 1; Gaps 1;					
11	QY	GATGCGCAGTTAGAAATTTGAGTTTGGGAACACAGGAGAGAGGCTTTGATGCGGATACAGA	70		
29299	DB	GAGAGAGAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGA	29358		
71	QY	CTTTGGAAGACATCAGTCGTCGACGAGTAATGATGATTCAGGAAGAGATTAACCTGGG	130		
29359	DB	AGAAGAAGAGAGAGAGAGAGAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAG	29418		
131	QY	AAAGAGACAGAGACAGAGGCTCAAGGAACATATTTAAGGACTGGGTAGAAAAACAAGAGAG	190		
29419	DB	AAAGAGAGAGAGAGAGAGAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGA	29478		
191	QY	TATGAAACAAGAGTGAGGAGATTATTAGCAGTGACCTTTGGAGAGTGATCATCTCTAGAGTGGT	250		
29479	DB	AAAAAANAAGGAAAGAGGANGAGAGAAANGAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAG	29538		
251	QY	ATGTGTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTCGGGGTGGAGGAAAA	310		
29539	DB	AAAAAANAANAAG	29598		
311	QY	GGAGCCATGAATCAAAAGGTGGGGAAGAGCCCTTTTGGAGAGTGCGGAGTGCGGTAGGGA	370		
29599	DB	GNAAAAAANAANAAGGNGGAAAAAAGGNNNANGGNGGAAAAAAGAGAAAGGAGGAGG	29658		
371	QY	GTAG-GGCTCCGTTAGATATACATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	429		
29659	DB	GAGAAANNNNAG	29718		
430	QY	AAACAGAAATTAACAGATTTCCAGCCCTCTAACCAAGAAAAACAAGATTTGGGAAACATCC	489		
29719	DB	ANNGGAAGAGAGAAAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	29778		
490	QY	TCCTCTCTGGAATATGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	549		
29779	DB	NNNAGGNGGAG	29838		
550	QY	AGAGAAAAAAGAGAAACA 567			
29839	DB	AAAGAAAAAAGAGAAACA 29856			

RESULT 10

AC128582/c

AC128582

221659 bp

DNA

linear

HTG 19-SEP-2002

DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL
------------	--	----------------------	--	--

Rattus norvegicus clone CH230-349P12, *** SEQUENCING IN PROGRESS

***, 2 unordered pieces.

AC126582

AC126582.2 GI:23196069

HTGS: PHASE1; HTGS DRAFT; HTGS_ENRICHED.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 221659)

Muzny,D,Marie., Metzger,M,Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angulano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egat,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowls,C., Kraft,C.L., Lebow,H., Levav,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Louleged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Maxwell,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaekeme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Polindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quirzo,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Stehlm,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C., Taylor,T., Thomas,N., Thomas,D., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasaas,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D. von Niederhausern,A., Weides,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 221659)

Worley,K.C.

Direct Submission

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 221659)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (19-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One

COMMENT

Baylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21909357.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYOF
Center clone name: CH230-349P12
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 204793 bases at least Q40
Consensus quality: 207893 bases at least Q30
Consensus quality: 210176 bases at least Q20
Estimated insert size: 232540; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
*
* 1 40671: contig of 40671 bp in length
* 40672 40771: gap of unknown length
* 40772 221659: contig of 180888 bp in length.
*
* Location/Qualifiers
1. 221659
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-349P12"

FEATURES

source

-ORIGIN

Query Match 7.2%; Score 49.8; DB 2; Length 221659;
Best Local Similarity 46.8%; Pred. No. 0.079;
Matches 156; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
Oy 75 GAAGACATCATGCTGACGACGATTAATGAGATGATTCAGGAAAGAGTATAAATCTGGGAAGA 134
Db 13434 GAGGAGGGGAG 13375
Oy 135 GGACAGAGGACAGGCTCAAGGAACATATTTAAGACTCGGTAGAAAACAAAGAGAGATATG 194
Db 13374 AG 13315
Oy 195 AACAGAGTACGAGAGATTTAGCAGTGACCTTTGAGAGTACATCTCTAGAGTGGTATGT 254
Db 13314 GAGAGGAG 13255
Oy 255 GTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTGGGGGTGGAGGAAAAGGAG 314
Db 13254 GAG 13195
Oy 315 CCATGAATCAAAAGTGGGGGAAAAGGCTTTTGGAGGTGCGAGTGTGGGTAGGGAGTAG 374
Db 13194 AGAAG 13135
Oy 375 GGCCTCCGTTTGAATACATGATCAAGAGAGG 407
Db 13134 GACGAGGAG 13102

RESULT 11

AC115498

LOCUS

DEFINITION

AC115498

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC115498 263081 bp DNA linear HTG 21-SEP-2002
Rattus norvegicus clone CH230-85C21, *** SEQUENCING IN PROGRESS

AC115498 GI:23265689
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 263081)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinb, H., Divya, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, I., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Guearregoris, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hughes, M.,
Hollins, B., Howells, S., Hulyar, S., Hume, J., Idlerbird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhera, L., Loulseghe, H., Lozano, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwackeleleh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, F., Poidexter, A., Popovic, D., Primus, E., Pu, L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajda, D.,
Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J.,
Staimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villanueva, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, P., Zhang, J., Zhou, X., Zhou, J., Zhao, S., Dunn, D., von
Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 263081)
Worley, K. C.
Direct Submission
Submitted (20-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

```
REFERENCE 3 (bases 1 to 263081)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Sep 21, 2002 this sequence version replaced gi:21735960.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GNWZ
Center clone name: CH230-85C21
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 238102 bases at least Q40
Consensus quality: 240920 bases at least Q30
Consensus quality: 242959 bases at least Q20
Estimated insert size: 268860; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 263081: contig of 263081 bp in length.
-----
FEATURES             source
source
1..263081
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-85C21"
1..1755
/note="wgs_end_extension
clone_end:Sp6"
misc_feature
complement(4454..5298)
/note="clone boundary
clone_end:Sp6
site:EcoRI
end_sequence:BH303343"
misc_feature
complement(259399..260012)
/note="clone boundary
clone_end:T7
site:EcoRI
end_sequence:BH303342"
misc_feature
261562..263081
/note="wgs_end_extension
clone_end:T7"
ORIGIN
Query Match 7.2%; Score 49.8; DB 2; Length 263081;
Best Local Similarity 46.8%; Pred. No. 0.078;
Matches 156; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
QY 75 GAAGACATCAGTCTGACGAGTAATGAGATGATTCAGGAAGATTAACCTCGGAGA 134
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191147 GAGGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 191206
QY 135 GGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTATG 194
DB 191207 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191266
QY 195 AACAGAGTGGAGAGATTTAGCAGTGCACCTTTTGGAGAGTACATCTCTAGAGTGTGTATGT 254
DB 191267 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191326
QY 255 GTAGAGCCAGATTTTTCAGCATCAGAACCATCAAGCATTTTGGGGGTGGAAGAAAGAG 314
DB 191327 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191386
QY 315 CCATCAATCAAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
DB 191387 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191446
QY 375 GCTCCGGTTAGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 407
DB 191447 GACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191479
DB 191447 GACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191479
RESULT 12
AL138681 126262 bp DNA linear PRI 31-JUL-2001
LOCUS Human DNA sequence from clone RP11-121019 on chromosome
DEFINITION 13q12.3-14.3, complete sequence.
ACCESSION AL138681
VERSION AL138681.17 GI:15072559
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 126262)
Tromans,A.
Direct Submission
Submitted (31-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 1, 2001 this sequence version replaced gi:14575076.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-121019 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-121019 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-121019 is at 126262 in this
sequence. The true left end of clone RP11-469L23 is at 55054 in
```

this sequence. The true right end of clone RP11-550P23 is at 2000 in this sequence.

FEATURES

source

```
Location/Qualifiers
1..126262
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="13"
/map="q12.3-14.3"
/clone="RP11-121O19"
(clone lib=vecori-11.1)
```

```

1284..1420
/note="FRAM repeat: matches 6..155 of consensus"
repeat_region
2106..2174
/note="I2 repeat: matches 1597..1666 of consensus"
repeat_region
2304..2403
/note="I2 repeat: matches 1888..1987 of consensus"
repeat_region
2410..2569
/note="MLR1A2 repeat: matches 1..153 of consensus"
repeat_region
2570..2869
/note="AluA repeat: matches 1..300 of consensus"
repeat_region
2870..3018
/note="MLR1A2 repeat: matches 153..387 of consensus"
repeat_region
3121..3326
/note="MIR repeat: matches 34..262 of consensus"
repeat_region
3341..3468
/note="I2 repeat: matches 2129..2254 of consensus"
repeat_region
3618..3953
/note="I2 repeat: matches 2388..2694 of consensus"
repeat_region
3977..4651
/note="I2 repeat: matches 1980..2697 of consensus"
repeat_region
5125..5251
/note="MIR repeat: matches 117..254 of consensus"
repeat_region
6068..6123
/note="I2 repeat: matches 2694..2746 of consensus"
repeat_region
6458..6616
/note="AluA repeat: matches 115..292 of consensus"
repeat_region
6871..7087
/note="MER58A repeat: matches 2..224 of consensus"
repeat_region
7866..8163
/note="AluY repeat: matches 1..298 of consensus"
repeat_region
8345..8514
/note="I2 repeat: matches 1927..2094 of consensus"
repeat_region
8543..8675
/note="AluA repeat: matches 1..133 of consensus"
repeat_region
8678..8746
/note="I2 repeat: matches 2131..2201 of consensus"
repeat_region
8760..9063
/note="AluA repeat: matches 1..309 of consensus"
repeat_region
9063..9363
/note="AluSc repeat: matches 1..308 of consensus"
repeat_region
9394..9532
/note="AluA/FRAM repeat: matches 163..304 of consensus"
repeat_region
9534..9633
/note="4 copies 25 mer 74% conserved"
repeat_region
9543..9638
/note="48 copies 2 mer aa 66% conserved"
repeat_region
9571..9626
/note="14 copies 4 mer agaa 71% conserved"
repeat_region
9642..10110
/note="I2 repeat: matches 2214..2744 of consensus"
repeat_region
10375..10672
/note="AluA repeat: matches 1..296 of consensus"
repeat_region
10673..10851
/note="AluA repeat: matches 132..310 of consensus"
repeat_region
10919..11192
/note="AluA repeat: matches 5..300 of consensus"
repeat_region
11376..11554
/note="I2 repeat: matches 1175..1372 of consensus"
repeat_region
11570..11732
/note="AluA repeat: matches 132..303 of consensus"
repeat_region
11741..11984
/note="I2 repeat: matches 1410..1711 of consensus"

```

```

repeat_region 11985..12264
/note="AluXk repeat: matches 29. .312 of consensus"
repeat_region 1265..12403
/note="12 repeat: matches 1711. .1834 of consensus"
repeat_region 12826..12894
/note="FAM repeat: matches 1. .175 of consensus"
repeat_region 13904..13994
/note="12 repeat: matches 2328. .2418 of consensus"
repeat_region 14144..14446
/note="AluXk repeat: matches 1. .299 of consensus"
repeat_region 14517..14813
/note="AluSp repeat: matches 1. .298 of consensus"
repeat_region 14814..14954
/note="MIR repeat: matches 8. .151 of consensus"
repeat_region 15096..15391
/note="AluXk repeat: matches 1. .295 of consensus"
repeat_region 15635..15804
/note="MER3 repeat: matches 2. .170 of consensus"
repeat_region 15968..16011
/note="AluUb repeat: matches 1. .141 of consensus"
repeat_region 16014..16062
/note="MER3 repeat: matches 155. .203 of consensus"
repeat_region 16026..16082
/note="MER3 repeat: matches 40. .90 of consensus"
repeat_region 16148..16490
/note="MLT1A1 repeat: matches 5. .365 of consensus"
repeat_region 16537..16840
/note="AluXk repeat: matches 1. .305 of consensus"
repeat_region 17017..17271
/note="AluUb repeat: matches 40. .304 of consensus"
repeat_region 18501..18574
/note="11P1a16 repeat: matches 5904. .5975 of consensus"
repeat_region 19246..19407
/note="11M03 repeat: matches 7324. .7476 of consensus"
repeat_region 19727..20455
/note="11P1a16 repeat: matches 5419. .6157 of consensus"
repeat_region 20457..20561
/note="11M04 repeat: matches 7867. .7977 of consensus"
repeat_region 21017..21533
/note="MLT1P repeat: matches 5. .541 of consensus"
repeat_region 22585..23026
/note="MLTIC repeat: matches 3. .466 of consensus"
misc_feature 22934..23082
/note="Sequence from clone PCR only."
repeat_region 23179..23359
/note="MER58C repeat: matches 1. .89 of consensus"
repeat_region 23932..23982
/note="MIR repeat: matches 200. .252 of consensus"
repeat_region 24422..24493
/note="36 Copies 2 mer ta 70% conserved"
repeat_region 24495..24586
/note="FLAN A repeat: matches 33. .123 of consensus"
repeat_region 24657..24695
/note="MLT1B repeat: matches 350. .390 of consensus"
repeat_region 24696..25004
/note="AluSp repeat: matches 1. .310 of consensus"
repeat_region 25005..25381
/note="MLT1B repeat: matches 1. .350 of consensus"
repeat_region 26088..26118
/note="MER46A repeat: matches 2. .32 of consensus"
repeat_region 26121..26222
/note="AluSp/q repeat: matches 194. .295 of consensus"
repeat_region 26223..26336
/note="MER46A repeat: matches 129. .232 of consensus"
repeat_region 26416..26874
/note="L1R7 repeat: matches 1. .448 of consensus"
repeat_region 26973..27284
/note="AluYa5 repeat: matches 1. .311 of consensus"
repeat_region 27380..27515
/note="MLT1F repeat: matches 153. .287 of consensus"
repeat_region 28349..28609
/note="AluJb repeat: matches 7. .266 of consensus"
repeat_region 28754..28876

```

```

/note="L2 repeat: matches 1667. 1784 of consensus"
29228. .29489
/repeat_region /notes="MER2 repeat: matches 72. 345 of consensus"
29661. .29881
/repeat_region /notes="L2 repeat: matches 2049. 2275 of consensus"
29900. .30087
Query Match
Best local similarity 64.5%; Pred. No. 0.29; Length 126262;
Matches 71; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 2 AAAATATCTGATGGCAGTTAGAAATTTGAGTTGGAAACACAGAGAGAGCGCTTTGATGG 61
Db 30729 AATCTATCAGTAGGACAGATGATGAATATGATCTGAGTTTCAGGAGAGGCTGGGTGG 30788
QY 62 CGATACAGACTTGAAGACATCACTGCTGACGAGTAAATGAGATGATCA 111
Db 30789 CAATATGAATCTGGAGCTCCACATCTGAATAGTATTTAAAGCTATACA 30838

RESULT 13
AC013828 143577 bp DNA linear PRI 04-SEP-2001
LOCUS Homo sapiens chromosome 1, clone RP11-23B7, complete sequence.
DEFINITION AC013828
ACCESSION AC013828
VERSION AC013828.10 GI:15294310
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143577)
Birken,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-23B7
Unpublished
2 (bases 1 to 143577)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lien,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 143577)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Canarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Chospel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Olivier,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Riback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,

```

Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,D., Zimmer,A. and Zody,M.
Direct Submission
Submitted (04-SEP-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 27, 2001 this sequence version replaced gi:14547834.
All repeats were identified using RepeatMasker:
Smit,A.P.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Genome Center
Center code: WBK
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4171
Center clone name: 23_B_7

FEATURES	Location/Qualifiers
source	1..143577
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/clone="RP11-23B7"
	/clone_lib="RPC1-11 Human Male BAC"
	/complement(670..775)
	/rpt_family="MIR3"
	/complement(2047..2329)
	/rpt_family="AluY"
	2876..2886
	/rpt_family="AT-rich"
	/complement(4044..4169)
	/rpt_family="FLAM_A"
	/complement(4199..4627)
	/rpt_family="MSTB1"
	/complement(4831..4872)
	/rpt_family="MER61B"
	5133..5453
	/rpt_family="MLT1G"
	5495..5623
	/rpt_family="MLT1G"
	5669..5690
	/rpt_family="AT-rich"
	6138..6346
	/rpt_family="MER58A"
	/complement(6378..6689)
	/rpt_family="AluJb"
	6889..7187
	/rpt_family="AluSx"
	/complement(7321..7456)
	/rpt_family="FLAM_C"
	/complement(8235..8396)
	/rpt_family="MIR"
	/complement(9700..9762)
	/rpt_family="MIR3"
	/complement(10332..10435)
	/rpt_family="HV1"
	/complement(110737..10822)
	/rpt_family="MIR"
	11523..11887
	/rpt_family="L1PA4"
	12381..12426
	/rpt_family="L2"
	/complement(12600..12711)
	/rpt_family="FLAM_A"
	12807..12919
	/rpt_family="MER94"
	/complement(12954..13651)
	/rpt_family="L1ME3"
	/complement(13652..13954)
	/rpt_family="AluSx"
	/complement(13955..14704)


```
repeat_region 14729.14749 /rpt_family="L1ME3"
repeat_region 14729.14749 /rpt_family="AT_rich"
repeat_region complement(14786..15179) /rpt_family="MLT1A1"
repeat_region complement(15180..15601) /rpt_family="L1ME5"
repeat_region 15602..15665 /rpt_family="MER46A"
repeat_region 15666..15954 /rpt_family="AluSx"
repeat_region 15955..16120 /rpt_family="MER46A"
repeat_region complement(16121..16340) /rpt_family="L1ME5"
repeat_region complement(16665..16744) /rpt_family="HAL1"
repeat_region 16874..17072 /rpt_family="MER30"
repeat_region complement(18234..18318) /rpt_family="MIR3"
repeat_region complement(19051..19186) /rpt_family="MIR"
repeat_region 19699..19730 /rpt_family="AT_rich"
repeat_region complement(20696..20883) /rpt_family="MER20"
repeat_region 20956..21257 /rpt_family="AluSx"
repeat_region 21773..21963 /rpt_family="L2"
repeat_region complement(22007..22121) /rpt_family="L2"
repeat_region 22261..22329 /rpt_family="L2"
repeat_region 22330..22623 /rpt_family="AluY"
repeat_region 22624..22847 /rpt_family="L2"
repeat_region 23118..23156 /rpt_family="AT_rich"
repeat_region 23800..23931 /rpt_family="MIR"
repeat_region 24755..24780 /rpt_family="AT_rich"
repeat_region 25038..25201 /rpt_family="L1MA5A"
repeat_region 25239..25311 /rpt_family="AluJb"
repeat_region 25312..25344 /rpt_family="AT_rich"
repeat_region 25627..25769 /rpt_family="MIR"
repeat_region 26152..26172 /rpt_family="AT_rich"
repeat_region complement(26951..27162) /rpt_family="AluJb"
repeat_region 27540..27842 /rpt_family="AluSx"
repeat_region complement(28209..28402) /rpt_family="MER5A"
repeat_region complement(28406..28465) /rpt_family="MER5A"
repeat_region complement(28591..28742) /rpt_family="MER5A"
repeat_region complement(30280..30490) /rpt_family="L1MA8"
repeat_region complement(30558..30781) /rpt_family="MIR"
repeat_region complement(30861..31046) /rpt_family="L1MC/D"
repeat_region 31425..31461 /rpt_family="AT_rich"

repeat_region 31902..32160 /rpt_family="AluSg"
repeat_region 32226..32259

Query Match 6.8%; Score 47.2; DB 9; Length 143577;
Best Local Similarity 52.5%; Pred. No. 0.36;
Matches 126; Conservative 0; Mismatches 113; Indels 1; Gaps 1;

QY 456 CTAACCAAGAAACAACAGTTTGGGAACATCTCTCTCTCTGAAATATGAAGAGAGGG 515
DB 125704 CCAGCTAACATATAAAGAAAACCTTGGATATTCGAAACACTTCAAGAGAAAGTAGGAAAAGA 125763
QY 516 GATAAATACCTGGAGTAGGATTGTGAAAAAGTCAAGAGAAAAAAGAAAAAGAACAGCCCAAGT 575
DB 125764 GAAAAAATACATCGGACACAGAGAAAGAAATCTTAATATCAATAAATTAACCCCAAT 125823
QY 576 GTAAACAGATATCTCCATGGATGGTAAAGAAAGATTTATTTCAATAAATGACCCCTT 635
DB 125824 GTATCAGTTA-TTATAATGAAATGAATTAATGCTCTGATTAATAAATAAAGATTACTA 125882
QY 636 GGAAGGAGTTCAAAACAGGTTCATATGCTTTATGATGGAGTTTGAATAATATATAAAA 695
DB 125883 GGTACTACTAAAAAATTTATGCTTTATACAGATATAGATAAATAAATATATATAGAA 125942

RESULT 14
AC027779 149059 bp DNA linear PRI 07-FEB-2002
LOCUS Homo sapiens chromosome 11, clone RP11-98J9, complete sequence.
DEFINITION AC027779
ACCESSION AC027779.10 GI:18182811
VERSION HTG.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,P.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Cheepel,Y., Colangelo,M., Collins,S.,
Collins,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W.S., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marcuis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivaz,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trillio,J.,
Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149059)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepl,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gird,S., Goyette,M., Graham,L., Grand-Pierre,N.,
```



```

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehotzky, J., Levine, R., Liu, G., Maclean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Riback, M., Riley, R., Risse, C., Rogov, P., Roman, J.,
Roberts, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zemek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (07-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 17, 2002 this sequence version replaced gi:17647018.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBK
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8960
Center clone name: 98_J_9
-----
Location/Qualifiers
1..149059
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-98J9"
/clone_lib="RPC1-11 Human Male BAC"
253..459
/rpt_family="MER106B"
854..894
/rpt_family="AT_rich"
/rpt_family="984..1105"
/rpt_family="MIR"
complement(1119..1482)
/rpt_family="MLT1A2"
1708..2132
/rpt_family="L2"
complement(2207..2365)
/rpt_family="MLT1A1"
complement(2366..2661)
/rpt_family="AluX"
complement(2662..2818)
/rpt_family="MLT1A1"
complement(4051..4176)
/rpt_family="L1ME"
4312..4596
/rpt_family="AluJo"
complement(4956..5112)
/rpt_family="VARNA"
complement(5202..5786)
/rpt_family="LTR50"
complement(5791..5909)
/rpt_family="MIR"
6052..6427
/rpt_family="THE1C"
complement(6744..6854)
/rpt_family="MIR"
complement(6920..7108)
/rpt_family="MIR"
complement(7109..7253)

```

```

repeat_region
complement(8488..8608)
/rpt_family="MER5A"
8617..8792
/rpt_family="L1ME1"
8783..8895
/rpt_family="MLT1H"
9558..9582
/rpt_family="MLT1H"
9687..9759
/rpt_family="(TG)n"
/rpt_family="(TA)n"
complement(9838..10104)
/rpt_family="MER115"
10146..10428
/rpt_family="MLT1A1"
complement(10461..10747)
/rpt_family="MER115"
complement(10845..11453)
/rpt_family="L1"
complement(11994..12079)
/rpt_family="LTR50"
12259..12499
/rpt_family="L1ME3A"
12540..12578
/rpt_family="(TTTA)n"
complement(12579..17985)
/rpt_family="L1PA2"
complement(17980..18071)
/rpt_family="L1PA2"
18119..18259
/rpt_family="L1ME3A"
complement(18308..18656)
/rpt_family="MLT2B1"
18657..19461
/rpt_family="L1PA5"
complement(19462..19585)
/rpt_family="MLT2B1"
19602..19930
/rpt_family="L1ME3A"
complement(19931..20282)
/rpt_family="THE1B"
20283..20382
/rpt_family="L1ME3A"
20434..20494
/rpt_family="AT_rich"
20697..21017
/rpt_family="L1ME3A"
21045..21174
/rpt_family="L1ME3A"
21175..21491
/rpt_family="AluJb"
21492..22185
/rpt_family="L1ME3A"
22186..22550
/rpt_family="MLT1A1"
22551..23305
/rpt_family="L1ME3A"
complement(23306..23394)
/rpt_family="L1PA13"
23395..23988
/rpt_family="L1ME3A"
23989..24027
/rpt_family="(TG)n"
24028..24136
/rpt_family="L1ME3A"
24135..24283
/rpt_family="LTR29"
complement(24386..24449)
/rpt_family="FLAN"
24575..25427
/rpt_family="L1MB2"
25428..25728
/rpt_family="AluJo"

```

```
repeat_region 25729..26075
repeat_region /rpt_family="L1MB2"
repeat_region 26094..26356
repeat_region /rpt_family="L1MB3A"
repeat_region complement(26358..26773)
repeat_region /rpt_family="WLRIC"
repeat_region 26774..27035
repeat_region /rpt_family="L1MB3A"

Query Match 6.8%; Score 47.2; DB 9; Length 149059;
Best Local Similarity 52.5%; Pred. No. 0.35;
Matches 126; Conservative 0; Mismatches 113; Indels 1; Gaps 1;

Qy 456 CTACCAAGAAACAAACAGTTGGGAACTTCTCTCTTCAATATCAAGAGAGGG 515
Db 20659 CCAGCTACATATAAGAAAGAACTTGGATTAATCGAACACTTCAAGAGAAAGTAGAAAGA 20718

Qy 516 GATAAATACCTGGAGTAGGATTGAAAAAGTCAAGAGAAAAAAGAACACCCCAAGT 575
Db 20719 GAAAAAATACATCGGACACAGAGAAAGAAATCTTAAATCATATAATTAACCCCAAT 20778

Qy 576 GTACACATATCTTCCATGGATGTTAAAGAGAGTATTTCAATAAATGACCCCTT 635
Db 20779 GTATCACTTA-TTATAATGAATGAATTAATGCTCTGATTAATAAATAAGATTACTA 20837

Qy 636 GGAAGGAGTTCAAAACAGGTTGCCATATGCTTTATGCGAGTTTGAATAATATAAAA 695
Db 20838 GGTACTACTAAAACTTTATGCTTTATACAGATAGATAAATAAATATATAGAA 20897

RESULT 15
AC074374 155185 bp DNA linear HTG 24-AUG-2000
LOCUS Homo sapiens chromosome 11 clone RP11-651C3, WORKING DRAFT
DEFINITION AC074374
ACCESSION AC074374
VERSION AC074374.3 GI:9887833
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155185)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 155185)
Waterston,R.H.
Direct Submission
Submitted (29-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 24, 2000 this sequence version replaced gi:9795994.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH051C03
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-primer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 14540 bases at least Q40
Consensus quality: 148426 bases at least Q30
Insert size: 157000; agarose-fp
Insert size: 153085; sum-of-contigs
Quality coverage: 4.43 in Q20 bases; agarose-fp
Quality coverage: 4.61 in Q20 bases; sum-of-contigs

----- This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 2478: contig of 2478 bp in length
* 2479 2578: gap of unknown length
* 2579 4930: contig of 2352 bp in length
* 4931 5030: gap of unknown length
* 5031 7763: contig of 2733 bp in length
* 7764 7863: gap of unknown length
* 7864 11285: contig of 3422 bp in length
* 11286 11385: gap of unknown length
* 11386 14925: contig of 3540 bp in length
* 14926 18227: gap of unknown length
* 18228 18327: contig of 3202 bp in length
* 18328 21955: gap of unknown length
* 21956 26074: contig of 4020 bp in length
* 26075 26174: gap of unknown length
* 26175 30628: contig of 4454 bp in length
* 30629 30728: gap of unknown length
* 30729 35614: contig of 4886 bp in length
* 35615 35714: gap of unknown length
* 35715 42284: contig of 6569 bp in length
* 42285 42383: gap of unknown length
* 42384 49108: contig of 6725 bp in length
* 49109 49208: gap of unknown length
* 49209 55858: contig of 6650 bp in length
* 55859 55958: gap of unknown length
* 55959 65238: contig of 9280 bp in length
* 65239 65338: gap of unknown length
* 65339 75265: contig of 9926 bp in length
* 75266 75364: gap of unknown length
* 75365 91540: contig of 16175 bp in length
* 91541 91639: gap of unknown length
* 91640 111316: contig of 19677 bp in length
* 111317 111416: gap of unknown length
* 111417 14737: contig of 36021 bp in length
* 14738 147537: gap of unknown length
* 147538 148789: contig of 1252 bp in length
* 148790 148889: gap of unknown length
* 148890 150390: contig of 1501 bp in length
* 150391 150490: gap of unknown length
* 150491 152240: contig of 1750 bp in length
* 152241 152340: gap of unknown length
* 152341 153185: contig of 2845 bp in length.
* 153186 153341: Location/Qualifiers
* 1..155185
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /chromosome="11"
* /clone="RP11-651C3"
* /note="assembly_name:Contig10"
* 2579..4930
* /note="assembly_name:Contig11"
* 5031..7763
* /note="assembly_name:Contig12"
* 7864..11285
* /note="assembly_name:Contig13"
* 11386..14925
* /note="assembly_name:Contig14"
* 15026..18227
* /note="assembly_name:Contig15"
* 18328..21954
* /note="assembly_name:Contig16"

FEATURES
source
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature
```

[illegible]

Search completed: April 25, 2004, 18:58:05
Job time : 1841.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 07:00:48 ; Search time 6359.53 Seconds
(without alignments)
16458.288 Million cell updates/sec

Title: US-10-051-835-13
Perfect score: 3505
Sequence: 1 ggccttgccatgatgggac.....tttgggccaaccacaggttg 3505

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
EST:*			
1:	em_estba:*		
2:	em_estum:*		
3:	em_estin:*		
4:	em_estmu:*		
5:	em_estov:*		
6:	em_estpl:*		
7:	em_estro:*		
8:	em_hci:*		
9:	gb_est1:*		
10:	gb_est2:*		
11:	gb_hic:*		
12:	gb_est3:*		
13:	gb_est4:*		
14:	gb_est5:*		
15:	em_estfun:*		
16:	em_estom:*		
17:	em_gss_hum:*		
18:	em_gss_inv:*		
19:	em_gss_pln:*		
20:	em_gss_vrt:*		
21:	em_gss_fun:*		
22:	em_gss_mam:*		
23:	em_gss_mus:*		
24:	em_gss_pro:*		
25:	em_gss_rod:*		
26:	em_gss_phg:*		
27:	em_gss_vrl:*		
28:	gb_gss1:*		
29:	gb_gss2:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1872.4	53.4	2172	29	AY402621 Homo sapi
2	1771.2	50.5	3206	11	AK077976 Mus muscu
3	1767	50.4	2133	29	AY402622 Pan trogl
4	1700.2	48.5	3086	11	AK035918 Mus muscu

5	1370.6	39.1	2172	29	AY402623
6	952.2	27.2	1114	13	EX367242
7	929.4	26.5	1201	13	EX363741
8	876.6	25.0	922	13	EX350606
9	856.6	24.4	926	13	EX328255
10	849.2	24.2	1201	13	EX384966
11	827.4	23.6	974	13	BQ057192
12	823.8	23.1	960	13	EX390196
13	775	22.5	801	13	EX112994
14	772.2	22.0	797	14	CB243787
15	768.2	21.9	912	13	BQ883972
16	768	21.9	1201	13	EX376660
17	759.2	21.7	892	14	CD107028
18	748.6	21.4	951	13	BQ056228
19	708.6	20.2	917	14	CA454892
20	698.2	19.9	775	9	AU122156
21	689.6	19.7	970	13	BQ707628
22	681	19.4	1066	12	EM806752
23	673	19.2	1090	13	EX367243
24	661.8	18.9	666	12	BG684636
25	655	18.7	666	10	BE868099
26	650	18.5	925	13	BQ937439
27	623	17.8	640	14	CA311774
28	608	17.3	1119	12	B1550650
29	604.4	17.2	624	12	BM666780
30	598.6	17.1	621	10	AM965845
31	595.2	17.0	618	13	BQ686374
32	594	16.9	634	13	BQ630065
33	583.6	16.7	881	13	CA315771
34	579.2	16.5	720	14	CA315771
35	551.4	15.7	695	12	BG685741
36	550.8	15.7	779	12	B1683727
37	546.6	15.6	709	13	BQ573544
38	543.4	15.5	547	12	EM128651
39	540.8	15.4	667	12	BG703963
40	540.6	15.4	784	12	BQ043061
41	537	15.3	841	14	CB566426
42	528	15.1	528	14	CA393520
43	527.8	15.1	796	13	BU052878
44	524.6	15.0	944	12	B1250501
45	522.8	14.9	858	14	CK022938

ALIGNMENTS

RESULT 1	AY402621	2172 bp	DNA	linear	GSS 12-DBC-2003
LOCUS	Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION	AY402621				
ACCESSION	AY402621.1	GI:39758607			
VERSION					
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2172)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trics				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2172)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				

JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..2172				
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>2172 /locus_tag="HCM1285"				
ORIGIN	Query Match 53.4%; Score 1872.4; DB 29; Length 2172; Best Local Similarity 86.2%; Pred. No. 0; Matches 1873; Conservative 0; Mismatches 299; Indels 0; Gaps 0;				
Qy	204	ATGGCCCTCCAGCCCTCGGCGCTGGACCCCTGGAGCCTCTGGGCTTTCTCTTCCAA	263		
Db	1	ATGGCCCTCCAGCCCTCGGCGCTGGACCCCTGGAGCCTCTGGGCTTTCTCTTCCAA	60		
Qy	264	CTGCTTCAGCTGCTGTCGACGACGACCGCGGGGGAGCGGGGCGGCGCCATGCC	323		
Db	61	CTGCTTCAGCTGCTGTCGACGACGACCGCGGGGGAGCGGGGCGGCGCCATGCC	120		
Qy	324	AGGCTCAGATATGACAGGGGATGACGTAGGCACTTAGCTTCTCCACAGAGGGC	383		
Db	121	AGGCTCAGATATGACAGGGGATGACGTAGGCACTTAGCTTCTCCACAGAGGGC	180		
Qy	384	CTCCAGGATTTGACACTCTGCTCTGAGTGGTATGGAAATACTCTCTACGTGGGGCT	443		
Db	181	CTCCAGGATTTGACACTCTGCTCTGAGTGGTATGGAAATACTCTCTACGTGGGGCT	240		
Qy	444	CGAAGCCATCTCGGCTTGGATATCCAGGATCCAGGGTCCCGAGCTTAAAGAACATG	503		
Db	241	CGAAGCCATCTCGGCTTGGATATCCAGGATCCAGGGTCCCGAGCTTAAAGAACATG	300		
Qy	504	ATACCGTGGCCAGCCAGTGCAGAAAAAAGAGTGAATGTGCTTTAAGAAAGAGCAAT	563		
Db	301	ATACCGTGGCCAGCCAGTGCAGAAAAAAGAGTGAATGTGCTTTAAGAAAGAGCAAT	360		
Qy	564	GAGACAGTGTTCACATTCATCCGTGCTGCTGTTCTTACATGTACCCATCTCTAC	623		
Db	361	GAGACAGTGTTCACATTCATCCGTGCTGCTGTTCTTACATGTACCCATCTCTAC	420		
Qy	624	ACCTGGGCACTTCGGCTTCAGCCCTGCTGTACCTTCAATTTCAAGATTCCTAC	683		
Db	421	ACCTGGGCACTTCGGCTTCAGCCCTGCTGTACCTTCAATTTCAAGATTCCTAC	480		
Qy	684	CTGTTCGCCATCTCGAGGACAAGGTCAATGAGGGGAAAGGCCAAGCCCTTTGACCC	743		
Db	481	CTGTTCGCCATCTCGAGGACAAGGTCAATGAGGGGAAAGGCCAAGCCCTTTGACCC	540		
Qy	744	GCTCACAGCATACGGCTGCTTGGTGGATGGGATGCTATTCTGGTACTATGAACAAC	803		
Db	541	GCTCACAGCATACGGCTGCTTGGTGGATGGGATGCTATTCTGGTACTATGAACAAC	600		
Qy	804	TTCTCGGCACTGAGCCCATCTGATGGGCACTCTGGATCCGAGCTGCTCAAGACC	863		
Db	601	TTCTCGGCACTGAGCCCATCTGATGGGCACTCTGGATCCGAGCTGCTCAAGACC	660		
Qy	864	GACAACTTCTCCGCTGGCTGATCATGACGCCCTCTTGTGGGAGGCACTCCCTTCGACC	923		
Db	661	GACAACTTCTCCGCTGGCTGATCATGACGCCCTCTTGTGGGAGGCACTCCCTTCGACC	720		
Qy	924	CAGGTCGTCTACTCTTCTTGAGAGACAGCCAGCGAGTTTGATCTCTTTGAGAGGCTC	983		
Db	721	NN	780		
Qy	984	CACACATCGCGGTGCTAGAGTCTGCAAGAATGACGTGGCGCGAAGAGCTCTGCAG	1043		
Db	781	NN	840		

Qy	1044	AAGAAGTGGACCACTTCTCTGAAGGCCAGCTGCTCTGACCCAGCGGGGAGCTGCC	1103		
Db	841	NN	900		
Qy	1104	TTCAACGTCATCGGCCAGCGGCTCTGCTCCCGCGGATTTCTCCACAGCTCCCAATC	1163		
Db	901	NN	960		
Qy	1164	TACGAGCTTTCACTCCAGTGGCAGGTTGGGGGACGAGGAGCTCTCGGTTTGTGCC	1223		
Db	961	NN	1020		
Qy	1224	TTCTCTCTCTGGACATTTGAACGCTCTTTAAAGGGGAAATACAAAGAGTTGAACAAGAA	1283		
Db	1021	TTCTCTCTCTGGACATTTGAACGCTCTTTAAAGGGGAAATACAAAGAGTTGAACAAGAA	1080		
Qy	1284	ACTTCAAGCTGGACTACTTATAGGGGCTTGAGAACAAACCCCGGCGAGGAGTTGTCTCA	1343		
Db	1081	ACTTCAAGCTGGACTACTTATAGGGGCTTGAGAACAAACCCCGGCGAGGAGTTGTCTCA	1140		
Qy	1344	GTGGGCCCCCTCTGATTAAGGCCCTGACCTTCAATGAAGACCAATTTCTCTGATGATGAG	1403		
Db	1141	GTGGGCCCCCTCTCTGATTAAGGCCCTGACCTTCAATGAAGACCAATTTCTCTGATGATGAG	1200		
Qy	1404	CAAGTGGTGGGACCGCCCTCTGCTGGTGAATCTGGGCTGGAGTATACACGGCTTGCAGTG	1463		
Db	1201	CAAGTGGTGGGACCGCCCTCTGCTGGTGAATCTGGGCTGGAGTATACACGGCTTGCAGTG	1260		
Qy	1464	GAGCAGCCAGGGCTTGATGGGACAGCCATCTTGTCTATGTACCTGGGAACCAACACACA	1523		
Db	1261	GAGCAGCCAGGGCTTGATGGGACAGCCATCTTGTCTATGTACCTGGGAACCAACACACA	1320		
Qy	1524	GGTCTGCTCCCAAGGGCTGTGAAGTGGGACAGCAGTGTCTATCTCTGGTGGAAAGAGATT	1583		
Db	1321	GGTCTGCTCCCAAGGGCTGTGAAGTGGGACAGCAGTGTCTATCTCTGGTGGAAAGAGATT	1380		
Qy	1584	CAGCTGTTCCCTGACCTTGAACTGTCGAACTGTCGAACTGTCGAACTGTCGAACTGTC	1643		
Db	1381	CAGCTGTTCCCTGACCTTGAACTGTCGAACTGTCGAACTGTCGAACTGTCGAACTGTC	1440		
Qy	1644	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGAGGGTGGCCCGGAGCCAACTGTAGTGTCTAT	1703		
Db	1441	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGAGGGTGGCCCGGAGCCAACTGTAGTGTCTAT	1500		
Qy	1704	GAGACTGTGTGAGTGTCTTCTGCGCGGACCCCACTGTGCTGGGACCTGAGTCC	1763		
Db	1501	GAGACTGTGTGAGTGTCTTCTGCGCGGACCCCACTGTGCTGGGACCTGAGTCC	1560		
Qy	1764	CGAACTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1823		
Db	1561	CGAACTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1620		
Qy	1824	GGGAAACCCAGAGTGGGCAATGTGCGGCGGACATGAGCAGGAGCTTGGGCTCAGAGC	1883		
Db	1621	GGGAAACCCAGAGTGGGCAATGTGCGGCGGACATGAGCAGGAGCTTGGGCTCAGAGC	1680		
Qy	1884	CGCCCGCAAACTCATTAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1943		
Db	1681	CGCCCGCAAACTCATTAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740		
Qy	1944	CCCACTCTGAGCTTGGCTCTTATTAATGGAGTCAATGGCCAGCAGCAGTCCCAAGAA	2003		
Db	1741	CCCACTCTGAGCTTGGCTCTTATTAATGGAGTCAATGGCCAGCAGCAGTCCCAAGAA	1800		
Qy	2004	GGCTCTTCCACTGTCTACAAATGGCTCCCTCTTGTGCTAGTGTGAGGATGGGAGTGGGGGT	2063		
Db	1801	GGCTCTTCCACTGTCTACAAATGGCTCCCTCTTGTGCTAGTGTGAGGATGGGAGTGGGGGT	1860		
Qy	2064	CTCTACAGTGTGGGCAACTGAGAAATGGCTTTTTCATACCTGTGATCTCTCTCTCTCTCTCT	2123		
Db	1861	CTCTACAGTGTGGGCAACTGAGAAATGGCTTTTTCATACCTGTGATCTCTCTCTCTCTCTCT	1920		
Qy	2124	GACAGCCAGGACCAAGCCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2183		

```

1921 GACAGCCAGCAGCAGACCCCTGGCCCTGGATCTCTAACTGCGAGCATCCCCGGGAGCAT 1980
QY 2184 GTGAAGTCCCGTGTGACAGGTCAGTGTGGGGCCGCCCTGGCTCCCGCAGCAGTCCCTAC 2243
Db 1981 GTGAAGTCCCGTGTGACAGGTCAGTGTGGGGCCGCCCTGGCTCCCGCAGCAGTCCCTAC 2040
QY 2244 TGGCCCACTTTCTCACTGTCCTCTTTGGCTTGTAGTCTTTCAGGAGCCCTCANC 2303
Db 2041 TGGCCCACTTTCTCACTGTCCTCTTTGGCTTGTAGTCTTTCAGGAGCCCTCANC 2100
QY 2304 ATCTCTGTCGCTCCCTCCCATTTGAGACGACCTCGGGCTCGGGCCAAAGTTTCAGGGCTGTGAG 2363
Db 2101 ATCTCTGTCGCTCCCTCCCATTTGAGACGACCTCGGGCTCGGGCCAAAGTTTCAGGGCTGTGAG 2160
QY 2364 ACCCTGGCCCT 2375
Db 2161 ACCCTGGCCCT 2172

RESULT 2
AK077976
LOCUS AK077976 3206 bp mRNA linear HTC 18-SEP-2003
DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030492A12 product:sema domain,
immunoglobulin domain (Ig), transmembrane domain (TM) and short
cytoplasmic domain, (semaphorin) 4A, full insert sequence.
ACCESSION AK077976
VERSION 1 GI:26057602
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 Carninci, P. and Hayashizaki, Y.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
2 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
4 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Taehiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kizawa, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
5 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
6 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
7 Nature 420, 563-573 (2002)
8 (bases 1 to 3206)

```

```

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
TITLE Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
FEATURES
Location/Qualifiers
source
1..3206
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="FANTOM_DB:6030492A12"
/db_xref="MG1:2394968"
/db_xref="taxon:10090"
/clone="6030492A12"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
224..2507
/note="putative
sema domain, immunoglobulin domain (Ig), transmembrane
domain (TM) and short cytoplasmic domain, (semaphorin) 4A
(MGI:MG1:107560, GB|NW_013658, evidence: BLASTN, 99%,
match=2517)"
polyA_signal 3181..3186
/note="putative"
polyA_site 3206
/note="putative"
ORIGIN
Query Match 50.5%; Score 1771.2; DB 11; Length 3206;
Best Local Similarity 75.8%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 663; Indels 121; Gaps 17;
QY 1 GGCTTTGGCATGATGGGACCTGGAGGGCGGACCTCCCGTTCCAGCCAGGCTGAGCCTTC 60
Db 47 GAGCTTGGCAGGATGGGTGCTCTGGAGGGCGGCGCGCTCCAGCCAGGCTGAGCCTGC 106
QY 61 TGTCCCTGCTCTGGGGCTGGGAAACCCCTTTCTTTCTCTCTGATGACACCCCGG 120
Db 107 TTGCTCTGCTTGGG-----CCCTTTCTTTGCTCGGATGCAACCTGA 150
QY 121 CCTAGATCCAGACACGAGTTTCCCACTGTGGGTGGTTCAAGGATATGTGAGAGCTCC 180
Db 151 TTCAGGGTTTGA-ACACAGGACTTCTCAGTGTGGGTGGCTCAAG-----GAACCAT 200
QY 181 CTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTTGACCCCTGAGCC 240
Db 201 CTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAGGACTCATGGAGTC 260

```



```
Db 2418 GACGACACCTCCAGCCCTCCAGACACACAGGACCTCTGCAGTAGCTAGATGCCGAC 2477
Qy 2460 AACAACTGCTAGGACCTAGAGTAACTTAGGCAAGCCGCGGCT--GCGGTG 2517
Db 2478 AACAACTATCTGGGCGCGAAAGTCTTAAACAGGACACAGATCCGAGCTGAGCAGAG 2537
Qy 2518 CAGGACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAG 2577
Db 2538 CAGGCACTGGCTTGTGGCTATGC-----CAG 2566
Qy 2578 CAAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTCATCTGATGACA 2637
Db 2567 GCACAGTGCCTGACAGAGGAGGCTCTCTGCTAACGTGTGTCACTACACGCA 2626
Qy 2638 CTCACAGGAGTATGACAGAGTCTGCTCCCTATGGAGTCCCTTCTACCAAGCACA 2697
Db 2627 CCGAGTAGGT-----CCTCCCTGTGGGACTCTCTCTCAAGCAGCAT 2669
Qy 2698 TGAGCTCTTAACAGGAGTGGGGCTACCCCCAGACCTCTCTCACTCATGATTTGAAGAA 2757
Db 2670 TGGGCTGTCT-----CCATACCTGTACTTGTGTGTGACAGGAAGA 2710
Qy 2758 CTTGAGAGGATCTTTCAGTTCTGCTGATTCAGGACCTCCAGAACACAGTGTTC 2817
Db 2711 GCCAGACAGGTTCTTGTATTTGATGACCAAGAGCCCTCCTGTAAACAACTGTCTCC 2770
Qy 2818 AGAGACCTTAAACACCTGCTCTCCAGGACCTTATGTTAATGAACACCAACATCTAA 2877
Db 2771 AGGAGACCATGAAGGTGTGCTGTGGATCTGTGTGTGACAGGAAGA 2829
Qy 2878 ACAATCATATGCTA-----ACATGCCACTCTCTGGAACCTCCACTCT- 2926
Db 2830 GCAAGCTGGGGCTATTCCTGCAAACTCCATCCTGAACTGCTGCTCACTCTAGAAGCAGCTGC 2889
Qy 2927 CGCTTTGACACCAACACTCCCTTC-TCACAGGGTCATGAGGATCTGCTCCCTCTGTC 2985
Db 2890 TGTCTTGAACACCAAGCCCTCTCTCCAGAGTCTCTATGAGTTGGCCCTCTGTGT 2949
Qy 2986 TTCCTTTACCACTGCTGACCGCTGACTCCAGGAAAGTCTTCCCTGAAAGTCTGACCACT 3045
Db 2950 TTCCTTTACCACTGCTGACCGCTGACTCCAGGAAAGTCTTCCCTGAAAGTCTGACCACT 3006
Qy 3046 TCTCTTCTGCTTCACTGCTGGGACACTCTGATCCCT---TCTGCCCTGGC-AGAATGGCA 3101
Db 3007 TCTCTTCTGCTTCACTGCTGGGACACTCTGATCCCT---TCTGCCCTGGC-AGAATGGG 3066
Qy 3102 GGGGTAATCTGAGCCTTCTTCACTCCCTTTACCTAGTGCACCCCTTCACTCTCCCTC 3161
Db 3067 GGCATAATCTGAGCCTTGTCTCCCTTGTCCAGTGTGGCTGACCCCTTGACCTCTT--CCTTC 3124
Qy 3162 CTTTCTCTTTTGGGATTCAGAACTGCTGTGTCAGAGCTGTATTATTTATTTATTA 3221
Db 3125 CTCTCCCTTTGTTTGGGATTCAGAACTGCTGTGTCAGAGCTGTATTATTTATTTATTA 3184
Qy 3222 AAAA 3225
Db 3185 AAAA 3188
```

```
RESULT 3
AY402622
LOCUS
DEFINITION
Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY402622
VERSION
AY402622.1
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (bases 1 to 2133)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
```

```
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriers,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
2 (bases 1 to 2133)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriers,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..2133
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>2133
/locus_tag="HCM1285"
```

```
Query Match 50.4%; Score 1767; DB 29; Length 2133;
Best Local Similarity 83.0%; Pred. No. 0;
Matches 1770; Conservative 0; Mismatches 363; Indels 0; Gaps 0;
```

```
Qy 204 ATGGCCCTCCAGCCCTGGGCTTGACCCCTGGAGCCTCTGGGCTTTCTCTTCCAA 263
Db 1 ATGGCCCTCCAGCCCTGGGCTTGACCCCTGGAGCCTCTGGGCTTTCTCTTCCAA 60
Qy 264 CTGCTTCAGCTGTCTGCTGCCAGCAGCCCGCGGGGAGGGGCGAGGGGCCCATGCC 323
Db 61 CTGCTTCAGCTGTCTGCTGCCAGCAGCCCGCGGGGAGGGGCGAGGGGCCCATGCC 120
Qy 324 AGGTCAGATATCTATGACGGGATGAACTAGGCGCTTAGCTTTCTCCAGAGAGGCG 383
Db 121 AGGTCAGATATCTATGACGGGATGAACTAGGCGCTTAGCTTTCTCCAGAGAGGCG 180
Qy 384 CTCAGGATTTTGACACTCTGCTGCTGAGTGTGATGAAATACTCTACGTGGGGCT 443
Db 181 CTCAGGATTTTGACACTCTGCTGCTGAGTGTGATGAAATACTCTACGTGGGGCT 240
Qy 444 CGAAGAGCAATCTTGCCCTTGATATCCAGGATCCAGGGGTCCTCCAGGCTAAGAACATG 503
Db 241 CGAAGAGCAATCTTGCCCTTGATATCCAGGATCCAGGGGTCCTCCAGGCTAAGAACATG 300
Qy 504 ATACCGTGGCCAGCCAGTGCAGAAAGAGTGAATGTGCCTTTAAGAGAGAGCAAT 563
Db 301 ATACCGTGGCCAGCCAGTGCAGAAAGAGTGAATGTGCCTTTAAGAGAGAGCAAT 360
Qy 564 GAGACACAGTGTTCAACTTCACTCCGTGCTCTGCTTCTTACAATGTACCCATCTCTAC 623
Db 361 GAGACACAGTGTTCAACTTCACTCCGTGCTCTGCTTCTTACAATGTACCCATCTCTAC 420
Qy 624 ACCTGGGCACTTCCCTTCAGCCCTGCTGTACTTCACTTGAAGTTCAGATTCCTAC 683
Db 421 ACCTGGGCACTTCCCTTCAGCCCTGCTGTACTTCACTTGAAGTTCAGATTCCTAC 480
Qy 684 CTCTTCCCATCTCTCGGAGGACAGGTCTATGAGGAGGAAAGGCAAGCCCTTTGACCC 743
Db 481 CTCTTCCCATCTCTCGGAGGACAGGTCTATGAGGAGGAAAGGCAAGCCCTTTGACCC 540
Qy 744 GCTCAGACATACGCTGTCTTGTGGATGGATGCTCTATTCTGGTACTATGAACAC 803
Db 541 GCTCAGACATACGCTGTCTTGTGGATGGATGCTCTATTCTGGTACTATGAACAC 600
Qy 804 TTCTTGGGAGTGGAGCCCATCTCTGATGCGCACACTGGGATCCAGGCTCTCTCTCAAGAC 863
Db 601 NTCTTGGGAGTGGAGCCCATCTCTGATGCGCACACTGGGATCCAGGCTCTCTCTCAAGAC 660
```


Qy	864	GACAACTTCCTCCGCTGGCTGCATCATCAGCGCTCCTTTGTGCGAGCCATCCCTTCGACC	923
Db	661		
Qy	924	CAGGTCGCTACTTCTTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTTGAGAGGCTC	983
Db	721	NN	780
Qy	984	CACACATCGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGGGGGGGAAAGACTGCTGCAG	1043
Db	781	NN	840
Qy	1044	AAGAAGTGGACCACTTCCTCGAAGGCCCGAGCTGCTCGACCCAGCGGGGCGAGCTGCC	1103
Db	841	NN	900
Qy	1104	TTCAAGTTCATCCGGCA CGCGGTCTGTCTCCCGCCGATTCCTCCACAGCTCCCAATC	1163
Db	901	NN	960
Qy	1164	TACGCACTCTTCACTCCAGTGGCAGGTTGGCGGACAGGAGCTCTGCGGTTTGTGTC	1223
Db	961	NN	1020
Qy	1224	TTCTCTCTCTTGGA CATTTGAACGTGTCTTTAAGGGGAAATAACAAGAGTTGAAACAAGAA	1283
Db	1021	TTCTCTCTCTTGGA CATTTGAACGTGTCTTTAAGGGGAAATAACAAGAGTTGAAACAAGAA	1080
Qy	1284	ACTTCAAGCTGCACTACTTATAGGGGCCCTGAGACCAACCCCGCCAGAGGAGTGTCTCA	1343
Db	1081	ACTTCAAGCTGCACTACTTATAGGGGCCCTGAGACCAACCCCGCCAGAGGAGTGTCTCA	1140
Qy	1344	GTGGGCCCTCTCTCTGATTAAGGCCCTGACCTTCATGAAGGACCAATTCCTGATCGATGAG	1403
Db	1141	GTGGGCCCTCTCTCTGATTAAGGCCCTGACCTTCATGAAGGACCAATTCCTGATCGATGAG	1200
Qy	1404	CAAGTGTGTGGGAGCGCCCTGCTGCTGAAATCTGCGCTGGAGTATACACGCTTGCGAGTG	1463
Db	1201	CAGTGTGTGGGAGCGCCCTGCTGCTGAAATCTGCGCTGGAGTATACACGCTTGCGAGTG	1260
Qy	1464	GAGACAGCCAGGCGCTTGATGGGCACAGCCATCTTGT CATGTACCTGGGAACCAACCACA	1523
Db	1261	GAGACAGCCAGGCGCTTGATGGGCACAGCCATCTTGT CATGTACCTGGGAACCAACCACA	1320
Qy	1524	GGGTGCTCCACAGGCTGTGTTAAGTGGGACAGAGTCTCATCTGTTGGGAAGAGATT	1583
Db	1321	GGGTGCTCCACAGGCTGTGTTAAGTGGGACAGAGTCTCATCTGTTGGGAAGAGATT	1380
Qy	1584	CAGCTGTTTCCCTGACCCCTGAAACCTGTTTCGCAACCTGCAGCTGGCGCCCAACCCAGGGTGA	1643
Db	1381	CAGCTGTTTCCCTGACCCCTGAAACCTGTTTCGCAACCTGCAGCTGGCGCCCAACCCAGGGTGA	1440
Qy	1644	GTGTTTGTAGGCTTCTCAGGAGTGTCTGAGGGTGGCCGAGGCAACTGTAGTGTCTAT	1703
Db	1441	GTGTTTGTAGGCTTCTCAGGAGTGTCTGAGGGTGGCCGAGGCAACTGTAGTGTCTAT	1500
Qy	1704	GAGAGCTGTGTGGACTGTGCTTTCGCCGGGACCCCACTGTGCTGGGACCTCTGAGTCC	1763
Db	1501	GAGAGCTGTGTGGACTGTGCTTTCGCCGGGACCCCACTGTGCTGGGACCTCTGAGTCC	1560
Qy	1764	CGAACTGTTGCTCTCTGTCTGCCCCCAACCTGAACTCTCTGGAAGCAGGACATGAGACGG	1823
Db	1561	CGAACTGTTGCTCTCTGTCTGCCCCCAACCTGGAAGCAGGACATGAGACGG	1620
Qy	1824	GGGAACCCAGAGTGGGCATGTGCCAGTGGGCCCATGAGCAGGAGCCTTCGCGCTCAGAGC	1883
Db	1621	GGGAACCCAGAGTGGGCATGTGCCAGTGGGCCCATGAGCAGGAGCCTTCGCGCTCAGAGC	1680
Qy	1884	CGCCCGCAAAATCAATAAGAAAGTCTCGCTGTCTTAACTCTCTGAGCTCCCTGTC	1943
Db	1681	CGCCCGCAAAATCAATAAGAAAGTCTCGCTGTCTTAACTCTCTGAGTCCCTGTC	1740

QY	1944	CCCCACCTGTCAAGCTTGGCCCTCTTATATATGGAGTCAATGGCCAGCAGCAGTCCAGAA	2003
Db	1741	CCCCACCTGTCAAGCTTGGCCCTCTTACTATATGGAGTCAATGGCCAGCAGCAGTCCAGAA	1800
QY	2004	GCCTCTTCCCACTGTCTCAATATGGCTCCCTCTTGTCTAGTATGAGGATGAGGATGGGGGT	2063
Db	1801	GCCTCTTCCCACTGTCTCAATATGGCTCCCTCTTGTCTAGTATGAGGATGAGGATGGGGGT	1860
QY	2064	CTCTACCAAGTCTGGGCAACTGAGATGGCTTTTCATACCTGTGATCTCTACTGGGTG	2123
Db	1861	CTCTACCAAGTCTGGGCAACTGAGATGGCTTTTCATACCTGTGATCTCTACTGGGTG	1920
QY	2124	GACAGCCAGGACACAGACCCCTGGCCCTGGATCTCTCAACTGGCAGGCAATCCCGGGGAGCAT	2183
Db	1921	GACAGCCAGGACACAGACCCCTGGCCCTGGATCTCTCAACTGGCAGGCAATCCCGGGGAGCAT	1980
QY	2184	GTGAAGTCTCCGTTGACAGAGGTCAGTGGTGGGGCGCCCTGGCTGCCAGCAGTCTCTAC	2243
Db	1981	GTGAAGTCTCCGTTGACAGAGGTCAGTGGTGGGGCGCCCTGGCTGCCAGCAGTCTCTAC	2040
QY	2244	TGGCCCACTTTGTCACTGTCACTGTCTCTCTTTGGCTTGTAGTGTCTTTCAGGAGCCCTCATC	2303
Db	2041	TGGCCCACTTTGTCACTGTCACTGTCTCTCTTTGGCTTGTAGTGTCTTTCAGGAGCCCTCATC	2100
QY	2304	ATCTCTGTGGCCCTCCCATTTAGAGCAGTCCGG	2336
Db	2101	ATCTCTGTGGCCCTCCCATTTAGAGCAGTCCGG	2133
RESULT 4			
LOCUS	AK035918	3086 bp mRNA linear HTC 19-SEP-2003	
DEFINITION	Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630018D15 product:sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, full insert sequence.		
ACCESSION	AK035918.1	GI:26084904	
VERSION	1		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	H-g-h-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Ozawa, Y., Iwata, M., Ohara, E., Watahiki, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		

Db 1226 CGAGGCCAGGAGTTGCTTCCATGGGCCCTTCTCTGACAAAGCCTTGACCTTCAAGAG 1285
Qy 1384 ACCATTTCTGATGATGAGAGCAAGTGGTGGGAGCGCCCTGCTGGTGAATCTGGCGTG 1443
Db 1286 ACCATTTCTGATGATGAGAGCAAGTGGTGGGAGCAAGTGGTGAATCTGGCGTG 1345
Qy 1444 AGTATACAGCGCTTGCAGTGGAGAGCAGCCAGGCGCTTGATGGGACAGCCATCTGTGCA 1503
Db 1346 AGTACACAGCGCTTGCAGTGGAGTCACTGGGCGCTTGATGGGAGAGCCATGTGCTCA 1405
Qy 1504 TGTACCTGGGAAACACACAGGCTGGTCCCAAGGCTGGTAAAGTGGGAGCAGCAGTG 1563
Db 1406 TGTATCTGGGTACCTCCAGCGGGTCCCTGACAGGCTGGTGGTGGCTCAAGGAGCAGTG 1465
Qy 1564 CTATCTGGTGGAGAGATTCAGCTGTTCCCTGACCTGAACCTGTTGCGAACCTGCAGC 1623
Db 1466 CTATCTGGTGGAGAGATTCAGCTGAGCCCTGACTCTGAGCCTGTTGGAACCTGCAGC 1525
Qy 1624 TGGCCCCCAACCCAGGCTGAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGGAGGTCGCC 1683
Db 1526 TGGCCCCCGCCAGGCTGAGTGTGTTGAGGCTTCTCAGGAGCACTCGAGAGTTCCCA 1585
Qy 1684 GAGCAACTGATGCTATGAGAGCTGTGAGCTGTCTCTGCTGGCGGACCCCACT 1743
Db 1586 GGGCAATTCAGTGTCTGAGAGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 1645
Qy 1744 GTGCTGGGACCTGAGTCCGCAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1803
Db 1646 GTGCTGGGACCTGAACTCAAGACTCTGAGCCTGCTGCTGCTGCTGCTGCTGCTGCT 1702
Qy 1804 GGAAGAGGACATGGAGCGGGGAGACCCAGAGTGGGATGTGCACTGGGCGCCCATGAGCA 1863
Db 1703 GGAAGAGGACATGGAGCGGGGAGACCCAGAGTGGGATGTGCACTGGGCGCCCATGAGCA 1762
Qy 1864 GGAAGCTTCGCGCTCAGAGCGCGCGCAATCAATTAAGAGTCTGCTGCTGCTGCTGCT 1923
Db 1763 GGAAGCTTCGCGCTCAGAGCGCGCGCAATCAATTAAGAGTCTGCTGCTGCTGCTGCT 1822
Qy 1924 CCATCTGGAGCTCCCTGCGGCGCACTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 1983
Db 1823 CCATCTGGAGCTGCTGCTGCGGCGCACTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCT 1882
Qy 1984 GCCAGAGAGTCCAGAGAGCTCTTCCACTGTCTACAAATGCTGCTGCTGCTGCTGCTGCT 2043
Db 1883 GCCAGAGAGTCTCAGAGAGCTCTGCTACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1942
Qy 2044 TGCAAGATGAGTGGGGTCTCTACAGCTGTGGGCACTGAGATGCTTTTCAATC 2103
Db 1943 CGCAGGATGCTGCGGGGCTCTACAGGCTGTGGGCACTGAGACGGCTACTCATACC 2002
Qy 2104 CTGTGATCTCTACTGCGGTGGAGAGCAGGAGCCAGAGCCCTGGGCTGCTGCTGCTGCTGCT 2163
Db 2003 CTGTGATCTCTACTGCGGTGGAGAGCAGGAGCCAGAGCCCTGGGCTGCTGCTGCTGCTGCT 2062
Qy 2164 CAGGATCCCGCGGAGCATGTGAAGTCCCGTTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2223
Db 2063 CGGCGTTCCTGCGGAGTGTGAGAGTCCCGTGTGAGAGTCCCGTGTGAGAGTCCCGTGTGAG 2122
Qy 2224 TGGCTGCGGAGCTCTACTGCGGCGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2283
Db 2123 TGGCTGCGGAGCTCTACTGCGGCGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2182
Qy 2284 TGCTTTGAGAGCGCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2343
Db 2183 TGCTTTGAGAGCGCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2242
Qy 2344 GCAAGGTTCAAGGCTGTGAGAGCTGCGGCTGCGGAGAGGCGGCTTAAAGCAGAGAGC 2403
Db 2243 GTAAGGTTCAAGGCTGTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2302
Qy 2404 AACACTTCAAGTCTCCCAAGGATGAGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2463

Db 2303 AGCACTCCAGCCCTCCAGGACCAAGGAGCTCTGCGAGCTGAGCTAGATGCCGACACA 2362
Qy 2464 ACTGCTAGGCACTGAGTGTGCTTAAACTCTGAGGCAACAGGCGGGGCT--GGGTGAGG 2521
Db 2363 ACCATCTGGGCGGAGTGGCTTAAACAGGAGACACAGATCCGAGCTGAGCAGAGCAAG 2422
Qy 2522 CACCTGGGCACTGCTGGTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACA 2581
Db 2423 CCACTGGGCTTGTGGCTATGC-----CAGGCAC 2451
Qy 2582 AAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGATCTGATGACACTCA 2641
Db 2452 AGTGCCTCTGACAGGAGGAGGCTCTCTGCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2511
Qy 2642 CGAGGTGATGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2701
Db 2512 GTAGT-----CCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2554
Qy 2702 CTCTCTAACAGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2761
Db 2555 CTGCT-----CCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2595
Qy 2762 GAGAGGATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2821
Db 2596 GACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2655
Qy 2822 ACCCTAAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2881
Db 2656 GACCATGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2714
Qy 2882 TCATATGCTA-----ACATGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2930
Db 2715 GCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2774
Qy 2931 TTGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2989
Db 2775 TTGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2834
Qy 2990 CTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3049
Db 2835 TTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2891
Qy 3050 TCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3105
Db 2892 TCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2951
Qy 3106 TAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3165
Db 2952 TAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3009
Qy 3166 TTCCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3225
Db 3010 TCCCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3069

RESULT 5
AY402623

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AY402623 2172 bp DNA linear GSS 12-DEC-2003
Mus musculus HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

AY402623
AY402623.1 GI:39758609
GSS.

Mus musculus (house mouse)
Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 2172)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

```
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2172)
AUTHORS Clark A.G., Glanowski S., Nielson R., Thomas P., Kejarawal A.,
        Todd M.A., Tenebaum D.M., Civello D.R., Lu F., Murphy B.,
        Ferreira S., Wang G., Zheng X.H., White T.J., Shinsky J.J.,
        Adams M.D. and Cargill M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
        Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
        them based on alignment.
FEATURES
    source
        1..2172
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            <1..>2172
            /locus_tag="HCM1285"
    gene
        1..2172
    ORIGIN
        Query Match 39.1%; Score 1370.6; DB 29; Length 2172;
        Best Local Similarity 71.8%; Pred. No. 0;
        Matches 1559; Conservative 0; Mismatches 612; Indels 0; Gaps 0;
        QY 204 ATGCGCTCCAGCCCTGGGCTGGAGCCCTGGAGCCTCTGGGCTTCTCTTCCAA 263
        DB 1 ATGCGCTTACCATCTCTGGGCGAGATCATGAGATCTCTGGTGTCTTCTTCCAA 60
        QY 264 CTGCTTACGTGCTGTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 323
        DB 61 CTCTCTCTGCTGCCATCACTGCCACCTGCTCTGGGACTGTGGTTCAGGGGCCATGCC 120
        QY 324 AGGTCAGATATGTCAGGGGATGAAGTATGAGGACCTAGCTCTCTCCACGAGAGGC 383
        DB 121 AGAGTCATATACCATGCTGGAGAGCGGCAAGGGCCCTCAGCTTCTTCCAAAGAGC 180
        QY 384 CTCAGGATTTGACACTCTCTCTGAGTGGTGATGGAATATCTCTACGTGGGGCT 443
        DB 181 CTCGAGACTTTGACAGCTCTCTCTGAGTGAACATGGCAACACTCTCTATGTGGGGCT 240
        QY 444 CGAGAGCCATCTTGGCTTGGATATCAGATCCAGGCTCCAGGCTCCAGCTTAAAGACATG 503
        DB 241 CGAGAGGCGCTTGGCTTGAATATCAGAACCCAGGAATCCCAAGGCTTAAAGACATG 300
        QY 504 ATACGCTGGCAGCAGTGAAGAGAGAGAGTGAATGTGCTTTTAAAGAGAGAGCAAT 563
        DB 301 ATACCTGGCAGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
        QY 564 GAGACAGTGTTCACATTCATCGGTGCTGCTGTTTCTTACATGTACCCATCTCTAC 623
        DB 361 GAGACAGTGTTCACATTCATCGGTGCTGCTGTTTCTTACATGTCTACCTCTAT 420
        QY 624 ACCTGGGCACTTGGCTTCCAGCCCTGCTGTACCTTCAATGAACTTCAAGATTCCTAC 683
        DB 421 GCCTGTGGGACCTTTGGCTTCCAGCCCTGCTGTACCTTCAATGAACTTCAAGATTC 480
        QY 684 CTGTGTCCTATCTCGAGGA CAAGGTATGAGGGAAGAGCCAAAGCCCTTTGACCC 743
        DB 481 CTGTGTCCTATCTTATAGACAGGTATGAGCAGGGAAGAGCCAAAGCCCTTTGACCC 540
        QY 744 GCTCAGAGCATAGGCTGTCTTGTGATGGGATGCTTATCTGTGTACTATGAAACAA 803
        DB 541 GTTCAAGCACACAGCTGTCTTGTGATGGGATGCTTATCTCGGCACTATGAAACAA 600
        QY 804 TTCTGGGAGTGAAGCCCATCTGATGCGACACTGGGATCCAGCTGTCTCAAGACC 863
        DB 601 TTCTGGGAGTGAAGCCCATCTGATGCGGACACTGGGATCCAGCTGTCTCAAGACT 660
        QY 864 GACAACTTCTCGCTGCTGCATCATGACGCTCTTTGTGGCAGCCATCCCTTCGACC 923
        DB 661 GACATCTTCTTACGCTGCTGCATCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720
        924 CAGGTGCTACTTCTTCTGAGGAGACGCGAGGAGTTTGACTTCTTTGAGAGGCTC 983
        DB 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
        QY 984 CACACATCGCGGTGGCTAGAGTCTGCAAGATACGTGGCGGCAAGAGCTGCTGCAG 1043
        DB 781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840
        QY 1044 AAGAGTGGACACCTTCTGAGGCGCAGCTGCTCTGACCCAGCGGGGAGCTGCC 1103
        DB 841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900
        QY 1104 TTCAAGCTCATCGCCACGCGCTCTGCTCCCGCGGATTTCTCCACAGCTCCCA 1163
        DB 901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960
        QY 1164 TAGCAGTCTTACCTCCAGTGGCGAGTGGCGGACAGAGCTCTGCGGTTGTGCC 1223
        DB 961 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020
        QY 1224 TTCTCTCTTGGACATTGAGCTCTTTAAGGGGAAATACAAAGCTTGAACAAAGAA 1283
        DB 1021 TTCTCTCTCACGACATTGAGCGAGTCTTTAAGGGAAGTACAGAGCTGAACAGAG 1080
        QY 1284 ACTTCAAGCTGACTACTTATAGGGGCTCTGAGACCAACCCCGCCAGGCAAGTTGCTCA 1343
        DB 1081 ACCTCCGCTGACCACTTACCGGCTCAGAGGTCAGCCCGAGGCAAGGCTGCTCC 1140
        QY 1344 GTGGGCTCTCTCTGATGAAGCCCTGACCTTCAAGAGGACCACTTCTGATGATGAG 1403
        DB 1141 ATGGGCTCTCTCTGACAAAGCTTGAACCTTCAAGAGGACCACTTCTGATGATGAG 1200
        QY 1404 CAAGTGTGGGACCGCTCTGCTGAAATCTGCGTGGAGTATACACGGCTTGCAGTG 1463
        DB 1201 CACTGTGAGAACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
        QY 1464 GAGACAGCCAGGCTTGAAGGACAGCCATCTTGTCTGATGCTGCTGCTGCTGCTGCTG 1523
        DB 1261 GAGTCAAGCTCGGGCTTGAAGGAGAGCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1320
        QY 1524 GGTGCTCCACAAAGCTGTGTAAGTGGGAGACAGCTGCTGCTGCTGCTGCTGCTGCTG 1583
        DB 1321 GGTGCTCCACAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
        QY 1584 CAGCTGCTTCCCTGACCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1643
        DB 1381 CAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
        QY 1644 GTGTTGTAGGCTTCTCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1703
        DB 1441 GTGTTGTAGGCTTCTCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
        QY 1704 GAGAGCTGTGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1763
        DB 1501 GAGAGCTGTGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
        QY 1764 CGNACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1823
        DB 1561 AGACTCTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
        QY 1824 GGGAAACCCAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1883
        DB 1621 GGCNACCCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
        QY 1884 CGCCCGCAATCATTTAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1943
        DB 1681 CCCCCTCACTAATTAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
        QY 1944 CCCCAGCTGTGAGCTTGGCTCTTATTTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2003
        DB 1741 CCCCAGCTGTGAGCTTGGCTCTTATTTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
```

2004 GCCTCTTCCACTGCTACATGGCTCCCTCTTGTGATAGTGCAGGATGGAGTTGGGGT 2063
|||||
1801 GCCTCTGCTACCGTCTACATGGCTCCCTCTTGTGCTGCGGAGAGATGCTGCGGGGC 1860
|||||
2064 CTCTACCAAGTCTGGGCAACTGAGAAAGGCTTTTATACACCTGTGATCTCTACTGGTG 2123
Db CTCTACCAAGTGTGTGGGCACTGAGAAAGGCTACTATACACCTGTGTCTCTCTATTGGGTA 1920
2124 GACAGCCAGGACCAAGACCCCTGGCCCTGATCTGAACTGGCAGGCAATCCCGGGAGCAT 2183
1921 GACAGCCAGGACCAAGACCCCTGGCCCTGATCTGAACTGGCAGGCAATCCCGGGAGCAT 1980
2184 GTGAAGTCCCGTTGACAGAGGTCAGTGTGGGCGCCCTGTGCTGCGCCAGCAGTCTTAC 2243
Db GTGAGGTCCCGTGTGACAGAGGTCAGTGTGGGCGCCCTGTGCTGCGCCAGCAGTCTTAC 2040
2244 TGGCCCACTTTGTCACTGTCACTGTCTCTTTGGCCCTTGTGCTTTCAGAGCCCTCATC 2303
2041 TGGCCCACTTTGTCACTGTCACTGTCTCTTTGGCCCTTGTGCTTTCAGAGGTCCTACT 2100
2304 ATCTCTGTGGCTCCCAATTGAGAGCACTCCGGCTCGGGCGCAAGGTTGAGGCTGTGAG 2363
Db CTCTCTCTGCTTCCCACTGGGGCGCTCGGGCTCGGGGTAAAGGTTGAGGCTGTGGG 2160
2364 ACCCTGCGCC 2374
2161 ATGCTGCCCC 2171

RESULT 6
BX367242/c
LOCUS
DEFINITION BX367242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL002Y004 3-PRIME, mRNA sequence.
ACCESSION BX367242
VERSION BX367242.1 GI:30455608
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1114)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 907.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AL002BH02NPI&cluster=907.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AL002BH02NPI.
Location/Qualifiers
1. .1114
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL002Y004"
/cell_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

Query Match 27.2%; Score 952.2; DB 13; Length 1114;
Best Local Similarity 94.9%; Pred. No. 3.2e-225;
Matches 997; Conservative 24; Mismatches 25; Indels 4; Gaps 4;

QY 2172 CCCCGGAGCAGTGTGAAGGTCCCCTTGAACCAAGGTCAGTGTGGGGCCGCCCTGGCTGCC 2231
Db 1055 CCCCGGAGCAGTGTGAAGGTCCCCTTGAACCAAGGTCAGTGTGGGGCCGCCCTGGCTGCC 998
QY 2232 CAGCAGTCTCTACTGGCCCC-ACCTTGTCACTGTCACTGTCTCTTTCCTTTCCTTTCCTTTC 2290
Db 997 CAGCAGTCTCTACTGGCCCC-ACCTTGTCACTGTCACTGTCTCTTTCCTTTCCTTTCCTTTC 938
QY 2291 AGGAGCCCTCATCATCTCTGCTGGCCCTCCCC-ATTGAGAGCACTCCGGCTCGGGGCAAGG 2349
Db 937 AGGAGCCCTCATCATCTCTGCTGGCCCTCCCC-ATTGAGAGCACTCCGGCTCGGGGCAAGG 878
QY 2350 TTCAGGGCTGTGAGACCTTCGGCCCTGGGAGAGAGCCCGCTTAAAGCAGAGAGCAACACC 2409
Db 877 TTCAGGGCTGTGAGACCTTCGGCCCTGGGAGAGAGCCCGCTTAAAGCAGAGAGCAACACC 818
QY 2410 TCCAGTCTCCCAAGAAATGCAAGACCTCTGCACTGTGAGAGCTGCAACCAACTGCC 2469
Db 817 TCCAGTCTCCCAAGAAATGCAAGACCTCTGCACTGTGAGAGCTGCAACCAACTGCC 758
QY 2470 TAGGCACTGAGTACTTAACTCTAGGCACAGGCCCGGGCTGGGTCAGGCACTGGC 2529
Db 757 TAGGCACTGAGTACTTAACTCTAGGCACAGGCCCGGGCTGGGTCAGGCACTGGC 698
QY 2530 CATGCTGGCTGGCGGCCCAAGCAGCAGCCCTGACTAGGATGACAGCAGCAGCAAAAGACCA 2589
Db 697 CATGCTGGCTGGCGGCCCAAGCAGCAGCCCTGACTAGGATGACAGCAGCAGCAAAAGACCA 638
QY 2590 CTTTCTCCCTGAGAGAGGCTTCTGCTACTGCTCACTGATGACACTCAGCAGGAGGTG 2649
Db 637 CTTTCTCCCTGAGAGAGGCTTCTGCTACTGCTCACTGATGACACTCAGCAGGAGGTG 578
QY 2650 ATGCACAGCAGTCTGCTCCCTATGGAGCTCCCTTCTACCAAGCAGCAGCTCTCTAA 2709
Db 577 ATGCACAGCAGTCTGCTCCCTATGGAGCTCCCTTCTACCAAGCAGCAGCTCTCTAA 518
QY 2710 CAGGCTGGGGCTACCCCGCAGCAGCTGCTCTCACTGATATGAAACCTGAGAGGAT 2769
Db 517 CAGGCTGGGGCTACCCCGCAGCAGCTGCTCTCACTGATATGAAACCTGAGAGGAT 458
QY 2770 CTTTCAGTCTGGGCATTTCCAGGAGCCCTCCAGAAACACAGTGTTCACAGAGCCCTAAA 2829
Db 457 CTTTCAGTCTGGGCATTTCCAGGAGCCCTCCAGAAACACAGTGTTCACAGAGCCCTAAA 398
QY 2830 AAACCTGCTGTCACAGACCCCTATGTAATGAACACCAACATCTTAAACATATATGC 2889
Db 397 AAACCTGCTGTCACAGACCCCTATGTAATGAACACCAACATCTTAAACATATATGC 338
QY 2890 TAACATGCCATCTCTGGAATCTCCACTCTGAAGCTGCGCTTTGGACACCAACCTCCCT 2949
Db 337 TAAATGCACTCTCTGGAATCTCCACTCTGAAGCTGCGCTTTGGACACCAACCTCCCT 278
QY 2950 TCTCCAGGGTCATGAGAGGATGCTCCCTCTGCTTCCCTTACCAAGTCTGACACCGCT 3009
Db 277 TCTCCAGGGTCATGAGAGGATGCTCCCTCTGCTTCCCTTACCAAGTCTGACACCGCT 218
QY 3010 GACTCCCGAGGAGCTTCCCTGAGTCTGACACCTTCTCTTCTTCTTCTTCTTCTTCTTCT 3069
Db 217 AACTCCAGGAGGAGCTTCCCTGAGTCTGACACCTTCTCTTCTTCTTCTTCTTCTTCT 158
QY 3070 ACTCTGATCCCTTCTGCTGCGCAGAAATGGCAGGGTAAATCTGAGCCCTTCTTCTTCT 3129
Db 157 ACTCTGATCCCTTCTGCTGCGCAGAAATGGCAGGGTAAATCTGAGCCCTTCTTCTTCT 98
QY 3130 TACCTAGCTGACCCCTTCACTCTCCCTCCCTCCCTTCTTCTTCTTCTTCTTCTTCTTCT 3189
Db 97 TACCTAGCTGACCCCTTCACTCTCCCTCCCTCCCTTCTTCTTCTTCTTCTTCTTCTTCT 38
QY 3190 ACTGCTTGTGACAGACTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3220

Invitrogen. This sequence belongs to sequence cluster 907.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BA1043ZD06_CS04076_1&cluster=907.f. Contact : Feng Liang Email : fliang@lifestech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BA1043ZD06_CS04076_1.

FEATURES
Location/Qualifiers
1..922
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL005YC17"
/cell_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 25.0%; Score 876; DB 13; Length 922;
Best Local Similarity 98.8%; Pred. No. 2.7e-206;
Matches 879; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1471 CCCAGGGCTTGATGGGACAGCAGCATCTGTGATGACCTGGGAAACACACAGGGTCGC 1530
DB 919 CCCAGGCTTGATGGGACAGCAGCATCTGTGATGACCTGGGAAACACACAGGGTCGC 860
QY 1531 TCCACAGGCTGTGTAAGTGGGACAGCAGCTGTCTATCTGTTGGAGAGATTGAGCTGT 1590
DB 859 TCCACAGAGCTGTGTAAGTGGGACAGCAGCTGTCTATCTGTTGGAGAGATTGAGCTGT 800
QY 1591 TCCCTGACCTGAACTGTTGCCAACTGTCAGCTGGGCCCCACCCAGGGTGCAGTGTG 1650
DB 799 TCCCTGACCTGAACTGTTGCCAACTGTCAGCTGGGCCCCACCCAGGGTGCAGTGTG 740
QY 1651 TAGGCTTCTCAGAGGCTCTGAGGGTGGCCCCAGAGCACTGATGATGCTATGAGAGCT 1710
DB 739 TAGGCTTCTCAGAGGCTCTGAGGGTGGCCCCAGAGCACTGATGATGCTATGAGAGCT 680
QY 1711 GTGTGGACTGTCTTCCCGGAGACCCCACTGTGCTGGGACCTGAGTCCCGAACCT 1770
DB 679 GTGTGGACTGTCTTCCCGGAGACCCCACTGTGCTGGGACCTGAGTCCCGAACCT 620
QY 1771 GTTGCCTCTGTCGCCCACTGACTGCTGAGAGCAGGACATGAGCGGGGAACC 1830
DB 619 GTTGCCTCTGTCGCCCACTGACTGCTGAGAGCAGGACATGAGCGGGGAACC 560
QY 1831 CAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCTTTCGGCCTCAGAGCGCCGC 1890
DB 559 CAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCTTTCGGCCTCAGAGCGCCGC 500
QY 1891 AATCATTAAGAAGTCTGCTGCTGCTTACTCCTGAGCTGCTGCTGCTGCTGCTGCTGCT 1950
DB 499 AATCATTAAGAAGTCTGCTGCTGCTTACTCCTGAGCTGCTGCTGCTGCTGCTGCTGCT 440
QY 1951 TGTGAGCTTGGCTCTTATTATTGAGTCTATGCTGAGCAGCAGTCCAGAGACCTCTT 2010
DB 439 TGTGAGCTTGGCTCTTATTATTGAGTCTATGCTGAGCAGCAGTCCAGAGACCTCTT 380
QY 2011 CAATGCTCAATGGCTCTTCTGCTGATGATGAGAGTGGAGTGGGGGTCTTACC 2070
DB 379 CAATGCTCAATGGCTCTTCTGCTGATGATGAGAGTGGAGTGGGGGTCTTACC 320
QY 2071 AGTGTGGGCACTGAGAGTGGCTTTTATACCTCTGATCTCTCTCTCTCTCTCTCTCTCT 2130
DB 319 AGTGTGGGCACTGAGAGTGGCTTTTATACCTCTGATCTCTCTCTCTCTCTCTCTCTCT 260
QY 2131 AGGACAGACCTTGGCTCTGATCTGAGCTGGAGGACATCCCCGGGAGCATGTGAAG 2190

DB 259 AGGACAGACCTTGGCTTGGATCTGAACCTGGCAGGATCCCCGGGAGCATGTGAAGG 200
QY 2191 TCCGTTTACCAGAGGTGAGTGGTGGGGCGGCTTGGTGGCCAGCAGTCTTACTGGGCCC 2250
DB 199 TCCGTTTACCAGAGGTGAGTGGTGGGGCGGCTTGGTGGCCAGCAGTCTTACTGGCCC 140
QY 2251 ACTTTGTCACTGTCACTGTCTCTTTTGGCTTAGTGTCTTTTGGAGGCCCTCATCATCTCG 2310
DB 139 ACTTTGTCACTGTCACTGTCTCTTTTGGCTTAGTGTCTTTTGGAGGCCCTCATCATCTCG 80
QY 2311 TGGCTTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGT 2360
DB 79 TGGCTTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGT 30

RESULT 9
BX328255 926 bp mRNA linear EST 01-MAY-2003
LOCUS BX328255 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.
ACCESSION BX328255
VERSION BX328255.1 GI:30307730
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 907.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG053ZH06_C
S05040_1&cluster=907.f. Contact : Feng Liang Email : fliang@lifestech.com URL : <http://fulllength.invitrogen.com/>
Invitrogen Corporation 1600 Parady Avenue Genoscope sequence ID : CS0BAG053ZH06_CS05040_1.

FEATURES
Location/Qualifiers
1..926
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL005YC17"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 24.4%; Score 856.6; DB 13; Length 926;
Best Local Similarity 98.1%; Pred. No. 1.8e-201;
Matches 909; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY 904 TGGCAGCATCTTCCAGCCAGGTCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 962
DB 1 TGGCAGCATCTTCCAGCCAGGTCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
QY 963 TTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1022
DB 61 TTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 1023 GCGGGGCAAAAGCTGCTGAGAGGAGTGGACACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1082

QY	858	AGAGCCGACAACTTCTCCGCTGGCTGCTCATATGAGCCCTCTTTGTGGCAGCCATCCCT	917
Db	728	AGAGCCGACAACTTCTCCGCTGGCTGCTCATATGAGCCCTCTTTGTGGCAGCCATCCCT	787
QY	918	TGACCCAGGTGCTGCTACTTCTTCTGAGGAGACAGCCAGGAGTTTGACTTCTTTGAG	977
Db	788	TGACCCAGGTGCTGCTACTTCTTCTGAGGAGACAGCCAGGAGTTTGACTTCTTTGAG	847
QY	978	AGCTCCACATATCGGGTGGCTAGAGTCTGCAAGATGAGTGGGGGGGAAAGCTG	1037
Db	848	AGCTCCACATATCGGGTGGCTAGAGTCTGCAAGATGAGTGGGGGGGAAAGCTG	906
QY	1038	CTCAGAGAGAGTGGACCACTTCTTGAAGCCAGCTGCTGCACCCAGCCGGGGC	1095
Db	907	CTCAGAGAGAGTGGACCACTTCTTGAAGCCAGCTGCTGCACCCAGCCGGGGC	964
RESULT 11			
LOCUS	BQ057192		
DEFINITION	AGENCOURT 6769628 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812383		
ACCESSION	BQ057192		
VERSION	BQ057192.1	GI:19816532	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	NH-MGC http://mgi.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-k@mail.nih.gov Tissue Procurement: Lou Staudt cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2062 row: 1 column: 16 High quality sequence stop: 714.		
FEATURES			
source	1..974		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5812383"		
	/tissue_type="lymphoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH_MGC_99"		
	/note="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	23.6%	Score 827.4; DB 13; Length 974;	
Best Local Similarity	92.6%	Pred. No. 3.4e-194;	
Matches 902; Conservative	0; Mismatches 67; Indels 5; Gaps 3;		
QY	191	TCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGCCCTCTGGGCCT	250
Db	1	TCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGCCCTCTGGGCCT	60

RESULT 12
BX390196
LOCUS
DEFINITION
BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CSDD003YE08 5-PRIME, mRNA sequence.
ACCESSION
BX390196
VERSION
BX390196.1
GI:30463276
KEYWORDS
EST.

QY	251	TTTCTCTTCCAACTGCTTTCAGCTGCTGCTGCGACGACGACCGCGGGGGAGCGCGGCA	310
Db	61	TTTCTCTTCCAACTGCTTTCAGCTGCTGCTGCGACGACGACCGCGGGGGAGCGCGGCA	120
QY	311	GGGGCCCATCCCGAGGGTCAGATACATATGAGGGGATGAACGTAGGGCACTTAGCTTCT	370
Db	121	GGGGCCCATCCCGAGGGTCAGATACATATGAGGGGATGAACGTAGGGCACTTAGCTTCT	180
QY	371	CCACCAAGAGGGCTCCAGGATTTTGCACACTCTGCTTCTCCCTGAGTGGTATGGAATACTCT	430
Db	181	CCACCAAGAGGGCTCCAGGATTTTGCACACTCTGCTTCTCCCTGAGTGGTATGGAATACTCT	240
QY	431	CTAGTGGGGGCTCGAGAGCCATTTGGCTTTGGATATCCAGGATCCAGGGGTGCCCCAG	490
Db	241	CTAGTGGGGGCTCGAGAGCCATTTGGCTTTGGATATCCAGGATCCAGGGGTGCCCCAG	300
QY	491	GCTAAAGAAATATGATACCGTGGCCAGCCAGTGCAGAAAAAGAGTGAATGTGCCTTTAA	550
Db	301	GCTAAAGAAATATGATACCGTGGCCAGCCAGTGCAGAAAAAGAGTGAATGTGCCTTTAA	360
QY	551	GAAGAGAGCAATGAGACACAGTGTGTTTAACTTCATCCCTGCTCTGTTTCTTACATGT	610
Db	361	GAAGAGAGCAATGAGACACAGTGTGTTTAACTTCATCCCTGCTCTGTTTCTTACATGT	420
QY	611	CACCATCTCTACACCTGCGGCACCTTCGCTTTCAGCCCTGCTTGTACCTTTCATTGAAC	670
Db	421	CACCATCTCTACACCTGCGGCACCTTCGCTTTCAGCCCTGCTTGTACCTTTCATTGAAC	480
QY	671	TCAAGATTCTTACCTGTTGCCATCTCGAGGACAGAGTTCATGAGGAGAAAGCCAAAG	730
Db	481	TCAAGATTCTTACCTGTTGCCATCTCGAGGACAGAGTTCATGAGGAGAAAGCCAAAG	540
QY	731	CCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATGGGATGCTCTATTCTGG	790
Db	541	CCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATGGGATGCTCTATTCTGG	600
QY	791	TACTATGAACAACTTCTCGGCACTGAGCCATCTGATGCGCACACTGGGATCCGAGCC	850
Db	601	TACTATGAACAACTTCTCGGCACTGAGCCATCTGATGCGCACACTGGGATCCGAGCC	660
QY	851	TGCTCTCAAGACCCAGCAACTTCTCCGCTGCTGATCATGAGCCCTCTTTGTGGCAGC	910
Db	661	TGCTCTCAAGACCCAGCAACTTCTCCGCTGCTGATCATGAGCCCTCTTTGTGGCAGC	720
QY	911	CATCCCTTCGACCCAGGTCGTTACTTCTTCTTTCGAGGAGACAGCCAGGATTTGACTT	970
Db	721	CATCCCTTCGACCCAGGTCGTTACTTCTTCTTTCGAGGAGACAGCCAGGATTTGACTT	780
QY	971	CTTTGAGAGGCTCCACACATCGCGGTGG-CTAGAGTCTGCAAGATGAGTGGGC-GGC	1028
Db	781	CTTTGAGAGGCTCCACACATCGCGGTGG-CTAGAGTCTGCAAGATGAGTGGGC-GGC	840
QY	1029	GAAAAGCTGCTGCAGAGAA---GTGGACCACTTCTTTCGAGGCGCCAGCTGCTCTGCACC	1085
Db	841	GAAAAGCTGCTGCAGAGAAAGTGGACCCCTCTTCTTGAAGCCCGAGCTGCTCTGGGCC	900
QY	1086	CAGCCGGGGAGTGGCCCTTCAAGTATTCGCGCAGCGGTCTCTGCTCCCGCGGATCT	1145
Db	901	CCAGCCGGGGAGTGGCCCTTTCAGTCTATTCGCGCCCGCGGTCTCTGCTCCCGCGGATCT	960
QY	1146	CCACAGCTTCCCCA 1159	
Db	961	CCGAATTTTCCCCA 974	

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 960)
TITLE	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished (2001)
CONTACT	Contact: Genoscope
Genoscope - Centre National de Sequencage	
BP 191 91006 Evry cedex - France	
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr	
Library was constructed by Life Technologies, a division of	
Invitrogen. This sequence belongs to sequence cluster 907.f For	
more information about this cluster, see	
http://www.genoscope.cns.fr/	
cgi-bin/cluster.cgi?seq=CS0BAG009ZD12_CS00860_1&cluster=907.f.	
Contact : Feng liang Email : fliang@lifetech.com URL :	
http://fulllength.invitrogen.com/ invitrogen Corporation 1600	
Faraday Avenue Genoscope sequence ID : CS0BAG009ZD12_CS00860_1.	
Location/Qualifiers	
1. .960	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="CS0DD003FE08"	
/tissue type="NEUROBLASTOMA COT 50-NORMALIZED"	
/clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"	
/note="First strand cDNA was primed with a NotI-oligo(dT)	
primer. Five prime end enriched, double-strand cDNA was	
digested with Not I and cloned into the Not I and EcoR V	
sites of the pCMVSPORT 6 vector. Library was normalized."	
FEATURES	
source	
1629	CCCACCCAGGTCGACGTCTTTGTAGGCTTCTCAGAGGTGTCCTGGAGGTGCCCGGAGCC 1688
10	CCCCACCCAGGTCGACGTCTTTGTAGGCTTCT-AGAGGTGTCCTGGAGGTGCCCGGAGCC 68
1689	AACTGTAGTCTATGACAGCTGTGTGACCTGTGTCTTGGCCGGGACCCCACTGTGCC 1748
69	AACTGTAGTCTATGACAGCTGTGTGACCTGTGTCTTGGCCGGGACCCCACTGTGCC 128
1749	TGGGACCTGAGTCCGAACTGTGTCTCTGTCTGTCTGCCCCCACTGAACTCTGGAAG 1808
129	TGGGACCTGAGTCCGAACTGTGTCTCTGTCTGTCTGCCCCCACTGAACTCTGGAAG 189
1809	CAGGACATGGAGCGGGGAAACCCAGATGGGATGTGCGAGTGGCCCCCATGAGCAGGAGC 1868
189	CAGGACATGGAGCGGGGAAACCCAGATGGGATGTGCGAGTGGCCCCCATGAGCAGGAGC 248
1869	CTTCGGCTCTAGAGCGCGCGCAATCATTAAGAGTCTGTGGCTGCTCCCTTAATCCATC 1928
249	CTTCGGCTCTAGAGCGCGCGCAATCATTAAGAGTCTGTGGCTGCTCCCTTAATCCATC 308
1929	CTGGAGTCTCCCTGCCCCCAGCTGTGAGCTTGGCTCTTATTATTGGAGTCATGGCCCA 1988
309	CTGGAGTCTCCCTGCCCCCAGCTGTGAGCTTGGCTCTTATTATTGGAGTCATGGCCCA 368
1989	GCAGCAGTCCCAAGAGCTCTTCCACTGTCTACATGCTCCCTTTCTGCTGATAGTCAG 2048
369	GCAGCAGTCCCAAGAGCTCTTCCACTGTCTACATGCTCCCTTTCTGCTGATAGTCAG 428
2049	GATGAGTGGGGTCTCTACAGTGGTGGGCACTGAGATGGCTTTTCATACCTCTGTG 2108
429	GATGAGTGGGGTCTCTACAGTGGTGGGCACTGAGATGGCTTTTCATACCTCTGTG 488
2109	ATCTCTCTACTGGGTGGACAGCAGGACGACAGCCCTGGCCCTGGATCTCTGAATGCGAGCC 2168
489	ATCTCTCTACTGGGTGGACAGCAGGACGACAGCCCTGGCCCTGGATCTCTGAATGCGAGCC 548
ORIGIN	
Query Match	23.5%; Score 823.8; DB 13; Length 960;
Best Local Similarity	97.3%; Pred. No. 2.7e-193;
Matches	901; Conservative 0; Mismatches 18; Indels 7; Gaps 6;
QY	1629
DB	10
QY	1689
DB	69
QY	1749
DB	129
QY	1809
DB	189
QY	1869
DB	249
QY	1929
DB	309
QY	1989
DB	369
QY	2049
DB	429
QY	2109
DB	489
QY	2169
DB	549
QY	2229
DB	609
QY	2289
DB	669
QY	2349
DB	729
QY	2406
DB	789
QY	2464
DB	849
QY	2524
DB	908
RESULT 13	
EX112994	
LOCUS	801 bp mRNA linear EST 07-FEB-2003
DEFINITION	EX112994 Soares placenta Nb2HP Homo sapiens cDNA clone
ACCESSION	IMAGE998F02225 ; IMAGE:147841, mRNA sequence.
VERSION	EX112994
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 801)
TITLE	Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
JOURNAL	Human Unigeneset - RZPD3
COMMENT	Unpublished (2003)
Contact: Ina Rolfs	
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany	
RZPD; IMAGE998F02225.	
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;	
Human Unigeneset - RZPD3 (RZPDLIB No.972)	
http://www.rzpd.de/CloneCards/cgi-	
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs	
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	
Heubnerweg 6, D-14059 Berlin, Germany	
Tel: +49 30 32639 101	
Fax: +49 30 32639 111	
www.rzpd.de	
This clone is available royalty-free from RZPD;	
contact RZPD (clone@rzpd.de) for further information. Seq primer:	
ML3r, Primer sequence: TTTCACAGGAAACAGCTATGAC.	
FEATURES	
source	
1. .801	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="IMAGE998F02225 ; IMAGE:147841"	
/sex="Female"	
/dev_stage="placenta obtained at birth (full term)"	
/lab_host="DH10B (ampicillin resistant)"	
/clone_lib="Soares placenta Nb2HP"	

Db 780 CCCCTTGACAGGTCATGGGTGGGCGCGCCTGGCTTGCCCAACAATCCTACTGGCCC 839

Qy 2250 C--ACTTGTCACTGTCACTGTCTCTTT 2276

Db 840 CCACTTGGCCACTGTACTGGCCCCCTT 868

Search completed: April 26, 2004, 01:59:12
Job time : 6369.53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 07:43:48 ; Search time 1024.65 Seconds

(without alignments)
15422.560 Million cell updates/sec

Title: US-10-051-835-13

Perfect score: 3505

Sequence: 1 ggcttgcatgatgggac.....tttgggccaaccaggttg 3505

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3505	100.0	3505	15	US-10-051-835-13
2	3060.8	87.3	3143	10	US-09-946-374-276
3	3060.8	87.3	3143	12	US-10-015-395A-276
4	3060.8	87.3	3143	13	US-10-006-485A-276
5	3060.8	87.3	3143	13	US-10-013-907A-276
6	3060.8	87.3	3143	13	US-10-015-499A-276
7	3060.8	87.3	3143	13	US-10-226-254A-276
8	3060.8	87.3	3143	15	US-10-006-856A-276
9	3060.8	87.3	3143	15	US-10-006-818A-276
10	3060.8	87.3	3143	15	US-10-015-393A-276
11	3060.8	87.3	3143	15	US-10-015-869A-276
12	3060.8	87.3	3143	15	US-10-012-121A-276
13	3060.8	87.3	3143	15	US-10-006-116A-276
14	3060.8	87.3	3143	15	US-10-006-117A-276

15	3060.8	87.3	3143	15	US-10-017-527A-276	Sequence 276, App
16	3060.8	87.3	3143	15	US-10-013-913A-276	Sequence 276, App
17	3060.8	87.3	3143	15	US-10-007-194A-276	Sequence 276, App
18	3060.8	87.3	3143	15	US-10-013-430A-276	Sequence 276, App
19	3060.8	87.3	3143	15	US-10-011-671A-276	Sequence 276, App
20	3060.8	87.3	3143	15	US-10-012-755A-276	Sequence 276, App
21	3060.8	87.3	3143	15	US-10-015-386A-276	Sequence 276, App
22	3060.8	87.3	3143	15	US-10-011-692A-276	Sequence 276, App
23	3060.8	87.3	3143	15	US-10-006-768A-276	Sequence 276, App
24	3060.8	87.3	3143	15	US-10-017-610A-276	Sequence 276, App
25	3060.8	87.3	3143	15	US-10-006-063A-276	Sequence 276, App
26	3060.8	87.3	3143	15	US-10-020-063A-276	Sequence 276, App
27	3060.8	87.3	3143	15	US-10-015-391A-276	Sequence 276, App
28	3060.8	87.3	3143	15	US-10-017-407A-276	Sequence 276, App
29	3060.8	87.3	3143	15	US-10-011-833A-276	Sequence 276, App
30	3060.8	87.3	3143	15	US-10-006-041A-276	Sequence 276, App
31	3060.8	87.3	3143	15	US-10-015-822A-276	Sequence 276, App
32	3060.8	87.3	3143	15	US-10-015-387A-276	Sequence 276, App
33	3060.8	87.3	3143	15	US-10-006-130A-276	Sequence 276, App
34	3060.8	87.3	3143	15	US-10-006-172A-276	Sequence 276, App
35	3060.8	87.3	3143	15	US-10-017-253A-276	Sequence 276, App
36	3060.8	87.3	3143	15	US-10-015-392A-276	Sequence 276, App
37	3060.8	87.3	3143	15	US-10-017-306A-276	Sequence 276, App
38	3060.8	87.3	3143	15	US-10-017-867A-276	Sequence 276, App
39	3060.8	87.3	3143	15	US-10-012-064A-276	Sequence 276, App
40	3060.8	87.3	3143	15	US-10-013-909A-276	Sequence 276, App
41	3060.8	87.3	3143	15	US-10-015-671A-276	Sequence 276, App
42	3060.8	87.3	3143	15	US-10-015-610A-276	Sequence 276, App
43	3060.8	87.3	3143	15	US-10-012-137A-276	Sequence 276, App
44	3060.8	87.3	3143	15	US-10-012-752A-276	Sequence 276, App
45	3060.8	87.3	3143	15	US-10-012-754A-276	Sequence 276, App

ALIGNMENTS

RESULT 1

US-10-051-835-13
; Sequence 13, Application US/10051835
; Publication No. US20030165864A1
; GENERAL INFORMATION:
; APPLICANT: Jones, David A.
; APPLICANT: Jasek, Amy W.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS
; FILE REFERENCE: PA-0044 US
; CURRENT APPLICATION NUMBER: US/10/051,835
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030165864A1 236992.2
US-10-051-835-13

Query Match	100.0%	Score	3505;	DB	15;	Length	3505;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	3505;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	GGCTTTGGCATATGGGACCTTGGAGGGCCGACCTCCCGTTCAGCCAGGCTGAGCCTTC	60				
Db	1	GGCTTTGGCATATGGGACCTTGGAGGGCCGACCTCCCGTTCAGCCAGGCTGAGCCTTC	60				
Qy	61	TGTCCCTCCCTCTGGGGCTGGGAACCCCTCTCTTTCTCTCTGAATGACCCCGG	120				
Db	61	TGTCCCTCCCTCTGGGGCTGGGAACCCCTCTCTTTCTCTCTGAATGACCCCGG	120				
Qy	121	CCTAGATCCAGACCCGAGTTCCACTGTGGCTTCAAGGGTATGTAGAGCTCC	180				
Db	121	CCTAGATCCAGACCCGAGTTCCACTGTGGCTTCAAGGGTATGTAGAGCTCC	180				

Db	2341	GGGGCAAGGTTTCAGGGCTGTGAGACCTTCGCGCCCTGGGGAGAAAGCCCGCTTAAGCAGAG	2400
Qy	2401	AGCAACACCTCCAGTCTCCCAAGGAATCAGGACCTCTGCCAGTGTATGTGACGCTGACA	2460
Db	2401	AGCAACACCTCCAGTCTCCCAAGGAATCAGGACCTCTGCCAGTGTATGTGACGCTGACA	2460
Qy	2461	ACAACTGGCTAGGCACTAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGAG	2520
Db	2461	ACAACTGGCTAGGCACTAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGAG	2520
Qy	2521	GCACCTGGCCATGCTGGCTGGCGCGGCCCAAGCACAGCCCTGACTAGGATGACACAGCAC	2580
Db	2521	GCACCTGGCCATGCTGGCTGGCGCGGCCCAAGCACAGCCCTGACTAGGATGACACAGCAC	2580
Qy	2581	AAAAGACCACTTTCTCCCTTGAGAGGAGCTTTGTCTACTCTGCATCACTGATGACACTC	2640
Db	2581	AAAAGACCACTTTCTCCCTTGAGAGGAGCTTTGTCTACTCTGCATCACTGATGACACTC	2640
Qy	2641	AGCAGGGTGATGCACAGCAGTCTGCCTCCCTATGCGGACTCCCTTCTACCAAGCACATGA	2700
Db	2641	AGCAGGGTGATGCACAGCAGTCTGCCTCCCTATGCGGACTCCCTTCTACCAAGCACATGA	2700
Qy	2701	GCTCTCTAAACAGGGTGGGGCTACCCCCAGACCTGCTCTACACTGATATTGAAGAACCT	2760
Db	2701	GCTCTCTAAACAGGGTGGGGCTACCCCCAGACCTGCTCTACACTGATATTGAAGAACCT	2760
Qy	2761	GGAGAGGATCCTTCAGTTCTGGCCCAATCCAGGGACCTTCAGAAACAACAGTGTTCAGA	2820
Db	2761	GGAGAGGATCCTTCAGTTCTGGCCCAATCCAGGGACCTTCAGAAACAACAGTGTTCAGA	2820
Qy	2821	GACCTTAAAAAACCTGCTGTGCCAGGACCCCTATGTTAAATGAACACCAACATCTAAACA	2880
Db	2821	GACCTTAAAAAACCTGCTGTGCCAGGACCCCTATGTTAAATGAACACCAACATCTAAACA	2880
Qy	2881	ATCATATGCTAACATGCCACTCTCTGGAAATCTCACTCTGAAGCTGCGCTTTGGACACCA	2940
Db	2881	ATCATATGCTAACATGCCACTCTCTGGAAATCTCACTCTGAAGCTGCGCTTTGGACACCA	2940
Qy	2941	ACACTCCCTTCTCCACAGGGTCATGCAGGGATCTCTCCCTCTGCTTCCCTTACCAGTCG	3000
Db	2941	ACACTCCCTTCTCCACAGGGTCATGCAGGGATCTCTCCCTCTGCTTCCCTTACCAGTCG	3000
Qy	3001	TGCACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTTCTGCTTCAG	3060
Db	3001	TGCACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTTCTGCTTCAG	3060
Qy	3061	TTGGGGCAGACTCTGATCCCTTCTGCGCTGSCAGAAATGGCAGAGGTAATCTGAGCCTTCT	3120
Db	3061	TTGGGGCAGACTCTGATCCCTTCTGCGCTGSCAGAAATGGCAGAGGTAATCTGAGCCTTCT	3120
Qy	3121	TCATCTCTTTACCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCTTTGTTGGG	3180
Db	3121	TCATCTCTTTACCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCTTTGTTGGG	3180
Qy	3181	ATTTCAGAAATCTGCTGTCAGAGACTCTTATTTTATTTTAAATAAAGGCTTATGTA	3240
Db	3181	ATTTCAGAAATCTGCTGTCAGAGACTCTTATTTTATTTTAAATAAAGGCTTATGTA	3240
Qy	3241	TGATGGGTGCTGTTTGTCTGGACAGAGTGCCTCCGCGACAGAAATGCTGGGATGTCAAG	3300
Db	3241	TGATGGGTGCTGTTTGTCTGGACAGAGTGCCTCCGCGACAGAAATGCTGGGATGTCAAG	3300
Qy	3301	GGACACAGCAGTCCAAGCAATCAAGTTGGAGAGGACTAGGTTTGTGGGGGATTTGTTTC	3360
Db	3301	GGACACAGCAGTCCAAGCAATCAAGTTGGAGAGGACTAGGTTTGTGGGGGATTTGTTTC	3360
Qy	3361	TCTCCAACTCCAGACTACCTCTCTGCGCTGCGCAGCTCCCAACCAAGAACCCACCC	3420
Db	3361	TCTCCAACTCCAGACTACCTCTCTGCGCTGCGCAGCTCCCAACCAAGAACCCACCC	3420
Qy	3421	AGAAACAGCCACAGCACTTCTCTCACTCTGAGCAATGCTAGAGGGTGTCTGCAAACTTT	3480

Db 3421 AGAACGAGCCGACAGCACTTCTCCACTGTAGAGGTGCTGCAAACTTT 3505

Qy 3481 TGCCTTTTGGGCCCAACACAGGTTG 3505
|||||

Db 3481 TGCCTTTTGGGCCCAACACAGGTTG 3505

RESULT 2

US-09-946-374-276

; Sequence 276, Application US/09946374

; Publication No. US20030073129A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2830PlCl

; CURRENT APPLICATION NUMBER: US/09/946,374

; CURRENT FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098803

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098821

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098843

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/099536

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099596

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099598

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099602

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099642

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099741

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099754

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099763

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099792

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099808

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099812

; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099815
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099816
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/100385
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100388
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100390
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100584
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100627
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100661
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100662
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100664
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100683
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100684
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100710
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100711
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100848
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/100849
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/100919
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/100930
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/101014
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/101068
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/101071
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/101279
 ; PRIOR FILING DATE: 1998-09-22
 ; PRIOR APPLICATION NUMBER: 60/101471
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101472
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101474
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101475
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101476
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101477
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101479
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101738
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101741
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101743
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101915
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101916
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/102207
 ; PRIOR FILING DATE: 1998-09-25
 ; PRIOR APPLICATION NUMBER: 60/102240
 ; PRIOR FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: 60/102307
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 60/102330
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 60/102331
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 60/102484
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: 60/102487
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: 60/102570
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: 60/102571
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: 60/102684
 ; PRIOR FILING DATE: 1998-10-01
 ; PRIOR APPLICATION NUMBER: 60/102687
 ; PRIOR FILING DATE: 1998-10-01
 ; PRIOR APPLICATION NUMBER: 60/102965
 ; PRIOR FILING DATE: 1998-10-02
 ; PRIOR APPLICATION NUMBER: 60/103258
 ; PRIOR FILING DATE: 1998-10-06
 ; PRIOR APPLICATION NUMBER: 60/103314
 ; PRIOR FILING DATE: 1998-10-07
 ; PRIOR APPLICATION NUMBER: 60/103315
 ; PRIOR FILING DATE: 1998-10-07
 ; PRIOR APPLICATION NUMBER: 60/103328
 ; PRIOR FILING DATE: 1998-10-07
 ; PRIOR APPLICATION NUMBER: 60/103395
 ; PRIOR FILING DATE: 1998-10-07
 ; PRIOR APPLICATION NUMBER: 60/103396
 ; PRIOR FILING DATE: 1998-10-07
 ; PRIOR APPLICATION NUMBER: 60/103401
 ; PRIOR FILING DATE: 1998-10-07
 ; PRIOR APPLICATION NUMBER: 60/103449
 ; PRIOR FILING DATE: 1998-10-06
 ; PRIOR APPLICATION NUMBER: 60/103633
 ; PRIOR FILING DATE: 1998-10-08
 ; PRIOR APPLICATION NUMBER: 60/103678
 ; PRIOR FILING DATE: 1998-10-08
 ; PRIOR APPLICATION NUMBER: 60/103679
 ; PRIOR FILING DATE: 1998-10-08
 ; PRIOR APPLICATION NUMBER: 60/103711
 ; PRIOR FILING DATE: 1998-10-08
 ; PRIOR APPLICATION NUMBER: 60/104257
 ; PRIOR FILING DATE: 1998-10-14
 ; PRIOR APPLICATION NUMBER: 60/104987
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/105000
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/105002
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/105104
 ; PRIOR FILING DATE: 1998-10-21
 ; PRIOR APPLICATION NUMBER: 60/105169
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: 60/105266
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: 60/105693
 ; PRIOR FILING DATE: 1998-10-26
 ; PRIOR APPLICATION NUMBER: 60/105694
 ; PRIOR FILING DATE: 1998-10-26
 ; PRIOR APPLICATION NUMBER: 60/105807

Query Match 87.3%; Score 3060.8; DB 10; Length 3143;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 173 AGAGCTCCCTGGTGCACGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 232
 Db 74 AGAGCTCCCTGGTGCACGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 133
 Qy 233 CTGGAGCCTCTGGGCCCTTTCTCTTCCAACTGCTTCAGCTGTGCTGCGGACGAC 292

134 CTGAGCCCTCTGGCCCTTTCTCTTCCAACTGCTTCAGCTGTGCTGCCAGCGAC 193
193
293 CGCGGGGAGCGCGGGCAGGGGCCCATGCCAGAGGTGAGATATGTCAGGGGATGAACG 352
194 CGCGGGGAGCGCGGGCAGGGGCCCATGCCAGAGGTGAGATATGTCAGGGGATGAACG 253
353 TAGGCACTTAGCTTCTTCCACCAAGAGGGGCTCCAGGATTTGACACTCTGCTCCTGAG 412
254 TAGGCACTTAGCTTCTTCCACCAAGAGGGGCTCCAGGATTTGACACTCTGCTCCTGAG 313
413 TGGTGATGGAATACTCTCTAGCTGGGGCTCGAGAGCCCATTTGCGCTTGGATATCCA 472
314 TGGTGATGGAATACTCTCTAGCTGGGGCTCGAGAGCCCATTTGCGCTTGGATATCCA 373
473 GGATCCAGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGAAGAAAAA 532
374 GGATCCAGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGAAGAAAAA 433
533 GAGTGAATGTCCTTTAAGAGAGAGAGCAATGAGACACAGTGTTCAACTTCATCGGTGT 592
434 GAGTGAATGTCCTTTAAGAGAGAGAGCAATGAGACACAGTGTTCAACTTCATCGGTGT 493
593 CCTGGTCTTTACAAATGTCACCACTCTCAACCTCGGGCACCCTTCGCCCTTCAGCCCTGC 652
494 CCTGGTCTTTACAAATGTCACCACTCTCAACCTCGGGCACCCTTCGCCCTTCAGCCCTGC 553
653 TTGTACCTTCATTTGAATTCAGATTCCTACTGTTGCCATCTCGAGAGCAAGTTCAT 712
554 TTGTACCTTCATTTGAATTCAGATTCCTACTGTTGCCATCTCGAGAGCAAGTTCAT 613
713 GGAGGAAAAAGGCCCAAGCCCTTTGACCCCGCTCAAGACATACCGCTGTCTTGGTGA 772
614 GGAGGAAAAAGGCCCAAGCCCTTTGACCCCGCTCAAGACATACCGCTGTCTTGGTGA 673
773 TGGATGCTCTATTCTGTGTACTATGAACATTCCTGGGCACTGAGCCCATCTGTATGCG 832
674 TGGATGCTCTATTCTGTGTACTATGAACATTCCTGGGCACTGAGCCCATCTGTATGCG 733
833 CACACTGGATCCCAAGCCCTGTCTCAAGACCGCAACTTCTCGCGTGGCTGATCATGA 892
734 CACACTGGATCCCAAGCCCTGTCTCAAGACCGCAACTTCTCGCGTGGCTGATCATGA 793
893 CGCTCTCTTTGTGGAGCCATCTTCAAGCCAGCTGTCTACTCTTCTTCGAGGAGAC 952
794 CGCTCTCTTTGTGGAGCCATCTTCAAGCCAGCTGTCTACTCTTCTTCGAGGAGAC 853
953 AGCCAGCGAGTTTCACTTTCTTGAGAGCTCCACACATCGGGTGGCTAGAGTCTGCAA 1012
854 AGCCAGCGAGTTTCACTTTCTTGAGAGCTCCACACATCGGGTGGCTAGAGTCTGCAA 913
1013 GAATGAAGTGGCGCGGAAAGCTGCTGCAAGAAAGTGAACCACTTCTGAGGCCCCA 1072
914 GAATGAAGTGGCGCGGAAAGCTGCTGCAAGAAAGTGAACCACTTCTGAGGCCCCA 973
1073 GCTGCTGACACCGAGCGGGGAGCTGCCCTTCAAGCTCATCCGCCAGCGGCTCTGCT 1132
974 GCTGCTGACACCGAGCGGGGAGCTGCCCTTCAAGCTCATCCGCCAGCGGCTCTGCT 1033
1133 CCCCAGGATTTCTCCACAGTCCCCCATCTAGCAGTCTTCACTCCAGTGGCAGGT 1192
1034 CCCCAGGATTTCTCCACAGTCCCCCATCTAGCAGTCTTCACTCCAGTGGCAGGT 1093
1193 TGGCGGACACGAGGCTCTGGGTTTGTGCTTCTCTCTTGGACATTTGAAGTGTCTT 1252
1094 TGGCGGACACGAGGCTCTGGGTTTGTGCTTCTCTCTTGGACATTTGAAGTGTCTT 1153
1253 TAAGGGAAATACAAAGAGTTGAACAAAGAACTTCAAGTGGACTTATAGGGGCC 1312
1154 TAAGGGAAATACAAAGAGTTGAACAAAGAACTTCAAGTGGACTTATAGGGGCC 1213
1313 TGAGACCAACCCCGGCGAGGCTGCTAGTGGGCCCTCTCTGATTAAGGCCCTGAC 1372

1214 TGAGACCAACCCCGCCAGGAGTGTCTAGTGGGCCCTCTCTCTGATAGAAGCCCTGAC 1273
1373 CTTTCAATGAAGGACCATTTCTCTGATGAGCAAGTGTGTGGGACGCCCTCTCTGTGAA 1432
1274 CTTTCAATGAAGGACCATTTCTCTGATGAGCAAGTGTGTGGGACGCCCTCTCTGTGAA 1333
1433 ATCTGGCTGGAGTATACACGGCTTTCAGTGGAGACGCCAGGGCCTTTGATGGGACAG 1492
1334 ATCTGGCTGGAGTATACACGGCTTTCAGTGGAGACGCCAGGGCCTTTGATGGGACAG 1393
1493 CATCTTGTTCATGTAACCTGGGAACACACAGGGTGCCTCCACAGAGTGTGTAGTGG 1552
1394 CATCTTGTTCATGTAACCTGGGAACACACAGGGTGCCTCCACAGAGTGTGTAGTGG 1453
1553 GGACAGCAGTGTCTATCTGTTGGAAGAGATTGAGTGTTCCTGACCCCTGAACTTTTGG 1612
1454 GGACAGCAGTGTCTATCTGTTGGAAGAGATTGAGTGTTCCTGACCCCTGAACTTTTGG 1513
1613 CAACCTGAGCTGGGCCCCACCCAGGGTGCAGTGTTCAGGCTTCTCAGAGGTGTCTG 1672
1514 CAACCTGAGCTGGGCCCCACCCAGGGTGCAGTGTTCAGGCTTCTCAGAGGTGTCTG 1573
1673 GAGGCTGCCCGAGGCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1732
1574 GAGGCTGCCCGAGGCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1633
1733 GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTTCGCTCTCTGTGCCCCAA 1792
1634 GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTTCGCTCTCTGTGCCCCAA 1693
1793 CTGAACTCTCTGGAGCAGGACATGGAGCGGGGAAACAGAGTGGGATGTGCGCAGTGG 1852
1694 CTGAACTCTCTGGAGCAGGACATGGAGCGGGGAAACAGAGTGGGATGTGCGCAGTGG 1753
1853 CCGATGAGCAGGAGCTTTCGCTCAGAGCGCGCCGCAAAATCATTAAGAAAGTCTCTGGC 1912
1754 CCGCATGAGCAGGAGCTTTCGCTCAGAGCGCGCCGCAAAATCATTAAGAAAGTCTCTGGC 1813
1913 TGTCCCTAACTCCATCTCTGGAGCTCCCTGCCCCCACTGTGAGCTTGTGCTCTTATTA 1972
1814 TGTCCCTAACTCCATCTCTGGAGCTCCCTGCCCCCACTGTGAGCTTGTGCTCTTATTA 1873
1973 TTGGATGATGCGCCAGCAGAGTCCAGAGAGCTTCTTCCACTGTCTCAATAGGCTCCCT 2032
1874 TTGGATGATGCGCCAGCAGAGTCCAGAGAGCTTCTTCCACTGTCTCAATAGGCTCCCT 1933
2033 CTTGTGTATGTCAGGATGGAGTTGGGGTCTCTACAGTGTGCGCAACTGAGAAAGG 2092
1934 CTTGTGTATGTCAGGATGGAGTTGGGGTCTCTACAGTGTGCGCAACTGAGAAAGG 1993
2093 CTTTTCATACCTGTGATCTCTACTGGGTGAGACAGCCAGGACCCCTTGGCCCTGGA 2152
1994 CTTTTCATACCTGTGATCTCTACTGGGTGAGACAGCCAGGACCCCTTGGCCCTGGA 2053
2153 TCCTGAATGGCAGGACATCCCGGGGAGCATGTGAAGTCCGCTGACACGGGTGAGTGG 2212
2054 TCCTGAATGGCAGGACATCCCGGGGAGCATGTGAAGTCCGCTGACACGGGTGAGTGG 2113
2213 TGGGCGCGCTTGGCTGCGCCAGCAGTCTCTACTGCGCCCACTTTTGTCACTGTCTCT 2272
2114 TGGGCGCGCTTGGCTGCGCCAGCAGTCTCTACTGCGCCCACTTTTGTCACTGTCTCT 2173
2273 CTTTGGCTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGCTGGCTTCCCATTTAGAGCACT 2332
2174 CTTTGGCTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGCTGGCTTCCCATTTAGAGCACT 2233
2333 CGGGCTCGGGCAAGTTCAGGGGTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCTT 2392
2234 CGGGCTCGGGCAAGTTCAGGGGTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCTT 2293
2393 AAGCAGAGAGCAACCTCTCAGTCTCCCAAGGAATGAGGACCTTGTGCGAGTGTGGA 2452
2294 AAGCAGAGAGCAACCTCTCAGTCTCCCAAGGAATGAGGACCTTGTGCGAGTGTGGA 2353

Qy	2453	CGCTGACAAACAACCTGCCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGCCCGGGCGTG	2512
Db	2354	CGCTGACAAACAACCTGCCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGCCCGGGCGTG	2413
Qy	2513	CGGTGCAGGCACCTGGCCATCTGGCTGGGGGGCCCAAGCAACGCCCTGACTAGGATGAC	2572
Db	2414	CGGTGCAGGCACCTGGCCATCTGGCTGGGGGGCCCAAGCAACGCCCTGACTAGGATGAC	2473
Qy	2573	AGCAGCAAAAAGAACCACTTCTCCCTCGAGAGGAGCTTCTGCTACTCTGTGCATCACTGA	2632
Db	2474	AGCAGCAAAAAGAACCACTTCTCCCTCGAGAGGAGCTTCTGCTACTCTGTGCATCACTGA	2533
Qy	2633	TGACACTCAGCAGGGTGATGACAGCAGTCTGCTCCCTGATAGGAGCTCCCTTCTACCAA	2692
Db	2534	TGACACTCAGCAGGGTGATGACAGCAGTCTGCTCCCTGATAGGAGCTCCCTTCTACCAA	2593
Qy	2693	GCACATGAGCTCTCTAAACAGGGTGGGGGTACCCCCAGAGCTGCTCCTACACTGATATTG	2752
Db	2594	GCACATGAGCTCTCTAAACAGGGTGGGGGTACCCCCAGAGCTGCTCCTACACTGATATTG	2653
Qy	2753	AAGAACTCGAGAGGATCCCTTCACTCTGGCCATTCCAGGAGCCCTCCAGAAACACAGTG	2812
Db	2654	AAGAACTCGAGAGGATCCCTTCACTCTGGCCATTCCAGGAGCCCTCCAGAAACACAGTG	2713
Qy	2813	TTTTCAAGAGACCCCTAAAACCTTGCCTGCTCCAGAGCCCTATGGTAATGAACCAACA	2872
Db	2714	TTTTCAAGAGACCCCTAAAACCTTGCCTGCTCCAGAGCCCTATGGTAATGAACCAACA	2773
Qy	2873	TCTAAAACAATCATATGCTAAATGCCACTCTCTGAAACTCCACTCTGAAGCTGCGGTTT	2932
Db	2774	TCTAAAACAATCATATGCTAAATGCCACTCTCTGAAACTCCACTCTGAAGCTGCGGTTT	2833
Qy	2933	GGACACAAACATCCCTTCTCCAGGTCATGACAGGATCTGTCCCTCTGTCTCCCTT	2992
Db	2834	GGACACAAACATCCCTTCTCCAGGTCATGACAGGATCTGTCCCTCTGTCTCCCTT	2893
Qy	2993	ACGAGTCGTGCACGGCTGACTCCAGAGACTCTCCCTGAAAGCTGACACACCTTCTCT	3052
Db	2894	ACGAGTCGTGCACGGCTGACTCCAGAGACTCTCCCTGAAAGCTGACACACCTTCTCT	2953
Qy	3053	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGTAATCTG	3112
Db	2954	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGTAATCTG	3013
Qy	3113	AGCCTTCTTCACTGCTTTAGCTAGTGAACCTTCACTCTCCCTCTCCCTTCTCCCTT	3172
Db	3014	AGCCTTCTTCACTGCTTTAGCTAGTGAACCTTCACTCTCCCTCTCCCTTCTCCCTT	3073
Qy	3173	GTTTTGGGATTGAGAAACCTGTTTGTGACAGAGCTGTTTATTTTATTAATAATAAAGG	3232
Db	3074	GTTTTGGGATTGAGAAACCTGTTTGTGACAGAGCTGTTTATTTTATTAATAATAAAGG	3133
Qy	3233	CTTA 3236	
Db	3134	CTTA 3137	

RESULT 3
US-10-015-395A-276
; Sequence 276, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

QY 953 AGCCAGCAGTTTGACTCTTTGAGAGCTCCACACATCGCGGTGGCTAGAGTCTGCAA 1012
DB 854 AGCCAGCAGTTTGACTCTTTGAGAGCTCCACACATCGCGGTGGCTAGAGTCTGCAA 913
QY 1013 GAATGACTGGCGCGCGGCGGAGAGTCTGCGAGAGAGTGGACCACTTCTCTGAAGGCCA 1072
DB 914 GAATGACTGGCGCGCGGCGGAGAGTCTGCGAGAGAGTGGACCACTTCTCTGAAGGCCA 973
QY 1073 GCTGCTCTGCAACCGCGGCGGAGCTGCCCTTCAAGTCAATCGCGGCTGCTGCT 1132
DB 974 GCTGCTCTGCAACCGCGGCGGAGCTGCCCTTCAAGTCAATCGCGGCTGCTGCT 1033
QY 1133 CCGCGCGGAGTCTCCCAAGCTCCCAATCTAGCGAGTCTTCACTCCCAAGTGGCAGGT 1192
DB 1034 CCGCGCGGAGTCTCCCAAGCTCCCAATCTAGCGAGTCTTCACTCCCAAGTGGCAGGT 1093
QY 1193 TGGCGGAGCAGGAGCTCTGCGGTTTGGCTTCTCTCTCTTGGACATTTGAAGTGTCTT 1252
DB 1094 TGGCGGAGCAGGAGCTCTGCGGTTTGGCTTCTCTCTCTTGGACATTTGAAGTGTCTT 1153
QY 1253 TAAGGGGAAATACAAAGAGTTGAAACAAAGAACTTCAAGTGGAGTACTTATAGGGGCC 1312
DB 1154 TAAGGGGAAATACAAAGAGTTGAAACAAAGAACTTCAAGTGGAGTACTTATAGGGGCC 1213
QY 1313 TGAGACCAACCCCGCGGCGGAGAGTCTGCTAGTGGGCCCTCTCTGATTAAGGCCCTGAC 1372
DB 1214 TGAGACCAACCCCGCGGCGGAGAGTCTGCTAGTGGGCCCTCTCTGATTAAGGCCCTGAC 1273
QY 1373 CTTATGAAGGACCAATTTCTGATGGATGAGCAAGTGGTGGGAGCGCCCTCTGCTGTGAA 1432
DB 1274 CTTATGAAGGACCAATTTCTGATGGATGAGCAAGTGGTGGGAGCGCCCTCTGCTGTGAA 1333
QY 1433 ATCTGGCGTGGAGTATACACGGCTTGGAGTGGAGAGCAGCCAGCGCTTGAAGGGACAG 1492
DB 1334 ATCTGGCGTGGAGTATACACGGCTTGGAGTGGAGAGCAGCCAGCGCTTGAAGGGACAG 1393
QY 1493 CCATCTGTCATGTACCTGGGAAACACCAAGAGTGGCTCCACAGGCTGGTGGTAACTGG 1552
DB 1394 CCATCTGTCATGTACCTGGGAAACACCAAGAGTGGCTCCACAGGCTGGTGGTAACTGG 1453
QY 1553 GGACAGCAGTCTCATCTGTGTGGAGAGATTCAGCTGTTCCTGACCTGAACCTGTTCG 1612
DB 1454 GGACAGCAGTCTCATCTGTGTGGAGAGATTCAGCTGTTCCTGACCTGAACCTGTTCG 1513
QY 1613 CAACCTGAGCTGGCCCCCAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1672
DB 1514 CAACCTGAGCTGGCCCCCAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1573
QY 1673 GAGGTGGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGAGTGTGTCTTGGCCG 1732
DB 1574 GAGGTGGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGAGTGTGTCTTGGCCG 1633
QY 1733 GGACCCCACTGTGCTGGGAGCTTGAAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1792
DB 1634 GGACCCCACTGTGCTGGGAGCTTGAAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1693
QY 1793 CCGTAACTCTCGGAGCAGGAGCATGGAGCGGGGAAACCCAGAGTGGGAGTGGCAGTGG 1852
DB 1694 CCGTAACTCTCGGAGCAGGAGCATGGAGCGGGGAAACCCAGAGTGGGAGTGGCAGTGG 1753
QY 1853 CCCATGAGCAGGAGCTTGGCTCTAGAGCGCGCGGCAAAATCAATTAAGAGTCTTGGC 1912
DB 1754 CCCATGAGCAGGAGCTTGGCTCTAGAGCGCGCGGCAAAATCAATTAAGAGTCTTGGC 1813
QY 1913 TGTCCCTAACTCCATCTCGGAGCTCCCTGCGCCCACTGTGAGCTTGGCTCTTATTA 1972
DB 1814 TGTCCCACTCCATCTCGGAGCTCCCTGCGCCCACTGTGAGCTTGGCTCTTATTA 1873
QY 1973 TTGAGTCAATGGCCAGCAGAGTCTTCCAGAGCTCTTCCAGTGTCTACAAATGCTCCCT 2032
DB 1874 TTGAGTCAATGGCCAGCAGAGTCTTCCAGAGCTCTTCCAGTGTCTACAAATGCTCCCT 1933
QY 2033 CTTGCTGATGTGAGGATGGATTGGGGTCTCTACAGTGGCTGGGCAACTGAGAGTGG 2092

DB 1934 CTTGCTGATGTGAGGATGGATTGGGGTCTCTACAGTCTCTGGGCACTGAGATGG 1993
QY 2093 CTTTTCATACCTGTGATCTCTACTTGGGTGACAGCCAGGACAGACCTTGGCCCTGGA 2152
DB 1994 CTTTTCATACCTGTGATCTCTACTTGGGTGACAGCCAGGACAGACCTTGGCCCTGGA 2053
QY 2153 TCTGAACTGGCAGGACATCCCCGGGAGCATGTGAAGTTCGGTTGACACAGAGTCAAGTGG 2212
DB 2054 TCTGAACTGGCAGGATCCCCGGGAGCATGTGAAGTTCGGTTGACACAGAGTCAAGTGG 2113
QY 2213 TGGGCGCGCTTGGCTGCGGAGCAGTCTTACTTGGGCCCACTTTTGTCACTGTCTCT 2272
DB 2114 TGGGCGCGCTTGGCTGCGGAGCAGTCTTACTTGGGCCCACTTTTGTCACTGTCTCT 2173
QY 2273 CTTTGGCTTAGTGTCTTTCAGGAGCCTCATCATCTCTGTTGGCTCCCACTTGGAGCAGT 2332
DB 2174 CTTTGGCTTAGTGTCTTTCAGGAGCCTCATCATCTCTGTTGGCTCCCACTTGGAGCAGT 2233
QY 2333 CCGGGCTCGGGCAAGGTTTCAGGGCTGTGAGACCTTGGCCCTGGGGAGAGGCCCGTT 2392
DB 2234 CCGGGCTCGGGCAAGGTTTCAGGGCTGTGAGACCTTGGCCCTGGGGAGAGGCCCGTT 2293
QY 2393 AAGCAGAGAGCAACCTTCCAGTCTCCAAAGAAATGACAGGACCTTGGCCAGTGTGGA 2452
DB 2294 AAGCAGAGAGCAACCTTCCAGTCTCCAAAGAAATGACAGGACCTTGGCCAGTGTGGA 2353
QY 2453 CGCTGACAACTGCTAGGACCTGAGTGTCTTAACTCTAGGCACAGGCGGGGCTG 2512
DB 2354 CGCTGACAACTGCTAGGACCTGAGTGTCTTAACTCTAGGCACAGGCGGGGCTG 2413
QY 2513 CGGTGAGCAGCTGGCCATGCTGGCTGGGGCCCAAGCAGCAGCCTGACTAGGATGAC 2572
DB 2414 CGGTGAGCAGCTGGCCATGCTGGCTGGGGCCCAAGCAGCAGCCTGACTAGGATGAC 2473
QY 2573 AGCAGCAGCAAAAGACCACTTCTCCCTGAGAGAGCTTCTGTACTCTGACTCACTGA 2632
DB 2474 AGCAGCAGCAAAAGACCACTTCTCCCTGAGAGAGGCTTCTGTACTCTGACTCACTGA 2533
QY 2633 TGAACCTGAGAGGAGTGTGACAGAGTCTGCTTCCCTTATGGAGTCTCCCTTCTACCAA 2692
DB 2534 TGAACCTGAGAGGAGTGTGACAGAGTCTGCTTCCCTTATGGAGTCTCCCTTCTACCAA 2593
QY 2693 GCACATGAGCTCTTAAACAGGAGTGGGGCTACCCCGAGAGCTCTCTTACATGATATG 2752
DB 2594 GCACATGAGCTCTTAAACAGGAGTGGGGCTACCCCGAGAGCTCTCTTACATGATATG 2653
QY 2753 AAGAACCTGAGAGGATCTTCAAGTCTGGCCATTCAGGGACCTTCCAGGAGACCTTCCAGAGAAACAGAGT 2812
DB 2654 AAGAACCTGAGAGGATCTTCAAGTCTGGCCATTCAGGGACCTTCCAGGAGACCTTCCAGAGAAACAGAGT 2713
QY 2813 TTTCAAGAGACCTTAAAGACCTTGGCTGTCAGAGGACCTTATGTAATGAACACCAACA 2872
DB 2714 TTTCAAGAGACCTTAAAGACCTTGGCTGTCAGAGGACCTTATGTAATGAACACCAACA 2773
QY 2873 TCTTAAACATCATATGTCTAACTGCACTCTCTGGAACCTTCCACTCTGAGAGTGGCGCTT 2932
DB 2774 TCTTAAACATCATATGTCTAACTGCACTCTCTGGAACCTTCCACTCTGAGAGTGGCGCTT 2833
QY 2933 GGACACCACTCTCCCTTCTCCAGGATCATGAGGATCTGCTCCCTCTCTCTTCCCTT 2992
DB 2834 GGACACCACTCTCCCTTCTCCAGGATCATGAGGATCTGCTCCCTCTCTCTTCCCTT 2893
QY 2993 ACCAGTCTGTCAGCTCCCAAGAGTCTTCCCTGAACTCTGACACCACTTCTCTTCT 3052
DB 2894 ACCAGTCTGTCAGCTCCCAAGAGTCTTCCCTGAACTCTTCTGAACTCTGACCACTTCTCT 2953
QY 3053 TGGCTTGGGCGAGCTCTGATCCCTTCTGCGCTTGGCAGAAATGGGAGGGGTAACTG 3112
DB 2954 TGGCTTGGGCGAGCTCTGATCCCTTCTGCGCTTGGCAGAAATGGGAGGGGTAACTG 3013
QY 3113 AGCCTTCTTCACTCTTCTTACCTTGTGACCTCTTCCCTCTCTCTCTCTCTCTTCTT 3172

Db	3014	AGCTTCTTCACTCTTTTACCTAGCTGACCCCTTGCACCTCTGCCCTCCCTTCCCTTT	3073
Qy	3173	GTTTGGGATTCAGAAACTGCTGTGCAGAGACTGTTATTTTTTATTTAAAAATATAAGG	3232
Db	3074	GTTTGGGATTCAGAAACTGCTGTGCAGAGACTGTTATTTTTTATTTAAAAATATAAGG	3133
Qy	3233	CTTA 3236	
Db	3134	CTTA 3137	
RESULT 4			
US-10-006-485A-276			
Sequence 276, Application US/10006485A			
Publication No. US20030064062A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Desnoyers, Luc			
APPLICANT: Eaton, Dan I.			
APPLICANT: Ferrara, Napoleone			
APPLICANT: Fong, Sherman			
APPLICANT: Gao, Wei-Qiang			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Grimaldi, Christopher J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Hillan, Kenneth J.			
APPLICANT: Pan, James			
APPLICANT: Pacini, Nicholas F.			
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
TITLE OF INVENTION: Acids Encoding the Same			
FILE REFERENCE: P2830P1C9			
CURRENT APPLICATION NUMBER: US/10/006,485A			
CURRENT FILING DATE: 2001-12-06			
PRIOR APPLICATION NUMBER: 60/098716			
PRIOR FILING DATE: 1998-09-01			
PRIOR APPLICATION NUMBER: 60/098723			
PRIOR FILING DATE: 1998-09-01			
PRIOR APPLICATION NUMBER: 60/098749			
PRIOR FILING DATE: 1998-09-01			
PRIOR APPLICATION NUMBER: 60/098750			
PRIOR FILING DATE: 1998-09-01			
PRIOR APPLICATION NUMBER: 60/098803			
PRIOR FILING DATE: 1998-09-02			
PRIOR APPLICATION NUMBER: 60/098821			
PRIOR FILING DATE: 1998-09-02			
PRIOR APPLICATION NUMBER: 60/098843			
PRIOR FILING DATE: 1998-09-02			
PRIOR APPLICATION NUMBER: 60/099536			
PRIOR FILING DATE: 1998-09-09			
PRIOR APPLICATION NUMBER: 60/099596			
PRIOR FILING DATE: 1998-09-09			
PRIOR APPLICATION NUMBER: 60/099598			
PRIOR FILING DATE: 1998-09-09			
PRIOR APPLICATION NUMBER: 60/099602			
PRIOR FILING DATE: 1998-09-09			
PRIOR APPLICATION NUMBER: 60/099642			
PRIOR FILING DATE: 1998-09-09			
PRIOR APPLICATION NUMBER: 60/099741			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: 60/099754			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: 60/099763			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: 60/099792			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: 60/099808			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: 60/099812			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: 60/099815			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: 60/100388			
PRIOR FILING DATE: 1998-09-15			
PRIOR APPLICATION NUMBER: 60/100390			
PRIOR FILING DATE: 1998-09-15			
PRIOR APPLICATION NUMBER: 60/100584			
PRIOR FILING DATE: 1998-09-16			
PRIOR APPLICATION NUMBER: 60/100627			
PRIOR FILING DATE: 1998-09-16			
PRIOR APPLICATION NUMBER: 60/100661			
PRIOR FILING DATE: 1998-09-16			
PRIOR APPLICATION NUMBER: 60/100662			
PRIOR FILING DATE: 1998-09-16			
PRIOR APPLICATION NUMBER: 60/100664			
PRIOR FILING DATE: 1998-09-16			
PRIOR APPLICATION NUMBER: 60/100683			
PRIOR FILING DATE: 1998-09-17			
PRIOR APPLICATION NUMBER: 60/100684			
PRIOR FILING DATE: 1998-09-17			
PRIOR APPLICATION NUMBER: 60/100710			
PRIOR FILING DATE: 1998-09-17			
PRIOR APPLICATION NUMBER: 60/100711			
PRIOR FILING DATE: 1998-09-17			
PRIOR APPLICATION NUMBER: 60/100848			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: 60/100849			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: 60/100919			
PRIOR FILING DATE: 1998-09-17			
PRIOR APPLICATION NUMBER: 60/100930			
PRIOR FILING DATE: 1998-09-17			
PRIOR APPLICATION NUMBER: 60/101014			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: 60/101068			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: 60/101071			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: 60/101279			
PRIOR FILING DATE: 1998-09-22			
PRIOR APPLICATION NUMBER: 60/101471			
PRIOR FILING DATE: 1998-09-23			
PRIOR APPLICATION NUMBER: 60/101472			
PRIOR FILING DATE: 1998-09-23			
PRIOR APPLICATION NUMBER: 60/101474			
PRIOR FILING DATE: 1998-09-23			
PRIOR APPLICATION NUMBER: 60/101475			
PRIOR FILING DATE: 1998-09-23			
PRIOR APPLICATION NUMBER: 60/101476			
PRIOR FILING DATE: 1998-09-23			
PRIOR APPLICATION NUMBER: 60/101477			
PRIOR FILING DATE: 1998-09-23			
PRIOR APPLICATION NUMBER: 60/101479			
PRIOR FILING DATE: 1998-09-23			
PRIOR APPLICATION NUMBER: 60/101738			
PRIOR FILING DATE: 1998-09-24			
PRIOR APPLICATION NUMBER: 60/101741			
PRIOR FILING DATE: 1998-09-24			
PRIOR APPLICATION NUMBER: 60/101743			
PRIOR FILING DATE: 1998-09-24			
PRIOR APPLICATION NUMBER: 60/101915			
PRIOR FILING DATE: 1998-09-24			
PRIOR APPLICATION NUMBER: 60/101916			
PRIOR FILING DATE: 1998-09-24			
PRIOR APPLICATION NUMBER: 60/102207			
PRIOR FILING DATE: 1998-09-29			
PRIOR APPLICATION NUMBER: 60/102240			
PRIOR FILING DATE: 1998-09-29			
PRIOR APPLICATION NUMBER: 60/102307			
PRIOR FILING DATE: 1998-09-29			
PRIOR APPLICATION NUMBER: 60/102330			
PRIOR FILING DATE: 1998-09			

Db 1154 TAAGGGGAATACAAAGAGTTGAACAAAGAAATTCACGCTGGACTACTTTATAGGGGCC 1213
Qy 1313 TGAGACCAACCCCGGCCAGGAGTTGCTCAGTGGGCCCTCTCTGTGAAGGCCCTGAC 1372
Db 1214 TGAGACCAACCCCGGCCAGGAGTTGCTCAGTGGGCCCTCTCTGTGAAGGCCCTGAC 1273
Qy 1373 CTTCAATGAAGACCATTTCTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGTGAA 1432
Db 1274 CTTCAATGAAGACCATTTCTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGTGAA 1333
Qy 1433 ATCTGGCGTGGAGTATACAGGCTTGCACTGGAGACAGCCAGGCCCTGTGATGGGACAG 1492
Db 1334 ATCTGGCGTGGAGTATACAGGCTTGCACTGGAGACAGCCAGGCCCTGTGATGGGACAG 1393
Qy 1493 CCATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1552
Db 1394 CCATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1453
Qy 1553 GGACAGAGTGTCTCATCTGGTGGAGAGATTCAGTGTTCCTTGACCCCTGAACCTGTTGG 1612
Db 1454 GGACAGAGTGTCTCATCTGGTGGAGAGATTCAGTGTTCCTTGACCCCTGAACCTGTTGG 1513
Qy 1613 CAACCTCAGTGTGCCCCCAGCCAGGCTGAGTGTTCCTTGACCCCTGAACCTGTTGG 1672
Db 1514 CAACCTCAGTGTGCCCCCAGCCAGGCTGAGTGTTCCTTGACCCCTGAACCTGTTGG 1573
Qy 1673 GAGGCTGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGAATGCTGCTGCCCG 1732
Db 1574 GAGGCTGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGAATGCTGCTGCCCG 1633
Qy 1733 GGACCCCACTGTGCTGGAGCCCTGAGTCCCGAAGCTGTGCTGCTGCTGCTGCTGCTGCT 1792
Db 1634 GGACCCCACTGTGCTGGAGCCCTGAGTCCCGAAGCTGTGCTGCTGCTGCTGCTGCTGCT 1693
Qy 1793 CTTGAATCTCTGGAAGCAGACATGAGCGGGGAAACCCAGAGTGGGCAATGTGCCAGTGG 1852
Db 1694 CTTGAATCTCTGGAAGCAGACATGAGCGGGGAAACCCAGAGTGGGCAATGTGCCAGTGG 1753
Qy 1853 CCCATGAGCAGAGCCTTGGGCTCAGAGCCCGCGCAATCATTAAGAGTCTGCTGGC 1912
Db 1754 CCCATGAGCAGAGCCTTGGGCTCAGAGCCCGCGCAATCATTAAGAGTCTGCTGGC 1813
Qy 1913 TGTCCCTAACTCCATCTGGAGTCTCCCTGCCCCCACTGTGAGCCTTGGCCTCTTATTA 1972
Db 1814 TGTCCCTAACTCCATCTGGAGTCTCCCTGCCCCCACTGTGAGCCTTGGCCTCTTATTA 1873
Qy 1973 TTGGAGTCATGCCCCCAGCAGCTCCAGAGGCTCTTCCACTGTCTCAATGGCTCCCT 2032
Db 1874 TTGGAGTCATGCCCCCAGCAGCTCCAGAGGCTCTTCCACTGTCTCAATGGCTCCCT 1933
Qy 2033 CTTGCTGATGTGAGGATGGAGTTGGGGGTCTCTACAGTGTGGGCAACTGAGAAATGG 2092
Db 1934 CTTGCTGATGTGAGGATGGAGTTGGGGGTCTCTACAGTGTGGGCAACTGAGAAATGG 1993
Qy 2093 CTTTTCATACCTGTGATCTCTACTGGGTGGAGCAGCAGGACCAACCTGGCCCTGGA 2152
Db 1994 CTTTTCATACCTGTGATCTCTACTGGGTGGAGCAGCAGGACCAACCTGGCCCTGGA 2053
Qy 2153 TCCTGAACTGGCAGGCAATCCCGGGAGCATGTGAAGTCCCGTTCACAGGGTCAGTGG 2212
Db 2054 TCCTGAACTGGCAGGCAATCCCGGGAGCATGTGAAGTCCCGTTCACAGGGTCAGTGG 2113
Qy 2213 TGGGCGCCGCTGGCTGCCAGAGTCTCTAAGTCTGGGCCCACTTTGTCACTGTCACTGCT 2272
Db 2114 TGGGCGCCGCTGGCTGCCAGAGTCTCTAAGTCTGGGCCCACTTTGTCACTGTCACTGCT 2173
Qy 2273 CTTTGGCTTGTGCTTTTTCAGAGCCCTCATCATCTCTGCTGGCTCCCATTTGAGACAT 2332
Db 2174 CTTTGGCTTGTGCTTTTTCAGAGCCCTCATCATCTCTGCTGGCTCCCATTTGAGACAT 2233
Qy 2333 CCGGGCTCGGGGCAAGGTTTTCAGGGCTGTGAGACCTTGGCCCTTGGGGAGAGGCCCTG 2392
Db 2234 CCGGGCTCGGGGCAAGGTTTTCAGGGCTGTGAGACCTTGGCCCTTGGGGAGAGGCCCTG 2293

Qy 2393 AAGCAGAGAGCAACACCTCCAGTCTCCNAGGATGAGGACCTCTCCAGTGTATGGA 2452
Db 2294 AAGCAGAGAGCAACACCTCCAGTCTCCNAGGATGAGGACCTCTCCAGTGTATGGA 2353
Qy 2453 CGCTGACAAACAACTGCCCTAGGCACTGAGGTAGTCTTAACTCTAGGCAAGCCCGGGCTG 2512
Db 2354 CGCTGACAAACAACTGCCCTAGGCACTGAGGTAGTCTTAACTCTAGGCAAGCCCGGGCTG 2413
Qy 2513 CGGTGACAGGACCTTGGGCACTGCTGGCTGGGGGGCCCAAGCACAGCCCTGACTAGATGAC 2572
Db 2414 CGGTGACAGGACCTTGGGCACTGCTGGCTGGGGGGCCCAAGCACAGCCCTGACTAGATGAC 2473
Qy 2573 AGCAGCAAAAGAGCAACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTCACTGA 2632
Db 2474 AGCAGCAAAAGAGCAACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTCACTGA 2533
Qy 2633 TGACACTCAGCAGGAGTATGACAGAGTCTGCTCCCTTATGGGACTCCCTTCTACAA 2692
Db 2534 TGACACTCAGCAGGAGTATGACAGAGTCTGCTCCCTTATGGGACTCCCTTCTACAA 2593
Qy 2693 GCACATGAGCTCTCTAAACAGGGTGGGGCTACCCCCAGAGCTGCTCCCTACACTGATATTG 2752
Db 2594 GCACATGAGCTCTCTAAACAGGGTGGGGCTACCCCCAGAGCTGCTCCCTACACTGATATTG 2653
Qy 2753 AAGAACCTGAGAGAGATTCCTTCACTTCTGAGGCAATCCAGGAGCCCTCCAGAAAACAGAGT 2812
Db 2654 AAGAACCTGAGAGAGATTCCTTCACTTCTGAGGCAATCCAGGAGCCCTCCAGAAAACAGAGT 2713
Qy 2813 TTTCAAGAGACCTTAAACAACTCCCTGCTCCAGAGCCCTATGTTATGAACACCAACA 2872
Db 2714 TTTCAAGAGACCTTAAACAACTCCCTGCTCCAGAGCCCTATGTTATGAACACCAACA 2773
Qy 2873 TCTAAACAAATCATATGCTAACTGCTCTCTGAGAACTCCACTCTGAAAGTCCGCTTT 2932
Db 2774 TCTAAACAAATCATATGCTAACTGCTCTCTGAGAACTCCACTCTGAAAGTCCGCTTT 2833
Qy 2933 GGACACAAACACTCCCTTCTCCAGGGTCTATGAGGAGTCTGCTCCCTCTGCTTCCCTT 2992
Db 2834 GGACACAAACACTCCCTTCTCCAGGGTCTATGAGGAGTCTGCTCCCTCTGCTTCCCTT 2893
Qy 2993 ACCAGTGTGCAACGCTGACTTCCAGAGAGTCTTCCCTGAGTGTGACCACTTCTTCT 3052
Db 2894 ACCAGTGTGCAACGCTGACTTCCAGAGAGTCTTCCCTGAGTGTGACCACTTCTTCT 2953
Qy 3053 TGCTTCTGAGTGGGCGAGACTCTGATCCCTTCTGCTGGCAGAGATGGCAGGGTAATCTG 3112
Db 2954 TGCTTCTGAGTGGGCGAGACTCTGATCCCTTCTGCTGGCAGAGATGGCAGGGTAATCTG 3013
Qy 3113 AGCCTTCTTCACTCTTTTACCTAGCTGAGCCCTTCACTCTCCCTCCCTTCTTCTT 3172
Db 3014 AGCCTTCTTCACTCTTTTACCTAGCTGAGCCCTTCACTCTCCCTCCCTTCTTCTT 3073
Qy 3173 GTTTTGGATTCAGAAAAGTCTTGTGAGAGCTTTTATTTTATTAATAATAATAGG 3232
Db 3074 GTTTTGGATTCAGAAAAGTCTTGTGAGAGCTTTTATTTTATTAATAATAATAGG 3133
Qy 3233 CTTA 3236
Db 3134 CTTA 3137

RESULT 5

US-10-013-907A-276
; Sequence 276, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

Db 374 GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGCAGAGAAAAA 433
Qy 533 GAGTGAATGTGCCCTTTAAGAGAGAGCAATGAGACACAGTGTGTTTCAACTTCTATCCGTGT 592
Db 434 GAGTGAATGTGCCCTTTAAGAGAGAGCAATGAGACACAGTGTGTTTCAACTTCTATCCGTGT 493
Qy 593 CTTGGTCTTTTACAAATGTACCCATCTCTACACCTGCGGACACTTGGCCCTTACGCCCTGC 652
Db 494 CTTGGTCTTTTACAAATGTACCCATCTCTACACCTGCGGACACTTGGCCCTTACGCCCTGC 553
Qy 653 TTGTACCTTCAATGAACTTCAAGATTCTACTCTGTGCCCCTCTCGGAGACAAAGGTCTAT 712
Db 554 TTGTACCTTCAATGAACTTCAAGATTCTACTCTGTGCCCCTCTCGGAGCAAGGTCTAT 613
Qy 713 GGAGGGAAGAGCCAAAGCCCTTTGACCCCGCTTCAAGCATACGCTGTCTTGTGTGA 772
Db 614 GGAGGGAAGAGCCAAAGCCCTTTGACCCCGCTTCAAGCATACGCTGTCTTGTGTGA 673
Qy 773 TGGGATGCTCTATTCTGTGTACTATGAACAACTTCTCGGCAAGTGGCCCATCTGTATGCG 832
Db 674 TGGGATGCTCTATTCTGTGTACTATGAACAACTTCTCGGCAAGTGGCCCATCTGTATGCG 733
Qy 833 CACACTGGGATCCAGCCCTGTCTCAAGACGCAAACTTCTCGGCTGGCTGTGATCTGA 892
Db 734 CACACTGGGATCCAGCCCTGTCTCAAGACGCAAACTTCTCGGCTGGCTGTGATCTGA 793
Qy 893 CGCCTCTTTGTGGCAGCATCCCTTCGACCCAGTGTCTACTTCTTTCGAGGAGAC 952
Db 794 CGCCTCTTTGTGGCAGCATCCCTTCGACCCAGTGTCTACTTCTTTCGAGGAGAC 853
Qy 953 AGCCAGCAGATTGACTTCTTTGAGAGGCTCCACATACGCGGTGTCTAGTCTGCAA 1012
Db 854 AGCCAGCAGATTGACTTCTTTGAGAGGCTCCACATACGCGGTGTCTAGTCTGCAA 913
Qy 1013 GAATGACGTGGCGGCGGAAGTGTCTGCAAGAGTGGACCACTTCTTGAAGGCCCA 1072
Db 914 GAATGACGTGGCGGCGGAAGTGTCTGCAAGAGTGGACCACTTCTTGAAGGCCCA 973
Qy 1073 GCTGCTCTGACCCAGCCGCGGAGCTGCTCCCTTCAAGCTCATCCGCCACGCGTCTGCT 1132
Db 974 GCTGCTCTGACCCAGCCGCGGAGCTGCTCCCTTCAAGCTCATCCGCCACGCGTCTGCT 1033
Qy 1133 CCGCGCCGATCTTCCACAGCTCCCCACATCTACGCACTTTCACCTCCACAGTGGCAGGT 1192
Db 1034 CCGCGCCGATCTTCCACAGCTCCCCACATCTACGCACTTTCACCTCCACAGTGGCAGGT 1093
Qy 1193 TGGCGGACACGAGGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATTTGAACGTGTCTT 1252
Db 1094 TGGCGGACACGAGGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATTTGAACGTGTCTT 1153
Qy 1253 TAAAGGGAATACAAAGATTGAACAAAGAACTTTCAGCTGTGACTATTATAGGCGCC 1312
Db 1154 TAAAGGGAATACAAAGATTGAACAAAGAACTTTCAGCTGTGACTATTATAGGCGCC 1213
Qy 1313 TGAGACCAACCCCGGCGGAGGTTGCTCAGTGGGCGCCCTCTCTGATAGGCGCTGAC 1372
Db 1214 TGAGACCAACCCCGGCGGAGGTTGCTCAGTGGGCGCCCTCTCTGATAGGCGCTGAC 1273
Qy 1373 CTTGATAGGACCAATTTCTGATGATGACAAAGTGTGGGAGCGCCCTCTGCTGTGTGA 1432
Db 1274 CTTGATAGGACCAATTTCTGATGATGACAAAGTGTGGGAGCGCCCTCTGCTGTGTGA 1333
Qy 1433 ATCTGGCTGTGAGTATACACGCTTTCAGTGGAGACGCCAGCGCTTGTATGGCACAG 1492
Db 1334 ATCTGGCTGTGAGTATACACGCTTTCAGTGGAGACGCCAGCGCTTGTATGGCACAG 1393
Qy 1493 CCATCTTGTATGTACCTGTGGAAACCAACAGGCTGTCTCCACAGGCTGTGTAAAGTGG 1552
Db 1394 CCATCTTGTATGTACCTGTGGAAACCAACAGGCTGTCTCCACAGGCTGTGTAAAGTGG 1453
Qy 1553 GGACAGCAGTGTCTATCTGTGGAGAGATTACAGTGTCTCCCTGACCTGACCTGTTCG 1612
Db 1454 GGACAGCAGTGTCTATCTGTGGAGAGATTACAGTGTCTCCCTGACCTGTTCG 1513

Qy 1613 CAACTGTGAGCTGGCCCCCAACCCAGGCTGCAAGTGTGTTGTAGGCTTCTCAGAGGTTGCTG 1672
Db 1514 CAACTGTGAGCTGGCCCCCAACCCAGGCTGCAAGTGTGTTGTAGGCTTCTCAGAGGTTGCTG 1573
Qy 1673 GAGGCTGGCCCCGAGCAAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCG 1732
Db 1574 GAGGCTGGCCCCGAGCAAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCG 1633
Qy 1733 GGAACCCCACTGTGTGCTGGGACCTTGAATCCCGAACTTGTGTGCTTGTGCTTGTGCCCCAA 1792
Db 1634 GGAACCCCACTGTGTGCTGGGACCTTGAATCCCGAACTTGTGTGCTTGTGCTTGTGCCCCAA 1693
Qy 1793 CTTGAATCTCTGGAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCAATGTGCCAGTGG 1852
Db 1694 CTTGAATCTCTGGAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCAATGTGCCAGTGG 1753
Qy 1853 CCCCATGAGCAGGACCTTTCGGCTTCAGAGCGCGCCGCAAACTATTAAAGAGTCTCTGGC 1912
Db 1754 CCCCATGAGCAGGACCTTTCGGCTTCAGAGCGCGCCGCAAACTATTAAAGAGTCTCTGGC 1813
Qy 1913 TGTCCCTAACTCCATCTGAGCTCCCTGCCCCACCTGTGAGCTTGGCTCTTATTATTA 1972
Db 1814 TGTCCCTAACTCCATCTGAGCTCCCTGCCCCACCTGTGAGCTTGGCTCTTATTATTA 1873
Qy 1973 TTGGAGTCAATGCCCCAGCAGCAGTCCCAAGAGCTTCTTCCAATGTCTTCAATGGCTCCCT 2032
Db 1874 TTGGAGTCAATGCCCCAGCAGCAGTCCCAAGAGCTTCTTCCAATGTCTTCAATGGCTCCCT 1933
Qy 2033 CTTGCTGATGTCAGGATGGAGTTGGGGTCTCTACAGTCTGCGGCAACTGAGAAATGG 2092
Db 1934 CTTGCTGATGTCAGGATGGAGTTGGGGTCTCTACAGTCTGCGGCAACTGAGAAATGG 1993
Qy 2093 CTTTTTATACCTGTGATCTCTACTGGGTGGAAGCCAGGACCCAGGACCCCTGGCCCTGGA 2152
Db 1994 CTTTTTATACCTGTGATCTCTACTGGGTGGAAGCCAGGACCCAGGACCCCTGGCCCTGGA 2053
Qy 2153 TCTGAACTGGGAGCATCCCCGGGAGCATGTGAAGTCCCGTTGACAGGAGTCAAGTGG 2212
Db 2054 TCTGAACTGGGAGCATCCCCGGGAGCATGTGAAGTCCCGTTGACAGGAGTCAAGTGG 2113
Qy 2213 TGGGCGGCTGGCTGGCTGCCCAGCAGTCTTACTTGGGCCCCCACTTTGTCACTGTCTCT 2272
Db 2114 TGGGCGGCTGGCTGGCTGCCCAGCAGTCTTACTTGGGCCCCCACTTTGTCACTGTCTCT 2173
Qy 2273 CTTTGGCTTAGTGTCTTTAGGAGCCCTCATCATCTCTGTGGCTCCCCATTGAGAGCACT 2332
Db 2174 CTTTGGCTTAGTGTCTTTAGGAGCCCTCATCATCTCTGTGGCTCCCCATTGAGAGCACT 2233
Qy 2333 CCGGGCTGGGCAAGGTTTCAGGCTGTGAGACCTCGCGCCCTGGGAGAAAGGCCCCGTT 2392
Db 2234 CCGGGCTGGGCAAGGTTTCAGGCTGTGAGACCTCGCGCCCTGGGAGAAAGGCCCCGTT 2293
Qy 2393 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAATGCAAGGACCTCTGCGAGTGTGGA 2452
Db 2294 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAATGCAAGGACCTCTGCGAGTGTGGA 2353
Qy 2453 CGCTGACAACTGCTAGGCACTGAGTACCTTAACTCTAGGACAGGCGCGGGCTG 2512
Db 2354 CGCTGACAACTGCTAGGCACTGAGTACCTTAACTCTAGGACAGGCGCGGGCTG 2413
Qy 2513 CGGTGAGGACACTTGGCCATGCTGGCGCGGCCCAAGCAAGCCCTGACTAGGATGAC 2572
Db 2414 CGGTGAGGACACTTGGCCATGCTGGCGCGGCCCAAGCAAGCCCTGACTAGGATGAC 2473
Qy 2573 AGCAGCAGAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCACTGA 2632
Db 2474 AGCAGCAGAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCACTGA 2533
Qy 2633 TGAACCTCAGCAGGCTGATGCAAGCAGTCTGCCCTCCCTATGGGACTCCCTTCTACCAA 2692
Db 2534 TGAACCTCAGCAGGCTGATGCAAGCAGTCTGCCCTCCCTATGGGACTCCCTTCTACCAA 2593

```
QY 2693 GCACATGAGCTCTTAACAGAGGTGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2752
Db 2594 GCACATGAGCTCTTAACAGAGGTGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2653
QY 2753 AAGAACCTGGAGAGGATCTCTCAGTTCTGGGCACTTCCAGGAGCCCTCCAGAAAACACAGTG 2812
Db 2654 AAGAACCTGGAGAGGATCTCTCAGTTCTGGGCACTTCCAGGAGCCCTCCAGAAAACACAGTG 2713
QY 2813 TTTCAAGAGACCTTAACAAACCTGCTGCTCCAGGAGCCCTTATGTAATGAACACCAACA 2872
Db 2714 TTTCAAGAGACCTTAACAAACCTGCTGCTCCAGGAGCCCTTATGTAATGAACACCAACA 2773
QY 2873 TCTAAACAATCATATGCTAAACATGCCACTCTCTGGAACCTCACTCTGAAGCTGCCGCTTT 2932
Db 2774 TCTAAACAATCATATGCTAAACATGCCACTCTCTGGAACCTCACTCTGAAGCTGCCGCTTT 2833
QY 2933 GGACACCAACACTCTCTCTCCAGGAGCTATGAGGAGTCTGCTCCCTCTGCTCTCCCTT 2992
Db 2834 GGACACCAACACTCTCTCTCCAGGAGCTATGAGGAGTCTGCTCCCTCTGCTCTCCCTT 2893
QY 2993 ACCAGTGTGACACCGCTCACTTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTCTCT 3052
Db 2894 ACCAGTGTGACACCGCTCACTTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTCTCT 2953
QY 3053 TGCTTCAGTTGGGCGACACTCTGATCCCTTCTGCTGCGGAGAAATGCGAGGGTAATCTG 3112
Db 2954 TGCTTCAGTTGGGCGACACTCTGATCCCTTCTGCTGCGGAGAAATGCGAGGGTAATCTG 3013
QY 3113 AGCTTCTTCACTCTCTTACCTAGCTGACCCCTTCACTCTCCCTCTCCCTTCTCTCTT 3172
Db 3014 AGCTTCTTCACTCTCTTACCTAGCTGACCCCTTCACTCTCCCTCTCCCTTCTCTCTT 3073
QY 3173 GTTTTGGGATTCAAAAACCTGTTGTGACAGACTGTTTATTTTATTTAAATAAAG 3232
Db 3074 GTTTTGGGATTCAAAAACCTGTTGTGACAGACTGTTTATTTTATTTAAATAAAG 3133
QY 3233 CTTA 3236
Db 3134 CTTA 3137
```

RESULT 7

```
US-10-226-254A-276
; Sequence 276, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830F1C68
; CURRENT APPLICATION NUMBER: US/10/226,254A
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 1998-09-01
; PRIOR FILING DATE: 1998-09-01
; PRIOR FILING DATE: 1998-09-01
; PRIOR FILING DATE: 1998-09-01
; PRIOR FILING DATE: 1998-09-01
; PRIOR FILING DATE: 1998-09-01
; PRIOR FILING DATE: 1998-09-01
```

```
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
; LENGTH: 3143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-226-254A-276

Query Match      87.3%; Score 3060.8; DB 13; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCCTGGACCC 232
Db 74 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCCTGGACCC 133
QY 233 CTGAGAGCTCTGGGCCCTTTTCTTCCACTGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 292
Db 134 CTGAGAGCTCTGGGCCCTTTTCTTCCACTGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 193
QY 293 CGCGGGGGAGCGCGGCGGAGGCGGCCCATGCCCAGGGTTCAGATATCTATGACGGGGATGAACG 352
Db 194 CGCGGGGGAGCGCGGCGGAGGCGGCCCATGCCCAGGGTTCAGATATCTATGACGGGGATGAACG 253
QY 353 TAGGGCACTTAGCTTCTTCCACAGAGAGGGCTCCAGGATTTTGACACTCTGCTCTCTGAG 412
Db 254 TAGGGCACTTAGCTTCTTCCACAGAGAGGGCTCCAGGATTTTGACACTCTGCTCTCTGAG 313
QY 413 TGGTGATGGAATACTCTCTACGTGGGGGCTCGAAGAGCCATTCTGGCTTGGATATCCA 472
Db 314 TGGTGATGGAATACTCTCTACGTGGGGGCTCGAAGAGCCATTCTGGCTTGGATATCCA 373
QY 473 GGATCCAGGGTCCCGAGGCTTAAAGAACATGATACCTGGCCAGCCAGTGAACAGAAAAA 532
Db 374 GGATCCAGGGTCCCGAGGCTTAAAGAACATGATACCTGGCCAGCCAGTGAACAGAAAAA 433
QY 533 GAGTGAATGTGCTTTTAAAGAAAGAGAGCAATGAGACACAGTGTTCATCTTCACTTCCCTGT 592
Db 434 GAGTGAATGTGCTTTTAAAGAAAGAGAGCAATGAGACACAGTGTTCATCTTCACTTCCCTGT 493
QY 593 CTGGTTTCTTAATGTCAACCTCACTCCATCTACCTCGGGACCTTCCCTTCCAGCCCTGC 652
Db 494 CTGGTTTCTTAATGTCAACCTCACTCCATCTACCTCGGGACCTTCCCTTCCAGCCCTGC 553
QY 653 TTGTACCTTTCATTAACCTTCAAGATTCCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
Db 554 TTGTACCTTTCATTAACCTTCAAGATTCCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
QY 713 GGAGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGCATACGCTGTCTTGTGTGA 772
Db 614 GGAGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGCATACGCTGTCTTGTGTGA 673
QY 773 TGGGATGCTCTATTCTGTATGAACAACTTCTGGGAGTGAAGCCCATCTGATGCG 832
Db 674 TGGGATGCTCTATTCTGTATGAACAACTTCTGGGAGTGAAGCCCATCTGATGCG 733
QY 833 CACACTGGGATCCAGGCTGTCTCAAGACCGAACTTCTCGGCTGGTGTGATCATGA 892
Db 734 CACACTGGGATCCAGGCTGTCTCAAGACCGAACTTCTCGGCTGGTGTGATCATGA 793
QY 893 CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTGCTCTACTTCTTCTTCTGAGGAGAC 952
```


Db	794		CGCTCTTTGTGGAGCCATCCCTTGACCCAGGTGGTCTACTTCTTCGAGGAGAC	853
Qy	953	AGCCAGCAGATTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGAGTCTGCAA	1012	
Db	854	AGCCAGCAGATTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGAGTCTGCAA	913	
Qy	1013	GAAATGACGTGGCGCGGAAAGCTGTGCGAAGAGTGGACACCTTCTCTGAAGGCCCA	1072	
Db	914	GAAATGACGTGGCGCGGAAAGCTGTGCGAAGAGTGGACACCTTCTCTGAAGGCCCA	973	
Qy	1073	GCTGCTGTGACCCAGCGCGGAGCTGCCCTTCAACGTCATCGCCACCGGTCCTGCT	1132	
Db	974	GCTGCTGTGACCCAGCGCGGAGCTGCCCTTCAACGTCATCGCCACCGGTCCTGCT	1033	
Qy	1133	CCCCGCCGATTCCTCCACAGCTCCCCACATCTACGCACTTACCTCCAGTGGCAGGT	1192	
Db	1034	CCCCGCCGATTCCTCCACAGCTCCCCACATCTACGCACTTACCTCCAGTGGCAGGT	1093	
Qy	1193	TGGCGGACACGAGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATGGAACGTGCTT	1252	
Db	1094	TGGCGGACACGAGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATGGAACGTGCTT	1153	
Qy	1253	TAAAGGGAATACAAAGATTGAACAAAGAACTTCAGCTGGACTACTTATAGGGCCC	1312	
Db	1154	TAAAGGGAATACAAAGATTGAACAAAGAACTTCAGCTGGACTACTTATAGGGCCC	1213	
Qy	1313	TGAGACCAACCCCGGCCAGCAGTTGCTCAGTGGGCCCCCTCTCTGATAGGCCCCTGAC	1372	
Db	1214	TGAGACCAACCCCGGCCAGCAGTTGCTCAGTGGGCCCCCTCTCTGATAGGCCCCTGAC	1273	
Qy	1373	CTTCATGAAGACACATTCCTGATGGATGACACAGTGGTGGGAGCGCCCTCTGTGTGAA	1432	
Db	1274	CTTCATGAAGACACATTCCTGATGGATGACACAGTGGTGGGAGCGCCCTCTGTGTGAA	1333	
Qy	1433	ATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCAGGCGCTTGATGGGCACAG	1492	
Db	1334	ATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCAGGCGCTTGATGGGCACAG	1393	
Qy	1493	CCATCTTGTATGATCTGGGAAACCAACAGGCTGGTTCACAGGCTGTGTGAAGTGG	1552	
Db	1394	CCATCTTGTATGATCTGGGAAACCAACAGGCTGGTTCACAGGCTGTGTGAAGTGG	1453	
Qy	1553	GGACAGCAGTGTCTATCTGGTGGAGAGATTTCAGCTGTTCCTGACCTGAACTGTTCG	1612	
Db	1454	GGACAGCAGTGTCTATCTGGTGGAGAGATTTCAGCTGTTCCTGACCTGAACTGTTCG	1513	
Qy	1613	CAACTGCACTGGCCCCCAACAGGCTGCAGTGTGTAGGCTTCTCAGAGGTGTCTG	1672	
Db	1514	CAACTGCACTGGCCCCCAACAGGCTGCAGTGTGTAGGCTTCTCAGAGGTGTCTG	1573	
Qy	1673	GAGGCTGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTCTTGGCCG	1732	
Db	1574	GAGGCTGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTCTTGGCCG	1633	
Qy	1733	GGACCCCACTGTGCTGGGACCTCTGAGTCCCGAACCTTGTTCCTCTCTGCTGCCCCCAA	1792	
Db	1634	GGACCCCACTGTGCTGGGACCTCTGAGTCCCGAACCTTGTTCCTCTCTGCTGCCCCCAA	1693	
Qy	1793	CCTGAATCTCTGGAAGACGACATGGACGGGGGAAACCCAGAGTGGGATGTGCCAGTGG	1852	
Db	1694	CCTGAATCTCTGGAAGACGACATGGACGGGGGAAACCCAGAGTGGGATGTGCCAGTGG	1753	
Qy	1853	CCCCATGAGCAGGAGCTTCGGCTCTCAGAGCGCGCCGAAATCAATTAAGAACTCTGGC	1912	
Db	1754	CCCCATGAGCAGGAGCTTCGGCTCTCAGAGCGCGCCGAAATCAATTAAGAACTCTGGC	1813	
Qy	1913	TGTCCCTAACTCCTGAGAGTCCCTTGCCGCCACCTGTGAGCTTGGCTCTTATTA	1972	
Db	1814	TGTCCCTAACTCCTGAGAGTCCCTTGCCGCCACCTGTGAGCTTGGCTCTTATTA	1873	
Qy	1973	TGGAGTCTATGSCCCAGCAGTCCCAAGAGCTTCTTCCACTGTCTACATGCTCCCT	2032	

Db	1874	TTGGAGTCAATGCCCCCAGCAGCAGTCCCAAGAGCCTCTTCCACTGTCTACAATGGCTCCT	1933	
Qy	2033	CTTGTGATAGTGCAGGATGGAGTTGGGGTCTCTACCACTGCTGGGCAACTGAGAAATGG	2092	
Db	1934	CTTGTGATAGTGCAGGATGGAGTTGGGGTCTCTACCACTGCTGGGCAACTGAGAAATGG	1993	
Qy	2093	CTTTTTCATACCTCTGATCTCTCTACTGGGTGGACAGCAGGACCAAGACCTTGGCCCTGGA	2152	
Db	1994	CTTTTTCATACCTCTGATCTCTCTACTGGGTGGACAGCAGGACCAAGACCTTGGCCCTGGA	2053	
Qy	2153	TCTGAACTGGCAGGATTCCTCCCGGAGCATGTGAAGTCCGTTGACAGAGGTCAATGG	2212	
Db	2054	TCTGAACTGGCAGGATTCCTCCCGGAGCATGTGAAGTCCGTTGACAGAGGTCAATGG	2113	
Qy	2213	TGGGGCCGCTGGCTGGCCAGCAGTCTCTACCTGGGCCCACTTTGTCACTGTCACTGTCT	2272	
Db	2114	TGGGGCCGCTGGCTGGCCAGCAGTCTCTACCTGGGCCCACTTTGTCACTGTCACTGTCT	2173	
Qy	2273	CTTTGCTTTAGTGTCTTTCAGGAGCCTCATCATCTCTGTGGCTCCCAATTGAGAGCACT	2332	
Db	2174	CTTTGCTTTAGTGTCTTTCAGGAGCCTCATCATCTCTGTGGCTCCCAATTGAGAGCACT	2233	
Qy	2333	CCGGCTCGGGCAAGGTTTCAGGCTGTGAGACCTCGCGCTGGGGAGAGGCCCGCTT	2392	
Db	2234	CCGGCTCGGGCAAGGTTTCAGGCTGTGAGACCTCGCGCTGGGGAGAGGCCCGCTT	2293	
Qy	2393	AAGCAGAGAGCAACCTCCTCAGTCTCCAGGAATGCAGGACCTCTGCCAGTGTATGGA	2452	
Db	2294	AAGCAGAGAGCAACCTCCTCAGTCTCCAGGAATGCAGGACCTCTGCCAGTGTATGGA	2353	
Qy	2453	CGCTGACAACTCGCTAGGCACTGAGGTAGCTTAACTCTAGGCACAGGCCGGGGCTG	2512	
Db	2354	CGCTGACAACTCGCTAGGCACTGAGGTAGCTTAACTCTAGGCACAGGCCGGGGCTG	2413	
Qy	2513	CGGTGAGGACACTGGCCACTGTGGCTGGCGGCCCAAGCAGCAGCCCTGATAGATGAC	2572	
Db	2414	CGGTGAGGACACTGGCCACTGTGGCTGGCGGCCCAAGCAGCAGCCCTGATAGATGAC	2473	
Qy	2573	AGCAGCAAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCAGTGA	2632	
Db	2474	AGCAGCAAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCAGTGA	2533	
Qy	2633	TGACACTCAGCAGGCTGATGCACAGCAGTCTCCCTCCCTATGGGACTCCCTTCTACCAA	2692	
Db	2534	TGACACTCAGCAGGCTGATGCACAGCAGTCTCCCTCCCTATGGGACTCCCTTCTACCAA	2593	
Qy	2693	GCAATGAGCTCTCTAAACAGGGTGGGGCTACCCCGAGCCTGCTCCTACATGATATG	2752	
Db	2594	GCAATGAGCTCTCTAAACAGGGTGGGGCTACCCCGAGCCTGCTCCTACATGATATG	2653	
Qy	2753	AAGAACTCGAGAGGATCCTTCAGTTCGGCCATTCAGGGACCTTCCAGAAACACAGTG	2812	
Db	2654	AAGAACTCGAGAGGATCCTTCAGTTCGGCCATTCAGGGACCTTCCAGAAACACAGTG	2713	
Qy	2813	TTTCAAGAGACCTTAAAAACCTGCTGTCAGGACCTTCCAGGACCTTGGTAATGAAACCA	2872	
Db	2714	TTTCAAGAGACCTTAAAAACCTGCTGTCAGGACCTTCCAGGACCTTGGTAATGAAACCA	2773	
Qy	2873	TCTAAACATCATATGCTAACTGCACTCTCTGGAACCTTCCACTCTGAGCTGCCGCTT	2932	
Db	2774	TCTAAACATCATATGCTAACTGCACTCTCTGGAACCTTCCACTCTGAGCTGCCGCTT	2833	
Qy	2933	GGACACCAACACTCCCTTCTCCAGGGTCATGACAGGATCTGCTCCCTCTCTTCCCTT	2992	
Db	2834	GGACACCAACACTCCCTTCTCCAGGGTCATGACAGGATCTGCTCCCTCTCTTCCCTT	2893	
Qy	2993	ACCACTGCTGCAACCTGACTCCAGGAGTCTTCCCTGAAGTCTGACCACTTCTTCT	3052	
Db	2894	ACCACTGCTGCAACCTGACTCCAGGAGTCTTCCCTGAAGTCTGACCACTTCTTCT	2953	
Qy	3053	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCTCCCTGCGAGAAATGGCAGGGTATCTG	3112	
Db	2954	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCTCCCTGCGAGAAATGGCAGGGTATCTG	3013	

2594	Db	GCATAGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCTCTACACTGATATG	2653
2753	Qy	AAGAACTCTGAGAGGATCCCTTCAGTTCTGSGCCATTCAGGGACCTCCAGAAACACAGTG	2812
2654	Db	AAGAACTCTGAGAGGATCCCTTCAGTTCTGSGCCATTCAGGGACCTCCAGAAACACAGTG	2713
2813	Qy	TTTCAAGAGACCCATAAAAACTGCGCTGTCCCAAGGACCTATGGTAATGAACACCAAAACA	2872
2714	Db	TTTCAAGAGACCCATAAAAACTGCGCTGTCCCAAGGACCTATGGTAATGAACACCAAAACA	2773
2873	Qy	TCTAAACAACTCATGCTAACTGCCACTCCTCGAAACTCCACTCTGAAGCTGCGCGTTT	2932
2774	Db	TCTAAACAACTCATGCTAACTGCCACTCCTCGAAACTCCACTCTGAAGCTGCGCGTTT	2833
2933	Qy	GGACACAAACATCCCTTTCTCCAGGTCATGACGGATCTGTCGCTCCTGTTTCCCTT	2992
2834	Db	GGACACAAACATCCCTTTCTCCAGGTCATGACGGATCTGTCGCTCCTGTTTCCCTT	2893
2993	Qy	ACGAGTCGTGCACCGCTGACTCCACGAGAGTCTTCCCTGAAGTCGACACCTTTCTTCT	3052
2894	Db	ACAGTCGTGCACCGCTGACTCCACGAGAGTCTTCCCTGAAGTCGACACCTTTCTTCT	2953
3053	Qy	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGCGGGGTAATCTG	3112
2954	Db	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGCGGGGTAATCTG	3013
3113	Qy	AGCCTTCTTCACATCCCTTACCCTAGCTGACCCCTTACCTCTCCCGCTCCCTTTCCCTT	3172
3014	Db	AGCCTTCTTCACATCCCTTACCCTAGCTGACCCCTTACCTCTCCCGCTCCCTTTCCCTT	3073
3173	Qy	GTTTTGGGATTCAAGAAACCTGCTTGTTCAGAGACTGTTTTATTTTTTATTAATAAATAAAGG	3232
3074	Db	GTTTTGGGATTCAAGAAACCTGCTTGTTCAGAGACTGTTTTATTTTTTATTAATAAATAAAGG	3133
3233	Qy	CTTA 3236	
3134	Db	CTTA 3137	

RESULT 9
UIS-10-006-818A-276

Query Match 87.3%; Score 3060.8; DB 15; Length 3143;

QY 2333 CCGGCTCGGGCAAGGTTTCAAGGCTGTGAGACCTTGGCCCTCGGGGAGAGGCCCGCTT 2392
 Db 2234 CCGGCTCGGGCAAGGTTTCAAGGCTGTGAGACCTTGGCCCTCGGGGAGAGGCCCGCTT 2293
 QY 2393 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGACAGGACCTCTGCGAGTGATGGGA 2452
 Db 2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGACAGGACCTCTGCGAGTGATGGGA 2353
 QY 2453 CGCTGACAAACCTCGCTAGGCACTGAGGTAGCTTAACTCTAGGCAAGGCGCGGGCTG 2512
 Db 2354 CGCTGACAAACCTCGCTAGGCACTGAGGTAGCTTAACTCTAGGCAAGGCGCGGGCTG 2413
 QY 2513 CGGTGACGACCTCGCTGCTGCTGCGGGCCCAAGCAGACCTCTGCTAGGCAAGGCGGGCTG 2572
 Db 2414 CGGTGACGACCTCGCTGCTGCTGCGGGCCCAAGCAGACCTCTGCTAGGCAAGGCGGGCTG 2473
 QY 2573 AGCAGCAAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTAGCTCTGCTAGCTGAC 2632
 Db 2474 AGCAGCAAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTAGCTCTGCTAGCTGAC 2533
 QY 2633 TGACACTGACAGGCTGATGACACAGCTGCTGCTCCCTATGGGACTCCCTTACCAA 2692
 Db 2534 TGACACTGACAGGCTGATGACACAGCTGCTGCTCCCTATGGGACTCCCTTACCAA 2593
 QY 2693 GCACATGAGCTCTTAACAGGCTGGGGCTACCCCGACACCTGCTCTTACACTGATTTG 2752
 Db 2594 GCACATGAGCTCTTAACAGGCTGGGGCTACCCCGACACCTGCTCTTACACTGATTTG 2653
 QY 2753 AGRACCTGGAGAGGATCTTCTGAGTCTGGCCATTCAGGAGCCCTCCAGAAACACAGTG 2812
 Db 2654 AGRACCTGGAGAGGATCTTCTGAGTCTGGCCATTCAGGAGCCCTCCAGAAACACAGTG 2713
 QY 2813 TTTCAAGAGACCTTAAACACCTGCTGTCCAGGACCTATGTAATGAACACCAACA 2872
 Db 2714 TTTCAAGAGACCTTAAACACCTGCTGTCCAGGACCTATGTAATGAACACCAACA 2773
 QY 2873 TCTAAACATCATATGCTAAGCATGCACTCTCTGGAACCTGCACTGAGCTGGCGTTT 2932
 Db 2774 TCTAAACATCATATGCTAAGCATGCACTCTCTGGAACCTGCACTGAGCTGGCGTTT 2833
 QY 2933 GCACACCAACCTCCCTTCTCCAGGCTCATGACGGATCTGCTCCCTCTGCTTCCCTT 2992
 Db 2834 GCACACCAACCTCCCTTCTCCAGGCTCATGACGGATCTGCTCCCTCTGCTTCCCTT 2893
 QY 2993 ACCAGTGTGACCGCTGACCTCCAGGAGCTTCCCTGAGTCTGACCACTTCTTCT 3052
 Db 2894 ACCAGTGTGACCGCTGACCTCCAGGAGCTTCTTCTGAGTCTGACCACTTCTTCT 2953
 QY 3053 TGCTTCAGTTGGGGAGACTCTGATCCCTTCTGCTGCGGAGATGGCAGGGGTAACTG 3112
 Db 2954 TGCTTCAGTTGGGGAGACTCTGATCCCTTCTGCTGCGGAGATGGCAGGGGTAACTG 3013
 QY 3113 AGCCTTCTTCACTCCCTTACCTAGTACCCCTTCACTCTCCCTCCCTTCCCTTCCCTT 3172
 Db 3014 AGCCTTCTTCACTCCCTTACCTAGTACCCCTTCACTCTCCCTCCCTTCCCTTCCCTT 3073
 QY 3173 GTTTTGGGATTCAGAAAACCTGCTCTGAGAGCTGTTATTTTATTAATAAATAAAGG 3232
 Db 3074 GTTTTGGGATTCAGAAAACCTGCTTGTGAGAGCTGTTATTTTATTAATAAATAAAGG 3133
 QY 3233 CTTA 3236
 Db 3134 CTTA 3137

RESULT 10
 US-10-015-393A-276
 ; Sequence 276, Application US/10015393A
 ; Publication No. US2003069179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2830P1C46
 ; CURRENT APPLICATION NUMBER: US/10/015,393A
 ; CURRENT Filing DATE: 2002-06-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 276
 ; LENGTH: 3143
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-015-393A-276

Query Match 87.3%; Score 3060.8; DB 15; Length 3143;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 173 AGAGCTCCCTGTGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGACCCCTGGGCTGAGCCC 232
 Db 74 AGAGCTCCCTGTGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGACCCCTGGGCTGAGCCC 133
 QY 233 CTGGAGCTCTCTGGGCTTTTCTCTTCCAACTGTCTGAGCTCTGCTCTGCTGCTGCTGCTG 292
 Db 134 CTGGAGCTCTCTGGGCTTTTCTCTTCCAACTGTCTGAGCTCTGCTCTGCTGCTGCTGCTG 193
 QY 293 CGGGGGGAGGG 352
 Db 194 CGGGGGGAGGG 253
 QY 353 TAGGGCACTTAGCTTCTTCCACAGAGGGGCTTCCAGGATTTTGAACACTCTGCTCTGCTGAG 412
 Db 254 TAGGGCACTTAGCTTCTTCCACAGAGGGGCTTCCAGGATTTTGAACACTCTGCTCTGCTGAG 313
 QY 413 TGCTGATGGAATACTCTCTACGTGGGGCTCGAGAGCCATCTGCGCTTGGATATCCA 472
 Db 314 TGCTGATGGAATACTCTCTACGTGGGGCTCGAGAGGCCATTTCTGGCTTGGATATCCA 373
 QY 473 GGATCCAGGGGCTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGCACAGAAAAA 532
 Db 374 GGATCCAGGGGCTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGCACAGAAAAA 433
 QY 533 GAGTGAATGTCCTTTAAGAGAGAGCAATGAGACACAGTGTTCACACTTCACTTCCGTGT 592
 Db 434 GAGTGAATGTCCTTTAAGAGAGAGCAATGAGACACAGTGTTCACACTTCACTTCCGTGT 493
 QY 593 CTTGTTTCTTACAAATGTCACCCATCTTACACCTCGGGCACCTTCCGCTTCCAGCCCTGC 652
 Db 494 CTTGTTTCTTACAAATGTCACCCATCTTACACCTCGGGCACCTTCCGCTTCCAGCCCTGC 553
 QY 653 TTGTACCTTCAATGAATTCAGATTCCTACTGTTTCCCATCTCGGAGGACAAAGTCTAT 712
 Db 554 TTGTACCTTCAATGAATTCAGATTCCTACTGTTTCCCATCTCGGAGGACAAAGTCTAT 613
 QY 713 GGAGGGAAGAGGCGGAGGCGGCTTTCACCCGCTCAAGCATACCGCTGTCTTGTGGA 772
 Db 614 GGAGGGAAGAGGCGGAGGCGGCTTTCACCCGCTCAAGCATACCGCTGTCTTGTGGA 673
 QY 773 TGGGATGCTCTATTCTGGTACTATGAACAACTTCTCTGGGAGTGAAGCCCACTCTGTATGCG 832
 Db 674 TGGGATGCTCTATTCTGGTACTATGAACAACTTCTCTGGGAGTGAAGCCCACTCTGTATGCG 733

QY 833 CACACTGGGATCCAGGCTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGA 892
DB 734 CACACTGGGATCCAGGCTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGA 793
QY 893 CGCCTCTTTGTGGGAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 952
DB 794 CGCCTCTTTGTGGGAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 853
QY 953 AGCCAGGAGTTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGAGTCTGCAA 1012
DB 854 AGCCAGGAGTTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGAGTCTGCAA 913
QY 1013 GAATGAGTGGGCGGCGGAGAGCTGCTCGAGAGAGAGTGCACACCTTCTGAAAGGCCCA 1072
DB 914 GAATGAGTGGGCGGCGGAGAGTGCCTCGAGAGAGTGCACACCTTCTGAAAGGCCCA 973
QY 1073 GCTGCTCTGCAACCCAGCGGGGAGCTGCCCTTCAACGTCATCCGCGACCGGTCCTGCT 1132
DB 974 GCTGCTCTGCAACCCAGCGGGGAGCTGCCCTTCAACGTCATCCGCGACCGGTCCTGCT 1033
QY 1133 CCCCAGGATTTCTCCACAGCTCCCACTACGACAGTCTTACACCTCCAGTGGCAGGT 1192
DB 1034 CCCCAGGATTTCTCCACAGCTCCCACTACGACAGTCTTACACCTCCAGTGGCAGGT 1093
QY 1193 TGGCGGACACGAGAGCTCTGCGGTTGTGCTCTCTCTTGTGACATTTGAAAGTGTCTT 1252
DB 1094 TGGCGGACACGAGAGCTCTGCGGTTGTGCTCTCTCTTGTGACATTTGAAAGTGTCTT 1153
QY 1253 TAAGGGGAAATACAAAGTGTGACAAAGAACTTACGCTGGACACTTATAGGGGCC 1312
DB 1154 TAAGGGGAAATACAAAGTGTGACAAAGAACTTACGCTGGACACTTATAGGGGCC 1213
QY 1313 TGAGAACCAACCCCGGCGGAGAGTGTGCTCAGTGGGCCCCCTCTCTCTGATTAAGGCCCTGAC 1372
DB 1214 TGAGAACCAACCCCGGCGGAGAGTGTGCTCAGTGGGCCCCCTCTCTCTGATTAAGGCCCTGAC 1273
QY 1373 CTTCAATGAGAACCAATTTCTGATGAGATGACAGTGGTGGGACCGCCCTCTGTTGAA 1432
DB 1274 CTTCAATGAGAACCAATTTCTGATGAGATGACAGTGGTGGGACCGCCCTCTGTTGAA 1333
QY 1433 ATCTGGCGTGAGATATACACGGCTTGACGTGGAGACAGCCAGGGCCCTTGATGGGACAG 1492
DB 1334 ATCTGGCGTGAGATATACACGGCTTGACGTGGAGACAGCCAGGGCCCTTGATGGGACAG 1393
QY 1493 CCACTTTGTATGATCTGGGAAACCAACAGGCTGGTCCACAGGCTGTGTAAAGTGG 1552
DB 1394 CCACTTTGTATGATCTGGGAAACCAACAGGCTGGTCCACAGGCTGTGTAAAGTGG 1453
QY 1553 GGACAGCAGTGTCTATCTGGTGGAGAGATTCAGCTGTTCCTGACCCCTGAAACCTGTTCG 1612
DB 1454 GGACAGCAGTGTCTATCTGGTGGAGAGATTCAGCTGTTCCTGACCCCTGAAACCTGTTCG 1513
QY 1613 CAACTGAGCTGGGCCCCCAACCGAGGTGACGTGTTGTAGGCTTCTCAGAGGTGTCTG 1672
DB 1514 CAACTGAGCTGGGCCCCCAACCGAGGTGACGTGTTGTAGGCTTCTCAGAGGTGTCTG 1573
QY 1673 GAGGCTGCCCGAGGCAACTGTAGTGTCTATGAGAGCTGTGTGACCTGTGCTTGGCCG 1732
DB 1574 GAGGCTGCCCGAGGCAACTGTAGTGTCTATGAGAGCTGTGTGACCTGTGCTTGGCCG 1633
QY 1733 GGACCCCACTGTGCTGGGACCTGTAGTGTCCGGAACCTGTGCTCTCTGCTGCCCCAA 1792
DB 1634 GGACCCCACTGTGCTGGGACCTGTAGTGTCCGGAACCTGTGCTCTCTGCTGCCCCAA 1693
QY 1793 CTTGAACCTCTGGAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCACTGTGCCAGTGG 1852
DB 1694 CTTGAACCTCTGGAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCACTGTGCCAGTGG 1753
QY 1853 CCCCATGAGCAGGAGCTTGGCTCTGAGCGCCCGGCAAAATCAATTAAGAGTCTCTGGC 1912
DB 1754 CCCCATGAGCAGGAGCTTGGCTCTGAGCGCCCGGCAAAATCAATTAAGAGTCTCTGGC 1813
QY 1913 TGTCCCTTAACCTCATCTGGAGCTCCCTGCGCCCGACCTGTGAGCTGTGACCACTTCTTCT 1972

DB 1814 TGTCCCAACTCCATCTCGAGCTCCCTGCCCCCACCCTGTGAGCCTTGGCCTCTTATTA 1873
QY 1973 TTGAGTCTATGGCCACGACAGTCCAGAGGCTCTTTCACATGTCTTACAAATGGCTCCCT 2032
DB 1874 TTGAGTCTATGGCCACGACAGTCCAGAGGCTCTTTCACATGTCTTACAAATGGCTCCCT 1933
QY 2033 CTTTCTGATAGTGCAGGATGGGTTGGGGTCTCTACAGTGTGGGCAACTGAGAAATGG 2092
DB 1934 CTTTCTGATAGTGCAGGATGGGTTGGGGTCTCTACAGTGTGGGCAACTGAGAAATGG 1993
QY 2093 CTTTCTCATACCTCTGTATCTCTACTG3GTGGACAGCAGGACAGACCCCTGGCCCTGGA 2152
DB 1994 CTTTCTCATACCTCTGTATCTCTACTG3GTGGACAGCAGGACAGACCCCTGGCCCTGGA 2053
QY 2153 TCCTGMACTGGCAGGACATCCCGGGGAGCATGTGAAGGTCCCGTTGACACAGGTCAGTGG 2212
DB 2054 TCCTGMACTGGCAGGACATCCCGGGGAGCATGTGAAGGTCCCGTTGACACAGGTCAGTGG 2113
QY 2213 TGGGGCCCGCCCTGGCTGCCAGCAGTCTCTACTG3CCCCACCTTTGTCTACTGTCACTGTCCT 2272
DB 2114 TGGGGCCCGCCCTGGCTGCCAGCAGTCTCTACTG3CCCCACCTTTGTCTACTGTCACTGTCCT 2173
QY 2273 CTTTTCCTTGTAGTCTTTCAGGAGCCCTCATCTCCTGTCGCTCCCTCCCATTTGAGAGACT 2332
DB 2174 CTTTTCCTTGTAGTCTTTCAGGAGCCCTCATCTCCTGTCGCTCCCTCCCATTTGAGAGACT 2233
QY 2333 CCGGGCTCGGGCGCAAGTTCAGGGGCTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCTGTT 2392
DB 2234 CCGGGCTCGGGCGCAAGTTCAGGGGCTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCTGTT 2293
QY 2393 AAGCAGAGAGCAACACTCTCAGTCTCCCAAGGATGAGGACCTTGCACGTGATGTTGA 2452
DB 2294 AAGCAGAGAGCAACACTCTCAGTCTCCCAAGGATGAGGACCTTGCACGTGATGTTGA 2353
QY 2453 CGCTCAACAACACTGCTAGGCACTGAGTGTAAACTCTTAGGCAAGGCGCGGGCTG 2512
DB 2354 CGCTCAACAACACTGCTAGGCACTGAGGCTGAGGCTGAGGCTTAGGCAAGGCGCGGGCTG 2413
QY 2513 CGGTGAGGACCTGGCCCATGCTGGCGGCGCCCAAGACAGCCCTGACTAGGATGAC 2572
DB 2414 CGGTGAGGACCTGGCCCATGCTGGCGGCGCCCAAGACAGCCCTGACTAGGATGAC 2473
QY 2573 AGCAGCACAAGAGACACCTTCTCCCTGAGAGAGCTTCTGTACTCTGTCATCACTGA 2632
DB 2474 AGCAGCACAAGAGACACCTTCTCCCTGAGAGAGCTTCTGTACTCTGCTACTCTGCTCACTGA 2533
QY 2633 TGACACTGAGAGGTGATGACAGAGTCTGCTCCCTCTATGGGACTCCCTTCTACCAA 2692
DB 2534 TGACACTGAGAGGTGATGACAGAGTCTGCTCCCTCTATGGGACTCCCTTCTACCAA 2593
QY 2693 GCACATGAGCTCTTAAACAGGTTGGGGCTACCCCGCAGACCTGTCTCTACAGTATATG 2752
DB 2594 GCACATGAGCTCTTAAACAGGTTGGGGCTACCCCGCAGACCTGTCTCTACAGTATATG 2653
QY 2753 AAGAACCTGGAGAGGATCTTTCAGTCTTGGCCATTTCCAGGGACCTCCAGAAAACAGAGT 2812
DB 2654 AAGAACCTGGAGAGGATCTTTCAGTCTTGGCCATTTCCAGGGACCTCCAGAAAACAGAGT 2713
QY 2813 TTTTCAGAGACCTTAAACACCTGCTGTCCAGGACCTATGTAATGAAACACCAACA 2872
DB 2714 TTTTCAGAGACCTTAAACACCTGCTGTCCAGGACCTATGTAATGAAACACCAACA 2773
QY 2873 TCTAAACAATCATATGCTAAACATGCTCTCTG3AAAATCTCACTCTGAGTGTGCGCTTT 2932
DB 2774 TCTAAACAATCATATGCTAAACATGCTCTCTG3AAAATCTCACTCTGAGTGTGCGCTTT 2833
QY 2933 GGACACCACTCTCCCTTCTCCAGGTCATGACAGGATCTGCTCCCTCTCTGCTTCCCTT 2992
DB 2834 GGACACCACTCTCCCTTCTCCAGGTCATGACAGGATCTGCTCCCTCTCTGCTTCCCTT 2893
QY 2993 ACCAGTCTGTGACCGCTGACTCCCGAGGAGTCTTCCCTGAAAGTGTGACCACTTCTTCT 3052

QY	1553	GGACAGAGTGTCTCATCTGTTGGAAGAGATT	CAGCTGTTCCTTGAAACCTGTGAAACCTGTTCG	1612
Db	1454	GGACAGCAGTGTCTCATCTGTTGGAAGAGATT	CAGCTGTTCCTTGAAACCTGTGAAACCTGTTCG	1513
QY	1613	CAACCTCAGCTGSCCCCCACCCAGGGTGCAGT	GTGTTGTAGGCTTCTCAGAGAGTGTCTG	1672
Db	1514	CAACCTCAGCTGSCCCCCACCCAGGGTGCAGT	GTGTTGTAGGCTTCTCAGAGAGTGTCTG	1573
QY	1673	GAGGGTSCCCGAGCCAACTGTATGTCTATGAG	AGAGCTGTGTGGACTGTCTTGTGCCGG	1732
Db	1574	GAGGGTSCCCGAGCCAACTGTATGTCTATGAG	AGAGCTGTGTGGACTGTCTTGTGCCGG	1633
QY	1733	GGACCCCACTGTGCTTGGGACCTGAGTCCCGA	ACCTGTTGCTCTGCTGCTGCCCCCAA	1792
Db	1634	GGACCCCACTGTGCTTGGGACCTGAGTCCCGA	ACCTGTTGCTCTGCTGCTGCCCCCAA	1693
QY	1793	CCTGAACTCCTTGGGAAGCAGGACATGGAGC	GGGGAAACCCAGAGTGGGCATGTGCCAGTGG	1852
Db	1694	CCTGAACTCCTTGGGAAGCAGGACATGGAGC	GGGGAAACCCAGAGTGGGCATGTGCCAGTGG	1753
QY	1853	CCCCATGACGAGGAGCCTTCGGGCTCAGAGC	CGCCGCAATCATTTAAAGAACTGCTCTGGC	1912
Db	1754	CCCCATGACGAGGAGCCTTCGGGCTCAGAGC	CGCCGCAATCATTTAAAGAACTGCTCTGGC	1813
QY	1913	TGTCCTTAACCTCCATCCTGGAGCTCCCGCT	CGCCCCACCTGTGAGCCTTGCCCTCTTATTA	1972
Db	1814	TGTCCTTAACCTCCATCCTGGAGCTCCCGCT	CGCCCCACCTGTGAGCCTTGCCCTCTTATTA	1873
QY	1973	TTGGAGTTCATGGCCCGACGACAGTCCAGAG	CCCTCTTCCACCTGTCTACAACTGGCTCCCT	2032
Db	1874	TTGGAGTTCATGGCCCGACGACAGTCCAGAG	CCCTCTTCCACCTGTCTACAACTGGCTCCCT	1933
QY	2033	CTTGCTCATATGTGCAGGATGGAGTTGGGGGT	CTCTACACAGTGTCTGGGCAACTGAGAATGG	2092
Db	1934	CTTGCTCATATGTGCAGGATGGAGTTGGGGGT	CTCTACACAGTGTCTGGGCAACTGAGAATGG	1993
QY	2093	CTTTTTCATACCTCTGTATCTCTTACTGGGT	GGGAGCAGGCAGGACACCTGCGCCCTGGA	2152
Db	1994	CTTTTTCATACCTCTGTATCTCTTACTGGGT	GGGAGCAGGCAGGACACCTGCGCCCTGGA	2053
QY	2153	TCCTGAACTGGCAGGCATCCCCCGGAGCAT	GTGAAGGTCCCGTTGACCAAGGGTCACTGG	2212
Db	2054	TCCTGAACTGGCAGGCATCCCCCGGAGCAT	GTGAAGGTCCCGTTGACCAAGGGTCACTGG	2113
QY	2213	TGGGGCGCCCTGCTGCGCAGCATCTTACTTG	GGCCCACTTTGTCTACTGTCTACTGTCTCT	2272
Db	2114	TGGGGCGCCCTGCTGCGCAGCATCTTACTTG	GGCCCACTTTGTCTACTGTCTACTGTCTCT	2173
QY	2273	CTTTTGCCTTAGTGTCTTTTCAGGAGCCCT	CATCATCTCGTGGCCCTCCCATTTGAGAGCACT	2332
Db	2174	CTTTTGCCTTAGTGTCTTTTCAGGAGCCCT	CATCATCTCGTGGCCCTCCCATTTGAGAGCACT	2233
QY	2333	CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	ACCTCGCCGCTTGGGGAGAGGCGCCCGTT	2392
Db	2234	CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	ACCTCGCCGCTTGGGGAGAGGCGCCCGTT	2293
QY	2393	AAGCAGAGAGCAACACTCCAGTCTCCCAAG	GAATGCAGGACCTCTCCCACTGATGTGGA	2452
Db	2294	AAGCAGAGAGCAACACTCCAGTCTCCCAAG	GAATGCAGGACCTCTCCCACTGATGTGGA	2353
QY	2453	CGCTGACAAACTGCTCTAGGCACTGAGGTA	GCTTTAACTCTAGGCAACAGCCGGGCGTG	2512
Db	2354	CGCTGACAAACTGCTCTAGGCACTGAGGTA	GCTTTAACTCTAGGCAACAGCCGGGCGTG	2413
QY	2513	CGGTGACGACCTTGCCCATCTGCTGGCTGGG	CGGCCCAAGCACACCTGACTAGGATGAC	2572
Db	2414	CGGTGACGACCTTGCCCATCTGCTGGCTGGG	CGGCCCAAGCACACCTGACTAGGATGAC	2473
QY	2573	AGCAGCAAAAGAACAACCTTTCTCCCTTGAG	AGGAGCTTCTGTCTACTGTGCACTCTGA	2632
Db	2474	AGCAGCAAAAGAACAACCTTTCTCCCTTGAG	AGGAGCTTCTGTCTACTGTGCACTCTGA	2533

Qy	2633	TGACATCTCAGCAGGCTGATGCAACAGCAGTCTGCCTCCCTATATGGGACTCCCTCTTACCAA	2699
Db	2534	TGACATCTCAGCAGGCTGATGCAACAGCAGTCTGCCTCCCTATATGGGACTCCCTCTTACCAA	2593
Qy	2693	GCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTCACTCATGATATTG	2752
Db	2594	GCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTCACTCATGATATTG	2653
Qy	2753	AAGAACTGTGAGAGGATCCTTCACTGTTCTGGCCATTCACGGGACCCCTCCAGAAACACAGT	2812
Db	2654	AAGAACTGTGAGAGGATCCTTCACTGTTCTGGCCATTCACGGGACCCCTCCAGAAACACAGT	2713
Qy	2813	TTTCAAGAGACCTTAATAAAACCTGCTGTCGCCAGGACCCCTATGGTAAATGAAACACCAACA	2872
Db	2714	TTTCAAGAGACCTTAATAAAACCTGCTGTCGCCAGGACCCCTATGGTAAATGAAACACCAACA	2773
Qy	2873	TCTAAACAAATCATATGCTAAATCATGCCACTCTTGAAACTCCACTCTGAAAGCTGCCGCTTT	2932
Db	2774	TCTAAACAAATCATATGCTAAATCATGCCACTCTTGAAACTCCACTCTGAAAGCTGCCGCTTT	2833
Qy	2933	GGACACAAACATCTCCTTCTCCAGGGTATGAGAGGATCTGCTCCCTCTGCTGCTTCCCTT	2992
Db	2834	GGACACAAACATCTCCTTCTCCAGGGTATGAGAGGATCTGCTCCCTCTGCTGCTTCCCTT	2893
Qy	2993	ACCAGTCTGTGCACCGCTGACTCCCCAGGAAAGTCTTCCCTGAAGTCTGACCACCTTTCTTCT	3052
Db	2894	ACCAGTCTGTGCACCGCTGACTCCCCAGGAAAGTCTTCCCTGAAGTCTGACCACCTTTCTTCT	2953
Qy	3053	TGCTTCAGTTTGGGGCAGACTCTGATCCCTCTGCTCCCTGGCAGAAATGGCAGGGGTATCTG	3112
Db	2954	TGCTTCAGTTTGGGGCAGACTCTGATCCCTTCTGCTCCCTGGCAGAAATGGCAGGGGTATCTG	3013
Qy	3113	AGCCTTCTTCACCTCCTTTACCTTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCCCTT	3172
Db	3014	AGCCTTCTTCACCTCCTTTACCTTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCCCTT	3073
Qy	3173	GTTTTGGGATTCAGAAACCTGCTGTTCAGAGACTGTTTATTTTTTATATAAAATAAAGG	3232
Db	3074	GTTTTGGGATTCAGAAACCTGCTGTTCAGAGACTGTTTATTTTTTATATAAAATAAAGG	3133
Qy	3233	CTTA 3236	
Db	3134	CTTA 3137	

```

RESULT 12
US-10-012-121A-276
; Sequence 276, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; TITLE OF INVENTION: Secured and Trans
; FILED INVENTION: Acids Encoding t
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
; LENGTH: 3143

```

TYPE: DNA	1034	CCCCCGGATTTCTCCACAGCTCCCCCATCTACGACAGTCTTCCCTCCAGTGGCAGGT	1093
ORGANISM: Homo sapiens	QY	TGGCGGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTGTGACATTTGAACGTGTCTT	1252
US-10-012-121A-276	Db	TGGCGGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTGTGACATTTGAACGTGTCTT	1153
Query Match 87.3%; Score 3060.8; DB 15; Length 3143;	QY	TAAGGGGAAATCAAAAGAGTTGAAACAAAGAACTTCAAGCTGGAGCTACTTATAGGGGCC	1312
Best Local Similarity 99.9%; Pred. No. 0;	Db	TAAGGGGAAATCAAAAGAGTTGAAACAAAGAACTTCAAGCTGGAGCTACTTATAGGGGCC	1213
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	QY	TGAGACCAACCCCGGACAGGAGTTGCTCAGTGGGCCCCCTCTCTGATAAGGGCCCTGAC	1372
	Db	TGAGACCAACCCCGGACAGGAGTTGCTCAGTGGGCCCCCTCTCTGATAAGGGCCCTGAC	1273
	QY	CTTCTATGAAGGACCAATTTCTGATGATGAGCAAGTGTGTGGGACGCCCCCTGTGTGAA	1432
	Db	CTTCTATGAAGGACCAATTTCTGATGATGAGCAAGTGTGTGGGACGCCCCCTGTGTGAA	1333
	QY	ATCTGGCTGGAGTATACACGGCTTGCAGTGGAGACGCCAGGSCCTTGATGGGCACAG	1492
	Db	ATCTGGCTGGAGTATACACGGCTTGCAGTGGAGACGCCAGGSCCTTGATGGGCACAG	1393
	QY	CCATCTTGTTCATGTATACCTGGGAAACCAACACAGGGTCTGCTCCACAGGCTGTGTAGTGG	1552
	Db	CCATCTTGTTCATGTATACCTGGGAAACCAACACAGGGTCTGCTCCACAGGCTGTGTAGTGG	1453
	QY	GGACAGAGTGTCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCTGACCTGTGTTCG	1612
	Db	GGACAGAGTGTCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCTGACCTGTGTTCG	1513
	QY	CAACCTGACGTGGGCCCCCACCACAGGGTCTGCTTGTAGGCTTCTCAGGAGGTGTCTGTG	1672
	Db	CAACCTGACGTGGGCCCCCACCACAGGGTCTGCTTGTAGGCTTCTCAGGAGGTGTCTGTG	1573
	QY	GAGGTTGCCCCGAGCAACTGTAGTGTCTATGAGAGCTGTGTGGAGTGTCTTGGCCG	1732
	Db	GAGGTTGCCCCGAGCAACTGTAGTGTCTATGAGAGCTGTGTGGAGTGTCTTGGCCG	1633
	QY	GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTGCTCCCTCTGTGCCCCCAA	1792
	Db	GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTGCTCCCTCTGTGCCCCCAA	1693
	QY	CTTGAACTCTCTGGAAGCAGACATGAGGCGGGGAAACCCAGAGTGGGCAATGTGCCAGTGG	1852
	Db	CTTGAACTCTCTGGAAGCAGACATGAGGCGGGGAAACCCAGAGTGGGCAATGTGCCAGTGG	1753
	QY	CCCCATGAGCAGGAGCTTTCGGCTTCAGAGCCGCGCAAAATCAATTAAGAAAGTCTCTGGC	1912
	Db	CCCCATGAGCAGGAGCTTTCGGCTTCAGAGCCGCGCAAAATCAATTAAGAAAGTCTCTGGC	1813
	QY	TGTCCCTAACTCCATCTGGAGCTCCCTGCCCCCACTGTGAGCCTTGGCCTCTTATTATTA	1972
	Db	TGTCCCTAACTCCATCTGGAGCTCCCTGCCCCCACTGTGAGCCTTGGCCTCTTATTATTA	1873
	QY	TTGGAGTCAATGGCCAGCAGCTCCAGAGCTCTTCCACTGTCTCAATGGCTCCCT	2032
	Db	TTGGAGTCAATGGCCAGCAGCTCCAGAGCTCTTCCACTGTCTCAATGGCTCCCT	1933
	QY	CTTGTCTATGATGAGGATGGAGTTGGGGGTCTCTACAGTGTGGGCAACTGAGAAATGG	2092
	Db	CTTGTCTATGATGAGGATGGAGTTGGGGGTCTCTACAGTGTGGGCAACTGAGAAATGG	1993
	QY	CTTTTCTATCCCTGTGATCTTCTGAGTGGGAGCAGCCAGGACCCCTGGCCCTTGA	2152
	Db	CTTTTCTATCCCTGTGATCTTCTGAGTGGGAGCAGCCAGGACCCCTGGCCCTTGA	2053
	QY	TCCTGAACTGGCAGGATCCCCCGGGAGCATGTGAAGGTCCCCCTTGACCAAGGTCTGAGTGG	2212
	Db	TCCTGAACTGGCAGGATCCCCCGGGAGCATGTGAAGGTCCCCCTTGACCAAGGTCTGAGTGG	2113
	QY	TGGGGCGCCCTGGCTGCCAGCAGTCTTACTGGCCCCACTTTGTCTACTGTCTCTCT	2272

Db 2114 TGGGGCCGCTGGCTGCCAGAGTCTCTAGTGGCCACCTTTGTCACTGTCCT 2173
QY 2273 CTTTGCCCTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTGGCCCTCCCATITGAGAGACT 2332
Db 2174 CTTTGCCCTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTGGCCCTCCCATITGAGAGACT 2233
QY 2333 CCGGCTCGGGCAAGGTTCAGGGCTGTGAGACCTCTGGCCCTCGGGAGAGGCCCCGCTT 2392
Db 2234 CCGGCTCGGGCAAGGTTCAGGGCTGTGAGACCTCTGGCCCTCGGGAGAGGCCCCGCTT 2293
QY 2393 AGCAGAGAGCAACACCTCCAGTCTCCCAAGGATGAGGACCTCTGCCAGTGTATGGA 2452
Db 2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGATGAGGACCTCTGCCAGTGTATGGA 2353
QY 2453 CGCTGACCAACTCCCTAGGCACTGAGGTAGCTTAACTCTAGGCAAGGCCCCGGGCTG 2512
Db 2354 CGCTGACCAACTCCCTAGGCACTGAGGTAGCTTAACTCTAGGCAAGGCCCCGGGCTG 2413
QY 2513 CGGTGAGGACCTGGCCATGCTGTGGCTGGGCGGCCCAAGCAAGCCCTGACTAGGATGAC 2572
Db 2414 CGGTGAGGACCTGGCCATGCTGTGGCTGGGCGGCCCAAGCAAGCCCTGACTAGGATGAC 2473
QY 2573 AGCAGCAAAAGACACCTTCTCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGA 2632
Db 2474 AGCAGCAAAAGACACCTTCTCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGA 2533
QY 2633 TGACACTCAGCAGGGTGTATGACAGAGCTGTGCTCCCTATGGACTCCCTTCAACAA 2692
Db 2534 TGACACTCAGCAGGGTGTATGACAGAGCTGTGCTCCCTATGGACTCCCTTCAACAA 2593
QY 2693 GCACATGAGCTCTTAAACAGGGTGGGGCTACCCGAGAGCTGCTCTACACTGATATG 2752
Db 2594 GCACATGAGCTCTTAAACAGGGTGGGGCTACCCGAGAGCTGCTCTACACTGATATG 2653
QY 2753 AAGAACTGGAGAGGATCCTTCAGTTCCTGGCCATTCAGGAGACCTCCAGAAACACAGTG 2812
Db 2654 AAGAACTGGAGAGGATCCTTCAGTTCCTGGCCATTCAGGAGACCTCCAGAAACACAGTG 2713
QY 2813 TTTCAGAGAGCCCTTAAACAGGGTGGGGCTACCCGAGAGCTGCTCTACACTGATATG 2872
Db 2714 TTTCAGAGAGCCCTTAAACAGGGTGGGGCTACCCGAGAGCTGCTCTACACTGATATG 2773
QY 2873 TCTAAACATCATATGCTTAAACATGCTTCTCCAGGAGCTGCTCTACACTGATATG 2932
Db 2774 TCTAAACATCATATGCTTAAACATGCTTCTCCAGGAGCTGCTCTACACTGATATG 2833
QY 2933 GGAACCAACACTCCCTTCTCCAGGAGCTGCTCTACACTGATATGCTTCTCTCTT 2992
Db 2834 GGAACCAACACTCCCTTCTCCAGGAGCTGCTCTACACTGATATGCTTCTCTCTT 2893
QY 2993 ACCAGTCTGCAACGCTGACTCCAGGAGGCTTCTCCCTGAGTCTGACCACTTCTTCT 3052
Db 2894 ACCAGTCTGCAACGCTGACTCCAGGAGGCTTCTCCCTGAGTCTGACCACTTCTTCT 2953
QY 3053 TGCTTCAGTGGGGAGAGCTGTATGCTTCTGCTGGGAGGATGCTGCTGCTGCTTCTCT 3112
Db 2954 TGCTTCAGTGGGGAGAGCTGTATGCTTCTGCTGGGAGGATGCTGCTGCTGCTTCTCT 3013
QY 3113 AGCTTCTTCACTCTTACCTAGCTGACCCCTTCACTCTCCCTGCTTCTCTTCTCTT 3172
Db 3014 AGCTTCTTCACTCTTACCTAGCTGACCCCTTCACTCTCCCTGCTTCTCTTCTCTT 3073
QY 3173 GTTTGGGATTCAGAAACCTGCTGTGAGAGCTGTTTATTTTATTAATAATAAGG 3232
Db 3074 GTTTGGGATTCAGAAACCTGCTGTGAGAGCTGTTTATTTTATTAATAATAAGG 3133
QY 3233 CTTA 3236
Db 3134 CTTA 3137

RESULT 13

US-10-006-116A-276

; Sequence 276, Application US/10006116A
; Publication No. US20030082826A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C15
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: US/10/006,116A
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661

```
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01

; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match      87.3%; Score 3060.8; DB 15; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 173 AGAGTCCCTGTGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTCCAGCCCTGGGCTGGACCC 232
Db 74 AGAGTCCCTGTGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTCCAGCCCTGGGCTGGACCC 133
Qy 233 CTGGAGCCTCCTGGGGCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCCGACGACGAC 292
Db 134 CTGGAGCCTCCTGGGGCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCCGACGACGAC 193
Qy 293 CGCGGGGGAGGCGGCGAGGCGCCCATGCCAGGGTTCAGATATGACAGGGATGAACG 352
Db 194 CGCGGGGGAGGCGGCGAGGCGCCCATGCCAGGGTTCAGATATGACAGGGATGAACG 253
Qy 353 TAGGGCATTAGCTTCTTCCACAGAGGCGCTCCAGGATTTTGACATCTCTCTCTGAG 412
```

Db 254 TAGGGCACTTAGCTTCTTCCACAGAGGGGCTCCAGGATTTTGACACTCTGCTCCTGAG 313
Qy 413 TGGTGAATGGAATACTCTCTACGTGGGGGCTCGAAGAGCAATTTCTTGCGCTTGGATATCCA 472
Db 314 TGGTGATGGAATACTCTCTACGTGGGGGCTCGAAGAGCAATTTCTTGCGCTTGGATATCCA 373
Qy 473 GGATCCAGGGGTCCCAAGGCTTAAAGAAACATGATACCGTGGCCAGGCTGACAGAAAGAAA 532
Db 374 GGATCCAGGGGTCCCAAGGCTTAAAGAAACATGATACCGTGGCCAGGCTGACAGAAAGAAA 433
Qy 533 GAGTGAATGTCCCTTTAAGAAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGT 592
Db 434 GAGTGAATGTCCCTTTAAGAAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGT 493
Qy 593 CCTGGTTTCTTACAAATGTACCCACTCTTACACCTGGCGACCTTTCGCCCTTCAGCCCTGC 652
Db 494 CCTGGTTTCTTACAAATGTACCCACTCTTACACCTGGCGACCTTTCGCCCTTCAGCCCTGC 553
Qy 653 TTGTACCTTCATTAAGATTTCTTACCTGTTCGCGCAATCTTCGAGGACAAAGGTAT 712
Db 554 TTGTACCTTCATTAAGATTTCTTACCTGTTCGCGCAATCTTCGAGGACAAAGGTAT 613
Qy 713 GGAGGAAAGGCGCAAGCCCTTTGACCCCGCTCAAGACATACGGCTGTCTTGGTGA 772
Db 614 GGAGGAAAGGCGCAAGCCCTTTGACCCCGCTCAAGACATACGGCTGTCTTGGTGA 673
Qy 773 TGGATGCTCTATTCTGGTACTATGAACAACTTCTCGGCGAGTGAGCCCATCTCTGATGCG 832
Db 674 TGGATGCTCTATTCTGGTACTATGAACAACTTCTCGGCGAGTGAGCCCATCTCTGATGCG 733
Qy 833 CACACTGGATCCAGCGCTGCTCAAGACCGACAACTTCTCGCGTGGTGGTGCATATGA 892
Db 734 CACACTGGATCCAGCGCTGCTCAAGACCGACAACTTCTCGCGTGGTGGTGCATATGA 793
Qy 893 CGCCTCTCTTTGTGGCAGCCATCCCTTCGACCAGGTCTCTACTTCTTCTTCGAGGAGAC 952
Db 794 CGCCTCTCTTTGTGGCAGCCATCCCTTCGACCAGGTCTCTACTTCTTCTTCGAGGAGAC 853
Qy 953 AGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACACATCGGGGTGGCTAGTCTGCAA 1012
Db 854 AGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACACATCGGGGTGGCTAGTCTGCAA 913
Qy 1013 GAAATGACGTGGCGCGGAGAAAGCTGCTGAGAAAGTGGACCACTTCTCTGAAAGCCCA 1072
Db 914 GAAATGACGTGGCGCGGAGAAAGCTGCTGAGAAAGTGGACCACTTCTCTGAAAGCCCA 973
Qy 1073 GCTGCTCTGCAACCGCGGCGAGCTGCTTCAAGTCTATCCGCCAGCGGTCTGCT 1132
Db 974 GCTGCTCTGCAACCGCGGCGAGCTGCTTCAAGTCTATCCGCCAGCGGTCTGCT 1033
Qy 1133 CCCCAGCGGATTTCTCCACAGCTCCCCACATCTAGCAGTCTTCACTCCAGTGGCAGGT 1192
Db 1034 CCCCAGCGGATTTCTCCACAGCTCCCCACATCTAGCAGTCTTCACTCCAGTGGCAGGT 1093
Qy 1193 TGGCGGGAACAGGAGCTCTGGGTTTGGCTTCTCTCTCTTGGACATGAACTGTCTT 1252
Db 1094 TGGCGGGAACAGGAGCTCTGGGTTTGGCTTCTCTCTCTTGGACATGAACTGTCTT 1153
Qy 1253 TAAAGGGAATAAAGAGTTGAAACAAAGAAACTTTCAGCTGGACTACTTATAGGGGCCC 1312
Db 1154 TAAAGGGAATAAAGAGTTGAAACAAAGAAACTTTCAGCTGGACTACTTATAGGGGCCC 1213
Qy 1313 TGAGACCAACCCCGCGCGAGGTTGCTCAGTGGGCCCCCTCTCTGATTAAGGCCCTGAC 1372
Db 1214 TGAGACCAACCCCGCGCGAGGTTGCTCAGTGGGCCCCCTCTCTGATTAAGGCCCTGAC 1273
Qy 1373 CTTTCATGAAGGACCAATTTCTTGATGATGAGCAAGTGTGGGAGCGCCCTCTGCTGGTGA 1432
Db 1274 CTTTCATGAAGGACCAATTTCTTGATGATGAGCAAGTGTGGGAGCGCCCTCTGCTGGTGA 1333
Qy 1433 ATCTGGCGTGGATATACCGGCTTTCAGTGGAGACGCCAGGCCCTTGTATGGGCAAG 1492
Db 1334 ATCTGGCGTGGATATACCGGCTTTCAGTGGAGACGCCAGGCCCTTGTATGGGCAAG 1393

Qy 1493 CCAATCTTGTATGTACTGGGAAACAACAAGGGTCCCTCCACAAGGCTGTGTAAAGTGG 1552
Db 1394 CCAATCTTGTATGTACTGGGAAACAACAAGGGTCCCTCCACAAGGCTGTGTAAAGTGG 1453
Qy 1553 GGACAGCAGTGTCTCATCTGGTGGAGAGATTCACTGTTCCTCAACCTGAACTGTTCG 1612
Db 1454 GGACAGCAGTGTCTCATCTGGTGGAGAGATTCACTGTTCCTCAACCTGAACTGTTCG 1513
Qy 1613 CAACTGTAGCTGGCCCCCAGGCTGAGTGTGTGTAGGCTTCTCAGGAGTGTCTG 1672
Db 1514 CAACTGTAGCTGGCCCCCAGGCTGAGTGTGTGTAGGCTTCTCAGGAGTGTCTG 1573
Qy 1673 GAGGCTGGCCCCGAGCAAACTGTAGTGTCTATAGAGCTGTGTGAGCTGTGTCTTTCG 1732
Db 1574 GAGGCTGGCCCCGAGCAAACTGTAGTGTCTATAGAGCTGTGTGAGCTGTGTCTTTCG 1633
Qy 1733 GGAACCCCACTGTGTCTGGGACCTGAGTCCCGAACCTGTTCCTCTGCTGCCCCAA 1792
Db 1634 GGAACCCCACTGTGTCTGGGACCTGAGTCCCGAACCTGTTCCTCTGCTGCCCCAA 1693
Qy 1793 CCTGAACCTCTGGAAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCACTGTGCGAGTGG 1852
Db 1694 CCTGAACCTCTGGAAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCACTGTGCGAGTGG 1753
Qy 1853 CCCCATGAGCAGGAGCTTTCGGCTCAGAGCGCGCCGCAAAATCATTAAGAGTCTCTGCG 1912
Db 1754 CCCCATGAGCAGGAGCTTTCGGCTCAGAGCGCGCCGCAAAATCATTAAGAGTCTCTGCG 1813
Qy 1913 TGTCTCTTAACCTCACTCTGGAGCTCCCTGCCCCCACCTGTGAGCTTGGCTCTTTATTA 1972
Db 1814 TGTCTCTTAACCTCACTCTGGAGCTCCCTGCCCCCACCTGTGAGCTTGGCTCTTTATTA 1873
Qy 1973 TTGGAGTCAATGCCCCAGCAGAGTCTCCAGAGCTCTTCCACTGTCTCAATAGGCTCTCT 2032
Db 1874 TTGGAGTCAATGCCCCAGCAGAGTCTCCAGAGCTCTTCCACTGTCTCAATAGGCTCTCT 1933
Qy 2033 CTTTGTGATAGTGCAGGATGGAGTTGGGGTCTCTTACCAAGTGTGGGCAACTGAGAAATGG 2092
Db 1934 CTTTGTGATAGTGCAGGATGGAGTTGGGGTCTCTTACCAAGTGTGGGCAACTGAGAAATGG 1993
Qy 2093 CTTTTCATACCTCTGTGATCTCTACTGGGTGAGCAGCAGGACAGACCTCTGGCCCTGGA 2152
Db 1994 CTTTTCATACCTCTGTGATCTCTACTGGGTGAGCAGCAGGACAGACCTCTGGCCCTGGA 2053
Qy 2153 TCTGAACCTGGCAGGACATCCCCGGGAGCATGTGAAGTCCCGTTGACAGGGTCACTGAGTGG 2212
Db 2054 TCTGAACCTGGCAGGACATCCCCGGGAGCATGTGAAGTCCCGTTGACAGGGTCACTGAGTGG 2113
Qy 2213 TGGGCGCGCTTGGCTGGCCAGCAGTCTCTATCTGGCCCCCACTTTTGTCTCATCTGTCTCT 2272
Db 2114 TGGGCGCGCTTGGCTGGCCAGCAGTCTCTATCTGGCCCCCACTTTTGTCTCATCTGTCTCT 2173
Qy 2273 CTTTGGCTTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTCGCTCCCACTTGGAGACT 2332
Db 2174 CTTTGGCTTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTCGCTCCCACTTGGAGACT 2233
Qy 2333 CCGGGCTCGGGCAAGGTTTCAAGGCTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCGCTT 2392
Db 2234 CCGGGCTCGGGCAAGGTTTCAAGGCTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCGCTT 2293
Qy 2393 AAGCAGAGAGCAACCTCCAGTCTCCAGGAATGACAGGCTCTGCGAGTGTGGA 2452
Db 2294 AAGCAGAGAGCAACCTCCAGTCTCCAGGAATGACAGGCTCTGCGAGTGTGGA 2353
Qy 2453 CGCTGACAACTGCTAGGCACTGAGTGTCTTAACTCTAGGCAAGGCCCGGGCTG 2512
Db 2354 CGCTGACAACTGCTAGGCACTGAGTGTCTTAACTCTAGGCAAGGCCCGGGCTG 2413
Qy 2513 CGGTGACGCACTGGCCATGCTGCTGGCGCGCCCAAGCAGGCTGTAGTGTGAC 2572
Db 2414 CGGTGACGCACTGGCCATGCTGCTGGCGCGCCCAAGCAGGCTGTAGTGTGAC 2473

Db 3134 CTTA 3137

RESULT 15

US-10-017-527A-276
; Sequence 276, Application US/10017527A
; Publication No. US20030082628A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gab, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C63
; CURRENT APPLICATION NUMBER: US/10/017,527A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570

Db	1274	CTTCATGAAGGACCATTTCTGATGATGAGCAAGTGGTGGGACGCCCCCTGCTGGTGAA	1333
Qy	1433	ATCTGGGTGGAGTATACAGGCTTGCACTGGAGACAGCCAGGGGCTTGAATGGGCACAG	1492
Db	1334	ATCTGGGTGGAGTATACAGGCTTGCACTGGAGACAGCCAGGGGCTTGAATGGGCACAG	1393
Qy	1493	CCATCTTGTGATGATACCTGGGAACACACAGGGTGGCTCCACAGGCTGGTGGTAAGTG	1552
Db	1394	CCATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1453
Qy	1553	GGACAGAGTGGCTCATCTGGTGGAGAGATTCAGCTGTTCCCTGACCCCTGAACCTGTCG	1612
Db	1454	GGACAGAGTGGCTCATCTGGTGGAGAGATTCAGCTGTTCCCTGACCCCTGAACCTGTCG	1513
Qy	1613	CAACCTGAGTGGCTCCACCCAGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1672
Db	1514	CAACCTGAGTGGCTCCACCCAGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1573
Qy	1673	GAGGGTGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1732
Db	1574	GAGGGTGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1633
Qy	1733	GGACCCCACTGCTGGGACCTGAGTCCGGAACCTGTTGGCTCTGCTGCTGCTGCTGCTGCTG	1792
Db	1634	GGACCCCACTGCTGGGACCTGAGTCCGGAACCTGTTGGCTCTGCTGCTGCTGCTGCTGCTG	1693
Qy	1793	CCTGAATCTCTGGAGCAGACATGGAGCGGGGGAACCCAGAGTGGGCTGTCAGTGG	1852
Db	1694	CCTGAATCTCTGGAGCAGACATGGAGCGGGGGAACCCAGAGTGGGCTGTCAGTGG	1753
Qy	1853	CCCCATGAGCAGGAGCCTTGGGCTCAGAGCGCGCCCAATCATTAAGAAAGTCTTGGC	1912
Db	1754	CCCCATGAGCAGGAGCCTTGGGCTCAGAGCGCGCCCAATCATTAAGAAAGTCTTGGC	1813
Qy	1913	TGTCCCTTAATCTCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1972
Db	1814	TGTCCCTTAATCTCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1873
Qy	1973	TTGAGTCAATGGCCAGCAGCAGTCCCAAGAGCCTCTTCCACTGTCTACAAATGCTCCCT	2032
Db	1874	TTGAGTCAATGGCCAGCAGCAGTCCCAAGAGCCTCTTCCACTGTCTACAAATGCTCCCT	1933
Qy	2033	CTTGTGATGATGAGTGGAGTGGGCTTCTACCAAGTGGTGGGCTGGGCTGGGCTGGGCTGG	2092
Db	1934	CTTGTGATGATGAGTGGAGTGGGCTTCTACCAAGTGGTGGGCTGGGCTGGGCTGGGCTGG	1993
Qy	2093	CTTTTTCATACCTGTGATCTCTACTGGGTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2152
Db	1994	CTTTTTCATACCTGTGATCTCTACTGGGTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2053
Qy	2153	TCCTGAATGGCAGGATCCCGGGGAGATGTGAGTGGCTCCGTTGACAGGCTGAGTGG	2212
Db	2054	TCCTGAATGGCAGGATCCCGGGGAGATGTGAGTGGCTCCGTTGACAGGCTGAGTGG	2113
Qy	2213	TGGGGCGCTGGCTGGCAGCAGTCTTACTGGGCGCCACTTTGTCAGTGGCTGCTGCT	2272
Db	2114	TGGGGCGCTGGCTGGCAGCAGTCTTACTGGGCGCCACTTTGTCAGTGGCTGCTGCT	2173
Qy	2273	CTTTGCTTGTGCTTTCAGGAGCCTCATCATCTCTGGCTCCCAATTTGAGAGCACT	2332
Db	2174	CTTTGCTTGTGCTTTCAGGAGCCTCATCATCTCTGGCTCCCAATTTGAGAGCACT	2233
Qy	2333	CGGGCTGGGCGAGGTTTGGGCTGTGAGACCTCGGCTGGGAGAGGCGCCGCTT	2392
Db	2234	CGGGCTGGGCGAGGTTTGGGCTGTGAGACCTCGGCTGGGAGAGGCGCCGCTT	2293
Qy	2393	AAGCAGAGAGCAACCTCCAGTCTTCCCAAGAAATGCAAGGACCTCTGCAAGTGTGGA	2452
Db	2294	AAGCAGAGAGCAACCTCCAGTCTTCCCAAGAAATGCAAGGACCTCTGCAAGTGTGGA	2353
Qy	2453	CGCTGACAACTGCTAGGACCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	2512
Db	2354	CGCTGACAACTGCTAGGACCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	2413

Qy	2513	CGTGCAGGCACTTGGCCATGCTGGCTGGGGGGCCCAAGCACACCCCTGCTAGGATGAC	2572
Db	2414	CGTGCAGGCACTTGGCCATGCTGGCTGGGGGGCCCAAGCACACCCCTGCTAGGATGAC	2473
Qy	2573	AGCAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGTCATCTGCA	2632
Db	2474	AGCAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGTCATCTGCA	2533
Qy	2633	TGACACTCAGCAGGGTGTGATGACAGCAGTCTGCTCCCTATGAGGACTCCCTTCTACCA	2692
Db	2534	TGACACTCAGCAGGGTGTGATGACAGCAGTCTGCTCCCTATGAGGACTCCCTTCTACCA	2593
Qy	2693	GCACATGAGCTCTCTAAACAGAGGCTGGGGCTACCCCCAGACCTGCTCTACATGATTTG	2752
Db	2594	GCACATGAGCTCTCTAAACAGAGGCTGGGGCTACCCCCAGACCTGCTCTACATGATTTG	2653
Qy	2753	AAGAACCTGGAGAGATCTTTCAGTCTGGGCTATCCAGGACCTCCAGAAACACAGTG	2812
Db	2654	AAGAACCTGGAGAGATCTTTCAGTCTGGGCTATCCAGGACCTCCAGAAACACAGTG	2713
Qy	2813	TTTCAAGAGACCTTAAACAACTGCTCTCCAGACCTATGTAATGAACACCAACA	2872
Db	2714	TTTCAAGAGACCTTAAACAACTGCTCTCCAGACCTATGTAATGAACACCAACA	2773
Qy	2873	TCTAAACAAATCATATGCTTAAACATGCTCTCTGGAACTCCACTCTGAGCTGCGCTTT	2932
Db	2774	TCTAAACAAATCATATGCTTAAACATGCTCTCTGGAACTCCACTCTGAGCTGCGCTTT	2833
Qy	2933	GGACACCACTCTCTCTCCAGGCTCATGAGGATCTGCTCCCTGCTGCTTCCCTT	2992
Db	2834	GGACACCACTCTCTCTCCAGGCTCATGAGGATCTGCTCCCTGCTGCTTCCCTT	2893
Qy	2993	ACCAGTCTGTGACCTGCTCTCCAGGAGTCTTCCCTGAGTCTGACCCCTTCTTCT	3052
Db	2894	ACCAGTCTGTGACCTGCTCTCCAGGAGTCTTCCCTGAGTCTGACCCCTTCTTCT	2953
Qy	3053	TGCTTCAGTGGGCGAGCTCTGATCCCTTCTGCTCCCTGCGAGAAATGCGGTAATCTG	3112
Db	2954	TGCTTCAGTGGGCGAGCTCTGATCCCTTCTGCTCCCTGCGAGAAATGCGGTAATCTG	3013
Qy	3113	AGCTTCTTCTCACTCTCTTACCCCTAGTCACTCCCTTCACTCTCCCTTCCCTTCTT	3172
Db	3014	AGCTTCTTCTCACTCTCTTACCCCTAGTCACTCCCTTCACTCTCCCTTCCCTTCTT	3073
Qy	3173	GTTCGGGATTCAGAAACCTGCTTGTGAGAGCTCTTATTTTATTTTATTAATAATAAGG	3232
Db	3074	GTTCGGGATTCAGAAACCTGCTTGTGAGAGCTCTTATTTTATTTTATTAATAATAAGG	3133
Qy	3233	CTTA 3236	
Db	3134	CTTA 3137	

Search completed: April 26, 2004, 03:19:12
Job time : 1032.65 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 07:15:18 ; Search time 173.879 Seconds
(without alignments)
11186.557 Million cell updates/sec

Title: US-10-051-835-13
Perfect score: 3505
Sequence: 1 ggcgttgcatgagggcac.....tttgggccaacacagggttg 3505

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgm2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230	6.6	2433	4	US-09-300-958A-24
2	153.4	4.4	4157	4	US-08-556-422A-1
3	126	3.6	3524	4	US-09-077-940A-3
4	125.4	3.6	3692	4	US-09-077-940A-1
5	102	2.9	2278	4	US-09-976-594-1002
6	98.6	2.8	121	4	US-08-833-381-202
7	98.6	2.8	2790	4	US-09-254-594-5
8	98.6	2.8	3432	4	US-09-254-594-4
9	89.8	2.6	2787	4	US-09-254-594-2
10	89.8	2.6	3195	4	US-09-254-594-1
11	84.2	2.4	4286	4	US-09-976-594-632
12	78.6	2.2	3560	1	US-08-121-713D-59
13	78.6	2.2	3560	1	US-08-835-268-59
14	78.6	2.2	3560	2	US-09-060-652-59
15	78.6	2.2	3560	3	US-08-833-391-59
16	78.6	2.2	3560	4	US-09-060-610-59
17	78.6	2.2	3560	5	PCT-US94-10151A-59
18	78.2	2.2	1923	4	US-09-653-274-12
19	78.2	2.2	3261	4	US-09-653-274-5
20	78.2	2.2	3694	4	US-09-653-274-3
21	69.8	2.0	2670	1	US-08-121-713D-61
22	69.8	2.0	2670	1	US-08-835-268-61
23	69.8	2.0	2670	1	US-09-060-652-61
24	69.8	2.0	2670	3	US-08-833-391-61
25	69.8	2.0	2670	4	US-09-060-610-61
26	69.8	2.0	2670	5	PCT-US94-10151A-61
27	63.8	1.8	2601	1	US-08-121-713D-53

28 63.8 1.8 2601 1 US-08-835-268-53 Sequence 53, Appl
29 63.8 1.8 2601 2 US-09-060-692-53 Sequence 53, Appl
30 63.8 1.8 2601 3 US-08-833-391-53 Sequence 53, Appl
31 63.8 1.8 2601 4 US-09-060-610-53 Sequence 53, Appl
32 63.8 1.8 2601 5 PCT-US94-10151A-53 Sequence 53, Appl
33 62.6 1.8 7218 1 US-08-232-463-14 Sequence 14, Appl
34 62 1.8 2854 1 US-08-121-713D-57 Sequence 57, Appl
35 62 1.8 2854 1 US-08-835-268-57 Sequence 57, Appl
36 62 1.8 2854 2 US-09-060-692-57 Sequence 57, Appl
37 62 1.8 2854 3 US-08-833-391-57 Sequence 57, Appl
38 62 1.8 2854 4 US-09-060-610-57 Sequence 57, Appl
39 62 1.8 2854 5 PCT-US94-10151A-57 Sequence 57, Appl
40 52.6 1.5 2898 4 US-09-308-179B-2 Sequence 2, Appl
41 50.2 1.4 2504 1 US-08-121-713D-63 Sequence 63, Appl
42 50.2 1.4 2504 1 US-08-835-268-63 Sequence 63, Appl
43 50.2 1.4 2504 2 US-09-060-692-63 Sequence 63, Appl
44 50.2 1.4 2504 3 US-08-833-391-63 Sequence 63, Appl
45 50.2 1.4 2504 4 US-09-060-610-63 Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-09-300-958A-24
; Sequence 24, Application US/09300958A

; Patent No. 6495319

; GENERAL INFORMATION:

; APPLICANT: McCrelland, Michael

; APPLICANT: Trengle, John

; APPLICANT: Welsh, John

; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of

; FILE REFERENCE: P-PH 3457

; CURRENT APPLICATION NUMBER: US/09/300,958A

; PRIOR FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: 60/083,331

; PRIOR FILING DATE: 1998-04-27

; PRIOR APPLICATION NUMBER: 60/098,070

; PRIOR FILING DATE: 1998-08-27

; PRIOR APPLICATION NUMBER: 60/118,624

; PRIOR FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 24

; LENGTH: 2433

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-300-958A-24

Query Match 6.6%; Score 230; DB 4; Length 2433;
Best Local Similarity 50.2%; Pred. No. 2.4e-53;
Matches 906; Conservative 0; Mismatches 805; Indels 93; Gaps 10;

QY 400 CTCGCTCTGAGTGGTATGGAATATCTCTAGCTGGGGCTGAGAGCCATCTCGG 459
DB 53 CCCTTCTGTGAGCCAGGATGGAAGAGCTGTATGTGGGGCCCGAGAGGCCCTCTTG 112
QY 460 CTTTGATATCAGGATCCAGGGGTCCC---CAGGCTAAAGAACATGATACCGTGGCCAG 516
DB 113 CACTTAACAGCAACCTCAGCTTCTTCCAGGGGGGAGTACCAAGAGCTACTGTGGAGTG 172
QY 517 CCAGTGCAGAGAAAAGAGTGAATGTGCTTTAAGAGAGAGCAATGAGACACAGTGT 576
DB 173 CAGATCTCAGAGGAAGCAGCAGTGCAGCTTCAAGGGGCAAGGCCCAAGCGTACTGTC 232
QY 577 TCAACTTTCATCGTGTCTTGTCTTCTTCAATGTCAACATCTTACACCTCGGCACT 636
DB 233 AMAACTACATCAGATCTCTTCCGACCTCAACAGAGCCACTGCTCACTTGGCACGG 292
QY 637 TCGCTTTCAGCCCTGCTGTATCTTCAATTTGAATTCACAGATTCCTACCTGTGGCCATCT 696
DB 293 CGCCCTTCAGCCCTGCTGTCTTCAATTCACATGACGAGCTTTACTTTAGCCCAAGATG 352

```
QY 697 CGAGAGCAAGGTCAAT-----GAGGGGAAAGGCGCAAGGCCCTTTGACCCCGCTCACA 750
Db 353 AGCGCGGTAAATGTCAATCTGAGAGGATGGCAAGGGTCAATGTCCCTTTGACCCCAACTTCA 412
QY 751 AGCATACGGCTGTCTGGTGGATGGATGCTCTATCTGTGTAATGTAACAACTTCTCTGG 810
Db 413 AGTCCACGGCTGTGGTGGTGTGATGAGTGTGACGTGTACACTGGAACAGTCACTAGTCTCCAG 472
QY 811 GCAGTGAGGCCATCTCTGATGCGGACACTGCGGATFCCAGAGCTCTCTCAAGACCGCAACT 870
Db 473 GAAACGACCCAGCCATTTCCCGAGAGCAGATTCCCGCCC-----CACCAAGACTGAGAGCT 529
QY 871 TCCTCCGCTGGCTGATCATGAGCCCTCTCTGTGGCAGCCATCCCTTCGACCCAGGTCG 930
Db 530 CCCTCAACTGGCTACAAGACCCCTGCTTGTGGCTCGCTACGTTCCCGGAGAGCTCGG 589
QY 931 -----TCTACTCTTCTTCAGAGAGCAGCAGCGAGT 963
Db 590 GCAGCCCCATAGGTGATGATGATAAGATCTACTTCTTCTTCAGCGAGAGCGGCCAGGAGT 649
QY 964 TTGACTTCTTTGAGAGGCTCCACACATCGGGTGGCTAGAGTCTGCAAGATGACGTGG 1023
Db 650 TTGAGTCTTTGAGAACACCATCGTGTCCGAGTTGCCGAGTCTGTAAAGGGCGATGAG 709
QY 1024 GCGGCGAAAGCTGCTCGAGAAAGATGGAACCACTTCTGGAAGGCCAGCTGCTCTGCA 1083
Db 710 GTGGAGAGCGGGTGTTCGAGCAACGCTGGACCTCTTCTCAAGGCTCAGCTCTGTGCT 769
QY 1084 CCAGCGCGGGCA--GCTGCCCTTCAAGCTCATCCGCGCGGCTCTGCTCCCGCGC 1140
Db 770 CCGGGCTGATGATGGCTTTCCTTTAACTGTGTCAAGATGCTTCACTCCCTGAACCCCA 829
QY 1141 ATTCTCCACAGCTCCCCACATCTA-----CGAGTCTTCACTCCAGTGGCGAGTTG 1194
Db 830 ACCCTCAGGATGGCGCAAGACCTTCTATCGGGTCTTTACTCCAGTGGCGACAGAG 889
QY 1195 GCGGACAGAGCTCTGGGTTGCTGCTTCTCTCTTGGACATGGAAGCTGTCTTGA 1254
Db 890 GGAACCAAGAGGCTCTGCACTCTGCTTCTTCACTTCACTGATGATGCAAGGCGCTTG 949
QY 1255 AGGGGAATCAAGAGCTGTGAACAAGAACTTTCAGCTGGACTTCTATAGGGGCGCTG 1314
Db 950 ACGGCTGTACAGAAAGTAAACAGAGAGACACAGAGTGTGTATACGAGACCCACAGG 1009
QY 1315 AGACCAACCCCGGCCAGGAGTTG-----CT 1341
Db 1010 TGCCCAACACCGCGCGCGGAGCGTGCATTACCAACAGTGCCTCGGGAACGGAAGATCA 1069
QY 1342 CAGTGGGCGCTCTCTCTGATAAGGCGCTGACCTTCATGAAGGACCACTTCTCTGATG 1401
Db 1070 CGTCCCTGCAGCTCCAGACCGAGTGTGAATTTCTCAAGGATCACTTCTGATGATG 1129
QY 1402 AGCAAGTGTGGGAGCGCCCTGTGTGTGAATCTGCGTGGAGTATACAGGCTTGCAG 1461
Db 1130 GGCAGGTCGCGAGTCTGTGTGTGTGTCAGCGCCAGAGCCGCTACCAAGCTGTGGCTG 1189
QY 1462 TGGAGACAGCCAGCGCTCTGATGGGACAGCCATCTGTGATGATCTCTGGGAACCA 1521
Db 1190 TGCACCGTGTGCTGGCTGACAG-----CACTATGATGCTCTATTTCTGGGCACTGGTG 1246
QY 1522 CAGGCTCGCTCCACAAAGCTGTGTAAGTGGGAGCAGAGTGTCTATCTGGTGGAGAGA 1581
Db 1247 ATGGCGGCTGCACAAAGCAGTGT---ACCTGAGCTCCAGATCCACATCAATTGAGAGC 1303
QY 1582 TTCAGCTGTCTCCCTGACCCCTGAACCTGTTCGCAACCTGCAAGTGGCCCGCCACAGGGTG 1641
Db 1304 TGCAGATCTTCCCTCAAGGACAGCTGTGCAAGACCTGCTCTTGGACAGCATATGGGGAC 1363
QY 1642 CAGTGTCTTGTAGGCTTCTCAAGAGGTGCTGTGGAGGGTGGCCCGGAGCCCACTGTAGTGTCT 1701
Db 1364 TGTGTATGCTCTCTCCCATTTCCGGGGTGGTGCAGAGTGGCCGCTGACCAACTGCGACCTGT 1423

QY 1702 ATGAGAGCTGTGGAGTGTGTCTTGGCCGGGAGCCCCCACTGTGTGCTGGGACCCCTGAGT 1761
Db 1424 ACCCACTGTGGAGACTGCCCTCTGCTCGAGACCCCTACTTGGGCTGGAGCTGTG 1483
QY 1762 CCGAACCCTGTTCCTCTGTGTGTCGCCCCCAACTGNACTTCTTGGAGCAGGACATGGAGC 1821
Db 1484 CCTGCGAGGCTCGCTAGCTCTTACCAGCTGTATGTCGCTTCCAGGCCCATGGACCCAGGACA 1543
QY 1822 GGGGGAACCCAGAGTGGGATGTGCCAGTGGGCCCATGAGCAGGAGCCCTTGGGCTTCAGA 1881
Db 1544 TTGAGGGTGCAGTGTCAAGGAATCTGCAAGAATTTCTCATACAAGGCCCGGTTTCTTG 1603
QY 1882 GCGGCCCGCAATCATTAAGAAAGTCTGTGCTGTCTTGTCTGATAGTGCAGGATGGAG 2055
Db 1604 TGCAGGTAAGCCATGTAAACAAGTCCAGATCAACCAACAACAGTGAACACACCTTGGCT 1663
QY 1942 GCGCCCACTGTGAGCCCTTGGCTCTTATTTATGGAGTCAATGGCCAGCAGCAGTCCCCAG 2001
Db 1664 GCCACTCTCTCAACCTTGGCCACTCGGCTCTGGGTGCACATGGAGGCCCACTCAATG 1723
QY 2002 AAGCTCTTCACTGTCTA-----CAATGGCTCCCTCTTGTCTGATAGTGCAGGATGGAG 2055
Db 1724 CCTCTGCTCTGCGCGTGTATTACCCACCGGGGACCTGCTGTGGTGGGCGAGCAGGAG 1783
QY 2056 TTGGGGGTCTTACAGTGTGGCAACTGAGAATGGCTTTTCATACCTCTGTGATCTCTCT 2115
Db 1784 GTTTGGGGGTGTTCAGTGTGGTGTGATAGAGAGGATTCAGCAGCTTGTGGCCAGCT 1843
QY 2116 ACTG 2119
Db 1844 ACTG 1847

RESULT 2
US-08-556-422A-1
; Sequence 1, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULZE, Joachim L.
; APPLICANT: BOUSSELOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)...(2673)
US-08-556-422A-1

Query Match 4.4%; Score 153.4; DB 4; Length 4157;
Best Local Similarity 50.0%; Pred. NO. 5.2e-32;
Matches 743; Conservative 0; Mismatches 636; Indels 108; Gaps 10;

QY 369 TTCACACAGAGGGCTCCAGGATTTTGACACTCTGCTCTGAGTGGTGGTGAATAACT 428
Db 211 TTTCATGAGCCAGACATCTTCAACTACTCAGCTTGTGCTGAGCGGAGCAAGGACACC 270
QY 429 CTCTACGTGGGGCTTCGAGAAGCCATTCTGGCTTGGATATCCAGGATCCAGGGGTCCCC 488
Db 271 TTGTACATAGGTGCGCGGAGGC-----GGTCTTGGCTGTGAACGCACTCAACATCTCC 324
QY 489 AGGCTTAAGAACATGATACCTGGCCAGCAGTGACAGAAAAAGAGTGAATGTCCCTTT 548
Db 325 GAGAACGACATGAGGTGTATTGGAGGTCTCAGAAACAAAGCAAAATGTGCAGAA 384
```

QY 549 AAGAAGAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGTTCTTACAAAT 608
Db 385 AAGGGGAATCAAAACAGACAGAGTGCCTCACTACATCGGGTGTGCGAGCCACTCAGC 444
QY 609 GTACCCATCTTACACCTCGGACCTTGGCCCTTCAGCCCTGCTGTGACCTTCAATGAA 668
Db 445 GCCACTTCCCTTTACGTGTGTGGGACCAACAGCATTCAGCCGCTGTGACCACTGAAC 504
QY 669 CTTCAAGATTCCTACCTGTTGCCATCTCGAGGACAAAGTCAATGAGGGAAGAAAGCCAA 728
Db 505 TTAACATCTTAAAGTTCTGGGGAATAATGAAGAT-----GGCAAGGAAGA 552
QY 729 AGCCCTTTGACCCCGCTCAAGACATACGGCTGTCTGTGTGATGGATGCTCTATTCT 788
Db 553 TGTCCCTTTGACCCAGCACACAGTACACATCGGTCAATGCTGTGATGGAGAACTTTATTCTG 612
QY 789 GGTACTATGACAACTTCCTGGGAGTGGCCATCTGATGCGCACATCGGATCCCAAG 848
Db 613 GGGACGTGCTAATATTTTGGGAAGTGAACCATCATCTCCGGAATCTTCCACAGT 672
QY 849 CCTGTCTCAAGACCGCAACTTCTCCGCTGGCTGATCATGACGCTCTCTTTTGGCA 908
Db 673 CCTCTGAGGACAGAAATGCAATCCCTTGGCTGAACGAGCTAGTTTCTGTGTTGCTGAC 732
QY 909 GCCATCCCTTGGACCCAGTCT-----GTCTACTTCTTCTTC 944
Db 733 GTGATCGGAAGAAACCCAGACAGCCCGAGCGGAGGATGACAGGCTCTACTTCTTCTTC 792
QY 945 GAGGAGACAGCACGCGAGTTTGTACTTCTTTGAGAGGCTCCACATCGCGGTGGGTAGA 1004
Db 793 ACGGAGTGTCTGTGGAGTATGAGTTTGTGTTACGGGTGTGATCCACCGATAGCAAGA 852
QY 1005 GTCTGCAAGATGAGTGGGGGGAAGCTGTCGAGAGAGTGGACCACTTCTCTG 1064
Db 853 GTGTGCAAGGGGACCAAGGGGGCTGAGGACCTTGACAGAAATGGACCTCTTCTCTG 912
QY 1065 AAGCCCAAGCTGTCTGTGACCCAGCCGCGG---GGCAGCTGCCCTTCAACGTCTCCGCCAC 1121
Db 913 AAGCCCGACTCATCTGCTCCCGGCAGACAGCGGCTTGGTCTTCAATGTGCTGCGGAT 972
QY 1122 GCGGTCTGTCTCCCGCGATCTTCCACAGCTCCCACTCCACAGTCTTCACTCC 1181
Db 973 GTCTTCTGTCTCAGTCCCGGGCTGAAGTGTCTGTGTTCTATGCACTCTTACCCCA 1032
QY 1182 CAGTGGCAGGTGTGGCGGACCAAGAGCTCTCGCGTTTGTGCTTCTCTCTTGGACATT 1241
Db 1033 CAGCTGAACAGTGGGCTGTGCGAGTGTGCGCTTCAACCTGTC---CACAGCGAG 1089
QY 1242 GAAGTGTCTTTAAGGGGAATAAAGAGTTGAACAAAG-----AAACTTCAGC 1292
Db 1090 GAGGTCTTCTCCACGGGAAGTACATGACAGACACCAAGTGGAGAGTCCCAACCAAG 1149
QY 1293 TGGACTACTTATAGGGGCTGTGAGACCAACCCCGCCAGGAGTGTGCTCAGTGGGC--- 1349
Db 1150 TGGTGGCTTAATGTCGCGGTACCCAAAGCGGGCTGTGAGGCTGATCGACAGGAG 1209
QY 1350 -----CCCTCTCTGTATAAGGCGCTTACCTCATG 1379
Db 1210 GCACGGGCGCCAACTACACAGCTCTCTTGAATTTGCCAGACAAGACGCTGAGTTGTT 1269
QY 1380 AAGGACCATTTCTGATGGATGA-----GCAAGTGTGGGAGCGCCCTCTGCTG 1430
Db 1270 AAGAACCACTTTTATGATGATGATCTCGGTAAACCCCAATAGACAACAGCCCGAGTTAATC 1329
QY 1431 AAATCTGGCGTGGATATACAGGCTTGCAGTGGAGACAGCCAGGGGCTTGTATGGGAC 1490
Db 1330 AAGAAAGATGTAACTACACCCAGATCGTGTGGACCGGACCGAGCCCTGGATGGAGT 1389
QY 1491 ACCCATCTTGTATGATCTGGGACCAACACAGGCTGCTCCCAAGAGGTGTGTAAGT 1550
Db 1390 GTCTATGATGTATGTTTGTGACGACAGACCGGGAGCTCTGCAAAAGCAATC---AGC 1446

QY 1551 GGGGACAGCAGTGTCTATCTGTGGAGAGATTACAGCTTCCCTGACCTGAACCTGTT 1610
Db 1447 CTCGACAGACGCTGTTCATCATATCGAGGAGACCCAGCTCTTCCAGACTTTCAGCCAGTC 1506
QY 1611 CGCAACCTGACAGCTGGGCCCCACCCAGGGTGCAGTGTGTTGT-----AGGCTTCTCAGGA 1664
Db 1507 CAGACCTGTCTGTCTTCAAGAAAGGCAACAGGTTTGTCTATGCTGTGCTCTTAACCTCG 1566
QY 1665 GGTGTGTGAGGGTGGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTC 1724
Db 1567 GCGGTGTGTCCAGGGCCCGCTGTGCTTCTGTGGGAAGCACGACCTCGAGGATGTGTG 1626
QY 1725 CTTGCCCGGAGCCCACTGTGCTGGGACCTGAGTCCCGAACCTG 1771
Db 1627 CTGGCGGAGACCCCTACTGCGCTGGAGCCCGCCACAGGACCTG 1673

RESULT 3
US-09-077-940A-3
; Sequence 3, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(38)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2706)..(3524)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (39)..(2702)
; OTHER INFORMATION:
US-09-077-940A-3

Query Match 3.6%; Score 126; DB 4; Length 3524;
Best Local Similarity 55.3%; Pred. No. 1.9e-24;
Matches 315; Conservative 0; Mismatches 240; Indels 15; Gaps 3;

QY 549 AAGAAGAGCAATGAGACACAGTGTTCAACTTTCATCCGTGTCCTGTTCTTACAAAT 608
Db 390 ATGAAGGGCAACAGAGGGCGAGTGTGAAACTTCGTAAGGTGCTGCTCTCGGAC 449
QY 609 GTCACCAATCTCTACACCTGCGGACCTTCGGCTTCAGCCCTGCTGTACCTTCAATGAA 668
Db 450 GAGTCCACGCTCTTTGTGTGCGGTTTCAACGCGCTTCAACCCGCTGTGCGCCAACTACAG 509
QY 669 CTTCAAGATTCCTACTCTGTGCTTCCCATCTCGGAGGACAAGGTCAATGAGGGAAGAAAGCCAA 728
Db 510 ATAGA-----CACCTCGAGCCGCTCGAGACAA-----CATCAGCGGTATGGCCCG 557
QY 729 AGCCCTTTGACCCCGCTCAAGACATACGGTGTCTGTGGTGGATGGGATGCTCTATTCT 788
Db 558 TGCCCGTACGACCCCAAGCAGCAATGTTGCCCTCTTCTGACGGGATGCTCTTCA 617
QY 789 GGTACTATGAACAACTTCCTGGGAGTGGACCATCTGATGCGCACACTGGGATCCCAAG 848
Db 618 GCTACTGTTACCGACTTCTTAGCCATTGATGTGTCATCTACCGAGCTTCGGGACAG 677
QY 849 CTTGTCTCAAGACCGACAACCTTCTCCCGCTGGCTGATCATGACGCCCTCTCTTTTGGCA 908
Db 678 CCACCCCTGGCACCCTGAAACATGACTCCAAAGTGTTCAAAGAGGCTTACTTTGTCAT 737

QY 909 GCATCCCTTCGACCCAGGTCGTCTACTTCTTCTCGAGAGACAGCCAGCGAGTTGAC 968
 Db 738 GCGGTGAGTGGGCGACGCCATGCTACTTCTTCTCCGGAGATTGCGATGAGTTAAC 797
 QY 969 TTCTTTGAGAGGTCACACATCGCGGTGGTGTGAGTCTGCAAGAAATGACGTGGCGGC 1028
 Db 798 TACTGAGAGAGTGGTGTGTCCTGCGGTGGTGTGTCAGAACAGCGTGGGAGC 857
 QY 1029 GAAAGC---TGTCGAGAGAGTGGACACCTTCTGAGGCCCGAGTGTCTGACCC 1085
 Db 858 TCCCCCGCGTGTGGAGAGCAGTGGACGCTCTCTGCAAGCGCGGCTCAACTGCTCT 917
 QY 1086 CAGCGGGGAGCTGCCCTTCAAGTTCATC 1115
 Db 918 GTACCCGAGACTCCCATTTCTACTTCAAC 947

RESULT 4
 US-09-077-940A-1
 ; Sequence 1, Application US/09077940A
 ; Patent No. 6576441
 ; GENERAL INFORMATION:
 ; APPLICANT: Kimura, Toru et al.
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
 ; FILE REFERENCE: 0020-4426P
 ; CURRENT APPLICATION NUMBER: US/09/077,940A
 ; CURRENT FILING DATE: 1998-06-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 3692
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: (1)...(18)
 ; NAME/KEY: CDS
 ; LOCATION: (19)...(2682)
 ; OTHER INFORMATION:
 ; NAME/KEY: 3'UTR
 ; LOCATION: (2683)...(3653)
 ; OTHER INFORMATION:
 ; NAME/KEY: PolyA site
 ; LOCATION: (3654)...(3692)
 ; OTHER INFORMATION:
 US-09-077-940A-1

Query Match 3.6%; Score 125.4; DB 4; Length 3692;
 Best Local Similarity 58.5%; Pred. No. 2.8e-24;
 Matches 238; Conservative 0; Mismatches 166; Indels 3; Gaps 1;
 QY 710 CATGAGGAGAAAGCCCAAGCCCTTTGACCCCGCTCAAGAGATACGGCTGCTTGGT 769
 Db 522 CATCAGTGGTATGGCGCGCTCCCTACGACCCCAAGCATGCCAATGCTCCCTCTTC 591
 QY 770 GGATGGGATGCTATTCTGTGTATGAAACAATCTCTGGGACAGTGGCCATCTCTGAT 829
 Db 582 AGATGGGATGCTTCTCAGAGCCACAGTAAGTCTCTAGCCATGACGCTGTATCTA 641
 QY 830 GCGCACACTGGGATCCAGCTGTCTCAAGACGACCAACTTCTCCGCTGGCTGACATCA 889
 Db 642 CCGTAGCCTTGGGAGCCGCGCCACACTGCGCACAGTAAGCATGACTCAAGTGGTTAA 701
 QY 890 TGAGCCTCTTGGGAGCCATCCCTTTCAGCCAGTGTCTTCTTCTTCGAGGA 949
 Db 702 AGAGCCATCTTTGTCATGCGTGGAGTGGGAGCCAGCTCTACTTCTTCTCCGGA 761
 QY 950 GACAGCCAGGATTTGATCTTCTTGGAGGCTCCACATCGCGGTGGCTAGAGCTG 1009
 Db 762 GATCGCCATGGAGTTAACTATCTGAAAAGTGTGTGTGTCGCGTGTGGCCCGTGTATG 821
 QY 1010 CAGAGATGACGTGGCGG---CGAAAAGCTGTGCGAGAGAGTGGAGCCACCTTCTCTGAA 1066

Db 822 CAAGATGATGTGGCGCTCCCAAGGTCGTCGAGAGCAGTGGACTTCTTCTCTGAA 881
 QY 1067 GCGCCAGCTGCTGACCCAGCGGGGAGCTGCGCTTCAAGTCA 1113
 Db 882 GCGCGGCTCAACTGCTCCGTCGCTGGGACTCACACTTCTACTTCA 928
 RESULT 5
 US-09-976-594-1002
 ; Sequence 1002, Application US/09976594
 ; Patent No. 6673549
 ; GENERAL INFORMATION:
 ; APPLICANT: Buchbinder, Jenny
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; CURRENT APPLICATION NUMBER: US/09/976,594
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1002
 ; LENGTH: 2278
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 411373.7
 US-09-976-594-1002

Query Match 2.9%; Score 102; DB 4; Length 2278;
 Best Local Similarity 50.0%; Pred. No. 6.4e-18;
 Matches 339; Conservative 0; Mismatches 330; Indels 9; Gaps 3;
 QY 717 GAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGG 776
 Db 761 GGAATGCCAGATGCCCATATGATGCCCAACATGCCAAGTGTGCTGTTTGCAGATGA 820
 QY 777 ATGCTTATTTCTGGTATATGAAACAATTCTGGGAGTGGAGCCATCTCTGATGGCACA 836
 Db 821 AAACCTATATCTCAGCCACAGTACGATCTCTTCCCATTTGACGAGTCAITTTACCGAGT 880
 QY 837 CTGGATCCAGCTGTCTCTCAAGACGACAACTTCTCCGCTGGCTGCTATCATGAGCC 896
 Db 881 CTGGAGAAAGCCCTTACCTCGGAGCCGTCAAGCAGATTCAAATGTTGAAAGAACCA 940
 QY 897 TCCTTTGTGGAGGCAATCCCTTGGACCCAGTGTCTACTTCTTCTTCTCGAGGACAGCC 956
 Db 941 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCTCAGGAAATACCA 1000
 QY 957 AGCGAGTTTGAATCTTTTGGAGAGGTCACACATCGCGGTGGCTAGAGTCTGCAAGAAT 1016
 Db 1001 GTGGAGTATTAACACATGGGAAAGGTAGTTTCCCAAGATGGTCTCAGTTTGTAAAGAT 1060
 QY 1017 GACGTGGCGG---CGAAAAGCTGTGAGAGAGTGGACCACTTCTCTGAAGCCGAG 1073
 Db 1061 GATATGGAGGATCTCAAGAGTCTCTGAGAAACAGTGGAGCTGCTTCTCTGAAGCGCGC 1120
 QY 1074 CTGCTCTGACCCAGCGGCGAGCTGCCCTTCAAGCTATCCGCGACGCGTCTGCTGTC 1133
 Db 1121 TTGAATCTGTCTAGTCTCTGGAGACTCTCTCATTTTATTTTCAACATCTTCCAGGAGTTACA 1180
 QY 1134 CCGCGCGATTTCTCCCAAGCTTCCCAATCTAGCAGTCTTCACTCCAGTGGCAGGTT 1193
 Db 1181 GATGTGATTCTGATCAACGCGGCTGATGT---TGTCCTGGCAACGTTTTTCTACACCTTAT 1237
 QY 1194 GCGGAGCAGGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATTAAGAGCTCTT 1253
 Db 1238 AACAGCATCCCTGGGTGTGAGTCTGTGCTTATGATGCTTGTGATGCTTCCAGTGTCTT 1297
 QY 1254 AAGGGGAAATACAAAGAGTGTGAACAAAGAACTTCACTCGCTGGAGTAC---TTATAGGGGC 1310

Db 1298 ACTGGGAGATTCAAGAAAGAGTCTCTGATTCACCTGGACACCAAGTTCTTGATGAA 1357
QY 1311 CCTGAGACCAACCCCGGCGGAGGAGTTGCTCAGTGGGCCCCCTCTCTGTGATAAGGCCCTG 1370
Db 1358 CGAGTTCTTAAAGCCAGGCGAGTTGCTGTGCTCATCTCTCTTAGAAGATATGCA 1417
QY 1371 ACCTTCATGAAGACCAT 1388
Db 1418 ACCTCCAAATGAGTTCCCT 1435

RESULT 6

US-09-833-381-202
; Sequence 202, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 202
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-202

Query Match 2.8%; Score 98.6; DB 4; Length 121;
Best Local Similarity 88.4%; Pred. No. 1.1e-17;
Matches 107; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 893 CGCTCTTGTGGCAGCCATCCCTTGGACCCAGGCTGCTACTTCTTCTTCGAGGAGAC 952
Db 1 CGCTCTTGTGGAGAGACATCCCTTCTACCCAGCGCCTACTTCTTCTTCAGGAGAC 60
QY 953 AGCCAGGAGTTGACTTCTTTGAGAGGCTCCACACATCGGGGTGGCTAGAGTCTCAA 1012
Db 61 AGCCAGGAGTTGACTTCTTTGAGAGGCTCCACACATCGGGGTGGCTAGAGTCTCAA 120
QY 1013 G 1013
Db 121 G 121

RESULT 7

US-09-254-594-5
; Sequence 5, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 2790
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: CDS
; LOCATION: (1)..(2790)
; OTHER INFORMATION: Identification Method: E

; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-5
Query Match 2.8%; Score 98.6; DB 4; Length 2790;
Best Local Similarity 50.1%; Pred. No. 6.3e-17;
Matches 369; Conservative 0; Mismatches 344; Indels 24; Gaps 4;
QY 571 AGTGTTCACATTCATCCGTGCTCTGTTGATACCTTCACTTGAACCTCAAGATTCTACCTGTTC 630
Db 359 AGTGTTCACATTCATTCGTGTTGTTGCTCCGAGCTCCAGACAGCTCTTGTGCTGTG 418
QY 631 GCACCTTCGCTTCAGCCCTCTGTTGATACCTTCACTTGAACCTCAAGATTCTACCTGTTC 690
Db 419 GAACGACTCATTCAGCCCTCTGTTGCTCCGAGCTATGGAT-----AATTCGC 466
QY 691 CCATTCGAGGAGCAAGTCTCATGGAGGAAAGGCCAAAGCCCTTTGACCCGCTCACA 750
Db 467 TGCAGCAGGAGGTGAGGAACTGATGGGCGAGCTCGATGCCCTTTGTATGCCACCCAGT 526
QY 751 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGTGTAATCTATGAACAACCTTCCTGG 810
Db 527 CCAACGTGGCCATCTTTCAGAGGGGAGCTGTACTCAGCCACAGCTGCGGATTTCCAGG 586
QY 811 GCAGTGAGCCCATCTCTGATGGGACACATGGGATCCGACCTGTCTCTCAAGACCGACAAT 870
Db 587 CCAAGTGTGCTGTAGTTTACAGAAAGCTTGGGGCCCAAGCTCCGCTCCGCTCCGCAAGT 646
QY 871 TCCTCCGCTGGCTGCATCATGACGCTCTCTTGTGGAGGACCATCCCTTCGACCCAGGTGC 930
Db 647 ATGACTCCAAAGTGGCTCCGAGAGCCACACTTTTGTCCAGGCTTGGAGCATGGAGCCATG 706
QY 931 TCTACTTCTTTCGAGGAGACAGCCAGGAGTTGACTTCTTTGAGAGGCTCCACACAT 990
Db 707 TCTACTTCTTTCGCGAGGCTCTCTGTGGAGGATGCTCGGCTGGGGAGGATGCACTTCT 766
QY 991 CCGGGGTGGCTAGAGTCTGCAAGAAATGACGTGGGCGCGGCAAAAGCTG---CTGCAGAGA 1047
Db 767 CCGGCTAGCCGAGTATGTAACGTGACATGGGCGGCTCGCTCGGCGCTTGGACCGCC 826
QY 1048 AGTGACACCTTCTCTGAGCCAGCTGCTGTCACCCAGCGGCGGAGCTGCTTCA 1107
Db 827 ACTGACATCTCTCTGAGCTTCGAGCTTCGAGCTCAACTCTCTGCTCCCTGGGAGTCTACTTCT 886
QY 1108 A---CGTCATCCGCCAGCGCTCTGCTCCCGCGGATTCCTCCACAGCTCCCAATCT 1164
Db 887 ATTTTGATGTTTACAGSCCTTGACTGGGCTGTGAACTGCTGCGCGCTCTGCTCTCT 946
QY 1165 AGCAGTCTTCACCTCCAGTGGGAGGTTGGCGGAGCAGGAGCTCTGCGGTTGTGCT 1224
Db 947 TTGGGGTCTTCACCAACCCAGACCAA-----TAGCATCCCTGGCTCTGCGCTCTGCGCT 1000
QY 1225 TCTCTCTCTGACATTCAGAGCTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAGAAA 1284
Db 1001 TCTACCTGGATGAGATTGAGGTTGGGTTTGGGGCAAGTTCAAGGAGCAGAGGATCTGG 1060
QY 1285 CTTGAGCTGGAGTACT 1301
Db 1061 ATGGGGCTGGAGTCTCT 1077

RESULT 8
US-09-254-594-4
; Sequence 4, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11

NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 3432
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1..7)
OTHER INFORMATION: Tissue Type: Child Brain
NAME/KEY: 5'UTR
LOCATION: (1..187)
OTHER INFORMATION: Identification Method: E
NAME/KEY: misc feature
LOCATION: (188)..(2977)
OTHER INFORMATION: CDS; Identification Method: E
NAME/KEY: 3'UTR
LOCATION: (2978)..(3407)
OTHER INFORMATION: Identification Method: E
NAME/KEY: PolyA signal
LOCATION: (3408)..(3432)
OTHER INFORMATION: Identification Method: E
US-09-254-594-4

Query Match 2.8%; Score 98.6; DB 4; Length 3432;
Best Local Similarity 50.1%; Pred. No. 7.1e-17;
Matches 369; Conservative 0; Mismatches 344; Indels 24; Gaps 4;

QY 571 AGTGTTCACCTCATCGGTCTCTGTTCTTACATGTCACCCATCTCTACACCTGCG 630
DB 546 AGTGCTACATATATCGTGTCTTCTTCTCCCTGGGACTCCAGAGCGCTCTTGGCTGTG 605
QY 631 GCACCTTCGCTTCAGCCCTGCTGTACCTTCATTTGAATTCAGATTCCTACCTGTGC 690
DB 606 GAACTACTCATTCAGCCCTGTGTGCGCAGCTATGGAT-----AACTTCGC 653
QY 691 CCATCTCGGAGCAAGTCTATGAGGAGAAAGCCAAAGCCCTTTGACCCCGCTCACA 750
DB 654 TGCAGCAGGAGGTGAGCAACTGATGCGCAGGCTCGATGCCCTTTGATGCCACCCAGT 713
QY 751 AGCATACGGCTCTTGTGTGATGGGATGCTCTATTCTGTGACTATGAACAATCTCTGG 810
DB 714 CCAAGTGGCCATCTTTGAGAGGAGGAGCTGTACTCAGCCACAGCTGCGGATTTCCAGG 773
QY 811 GCAGTGAACCCATCTGTATGCGCACAATGGGATCCAGAGCTGTCTTCAAGACCGACA 870
DB 774 CCAGTGATGCTGTATTTACAGAGGCTTTGGGCGCCAGCCCACTCCGCTCCGCGCAAGT 833
QY 871 TCCTCCGCTGGCTCATCATGACGCTCTTTGTGGCAGCCATCCCTTCGACCCAGGTG 930
DB 834 ATGACTCCAAAGTGGCTCCGAGAGCCACACTTTGTCCAGGCTTTGGAGCATTGGAGCATG 893
QY 931 TCTACTTCTTTTCGAGGAGCAGCCAGCGAGTTTGACTTTCTTTGAGAGGCTCCACAT 990
DB 894 TCTACTTCTTTTCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGTGCAGTTCT 953
QY 991 CGCGGTGGCTAGATCTGCAAGATGACGTGGGCGGAGAAAGCTG---CTGCAGAGA 1047
DB 954 CCGCGGTAGCCGAGTATGTAAAGTGAATGGGCGGCTCCGCTCGGCGCTTGAACCGCC 1013
QY 1048 AGTGACACACCTTCTGAAGCCAGCTGTCTGCAACCCAGCCGCGGCGAGCTGCCCTTCA 1107
DB 1014 ACTGACATCTTCTGAAGCTTCGGCTCAACTGTCTGTCTCCCTGGGAGCTCTACTTCT 1073
QY 1108 A---CGTCATCGGCGAGTCTGTCTCCCGCGGATCTTCCACAGCTCCCACTCT 1164
DB 1074 ATTTTGTATGTTTACAGGCGCTTGAATGGGCGCTGTGAACCTGCATGGGCGCTCTGCTCT 1133
QY 1165 AGCGAGTCTTTCACCTCCAGTGGCAGGTGTGGCGGAGCCAGGAGCTCTGCGGTTTGTGCT 1224
DB 1134 TTGGGGTCTTTCACCAACCCAGACCA-----TAGCATCCCTGGCTCTGCGCTCTGCGCT 1187
QY 1225 TCTCTCTCTTGACATTTGAACGTGTCTTTAAGGGGAAATACAAAGATTGAACAAAGAA 1284

DB 1188 TCTACCTGGATGAGATTGAGCTGGGTTTGAAGGCAAGTTCAAGGACAGAGGATCTGG 1247
QY 1285 CTTTACCGCTGGACTACT 1301
DB 1248 ATGGGGCTGGACTCT 1264

RESULT 9
US-09-254-594-2
Sequence 2, Application US/09254594
Patent No. 6566094
GENERAL INFORMATION:
APPLICANT: KIMURA, Toru
APPLICANT: KIKUCHI, Kaoru
TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
FILE REFERENCE: 0020-4527P
CURRENT APPLICATION NUMBER: US/09/254,594
CURRENT FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 2787
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1..7)
OTHER INFORMATION: Tissue Type: Brain
NAME/KEY: CDS
LOCATION: (1)..(2787)
OTHER INFORMATION: Identification Method: E
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-2

Query Match 2.6%; Score 89.8; DB 4; Length 2787;
Best Local Similarity 50.1%; Pred. No. 1.7e-14;
Matches 369; Conservative 0; Mismatches 347; Indels 21; Gaps 5;

QY 571 AGTGTTCACCTCATCGGTCTCTGTTCTTCAATATGTCAACCATCTCTACACCTGCG 630
DB 356 AATGCTACACTACATCCGTGTTCTTGTTCCTGGAGCTCGCAGACACTCTCTGCTGTG 415
QY 631 GCACCTTCGCTTCAGCCCTGCTGTACCTTCATTTCAAGATTCCTACCTGTTC 690
DB 416 GAACAAATTCCTTCAGCCCTGTGTGTCGACGTATGGGATTAACATCTCTGCAAC----- 469
QY 691 CCATCTCGGAGGACAAAGTCTATGGAGGAAAGGCCAAAGCCCTTTGACCCCGCTCACA 750
DB 470 -----AGGAGGCTGAGGAGCTGAGTGGGCAAGCTCGATGCCCTTTGATGCCACCCAGT 523
QY 751 AGCATACGGCTCTTGTGTGATGGGATGCTCTATTCTGTGTAATATGAACAATCTCTG 810
DB 524 CCAGTGTGGCCATCTCTGAGAGGAGTGTGTGTAATCAGCCACAGCAGCAGATTTCCAGG 583
QY 811 GCAGTGAACCCATCTGTATGCGCACATCGGATCCAGCCTGTCTCAAGACCCGACAACT 870
DB 584 CAGTGTATGCTGTGTTTACAGAGCCTTGGACCTCAGCCCCCACTCTCCGTTCTGCAAGT 643
QY 871 TCCTCGGTGGCTGATCATATGACGCTCTTTTGTGGCAGCCAT-----CCCTTCGACCCAGG 927
DB 644 ATGACTTCCAAGTGGCTTCGAGAGCCACACTTTTGTCTATGTCTTGGAGATGGAGACCATG 703
QY 928 TGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTTCTTTGAGAGCTCTCACA 987
DB 704 TCTACTTCTTCTTCGAGAGAACTCTCTGTGAGAGACGCCCGCTTGGGAGGCTGCAAT 763
QY 988 CATCGCGGTGGCTAGAGTCTCAAGAAATGAGCTGGGCGGCGAAAGCTG-----CTGCAGA 1044
DB 764 TTTCCCGGTGGCGCGGTGTGTAAACGTGACATGGGTGGCTCAGCAGCGGCTTTGGATC 823

QY 1045 AGAAGTGGACACCTTCTGAAGCCAGCTGCTCTGACCCAGCCGGGCGAGCTGCCCT 1104
DB 824 GCCACTGGACATCTCTCTTAAGCTGAGGCTCAACTGCTCGTCCCTGGGACTCTTACCT 883
QY 1105 TCAAGTCATCCGCCACCGGCTCTGCTCCCGCGGATTTCCACACAGCTCCCACTCT 1164
DB 884 TCTAC-TTTGATGCTTTACAGTCTTAACTGGGCTGTGAACCTGCAATGGGCGCTCTGC- 941
QY 1165 ACGAGTCTTCACTCTCCAGTGGGAGGTTGGCGGGAACAGGAGCTCTGCGGTTTGTGCT 1224
DB 942 -CCTCTTTGGGGTCTTCACTACTCAGACCAATAGCAATCTCGGTCTGCACTCTGCGCT 1000
QY 1295 TCTCTCTCTGGACATTAAGCTGCTTTAAGGGGAATACAAAGAGTTGAACAAAGAA 1284
DB 1001 TCTACTAGATGACATTAAGCTGCTTTAAGGGGAAGTTCAAGGAGCAGAGGAGTCTGG 1060
QY 1285 CTTACGCTGGACTACT 1301
DB 1061 ATGGGGCTGGACTCT 1077

RESULT 10

US-09-254-594-1

; Sequence 1, Application US/09254594

; Patent No. 6566094

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru

; APPLICANT: KIMURA, Toru

; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y

; FILE REFERENCE: 0020-4527P

; CURRENT APPLICATION NUMBER: US/09/254,594

; CURRENT FILING DATE: 1998-05-11

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3195

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(50)

; OTHER INFORMATION: Tissue Type: Brain

; NAME/KEY: 5'UTR

; LOCATION: (1)..(50)

; OTHER INFORMATION: Identification Method: E

; NAME/KEY: misc_feature

; LOCATION: (51)..(2837)

; OTHER INFORMATION: CDS; Identification Method: E

; NAME/KEY: 3'UTR

; LOCATION: (2838)..(3195)

; OTHER INFORMATION: Identification Method: E

; US-09-254-594-1

Query Match 2.6%; Score 89.8; DB 4; Length 3195;
Best Local Similarity 50.1%; Pred. No. 1.9e-14;
Matches 369; Conservative 0; Mismatches 34; Indels 21; Gaps 5;
QY 571 AGTGTTCACACTTCATCGTGTCTCTGTTTCTTACAAATGTACCCCACTCTACACCTGCG 630
DB 406 AATGCTACAACTACATCGTGTCTCTGTTTCTTCCCTGGGACTCGGAGACACTCTCTGCTGTG 465
QY 631 GCACCTTCGCTTCAGCCCTGTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTTCG 690
DB 466 GAACAAATTCCTTCAGCCCTGTGTGTCGAGCTATGGGATACATCTCTGCAAC----- 519
QY 691 CCATCTCGGAGGACAAAGTTCATGGAGGGAAGGCAAGCCCTTTGACCCCGCTCACA 750
DB 520 -----AGAGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCCTTTGATGCCACCCAGT 573
QY 751 AGCAATACGCTGTCTGTTGGTGGATGCTCTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 810
DB 574 CCACCTGTGGCCATCTCTGACAGAGGGTGTGTTGTCTGACCCCAACGACGACGAGATTTCCAGG 633

QY 811 GCAGTGGAGCCCATCTCTGATGGGCACTGGGATCCAGGCTGTCTCAAGACCGACAACCT 870
DB 634 CCAGTGTATGCTGTGGTCTTACAGAGCTTGGACCTTCAGCCCCCACTCCGTTCTGCAAGT 693
QY 871 TCCTCCGCTGGCTGATCATATGACGCTCTCTTTGTGGCAGCCAT---CCTTCGACCCAGG 927
DB 694 ATGACTCCCAAGTGGCTTCAGAGGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATG 753
QY 928 TCGTCTACTTCTTCTGAGGAGAGACAGCGAGGATTTGAATTTTGTGAGAGGCTCCACA 987
DB 754 TCTACTTCTTCTTCCGGAGAAAGTCTCTGTGGAGGACGCCCGGCTGGGGAGGGTGCAGT 813
QY 988 CATCGGGGTGCTAGAGTCTCAAGAAATGACGTGGGGGCGGAAAGCTG---CTGCAGA 1044
DB 814 TTTCCGGGTGCGCGGGTGTGTAAAGTGAATGGTGGCTCACACCGGGCTTTGGATC 873
QY 1045 AGAAGTGGACCACTTCTTGAAGGCCAGCTCTGTGACCCAGCGGGGAGCTGCCCT 1104
DB 874 GCCACTGGACATCTTCTTAAAGCTGAGGCTCAACTGTCTCCGTCCCTGGGAGCTCTACCT 933
QY 1105 TCAAGTTCATCGGACAGCGGTCTCTGCCCGCGATTTCTCCACAGCTCCCCACATCT 1164
DB 934 TCTAC-TTTGATGCTTTACAGTCTTAACTGGGCTGTGAACCTGATGGGCGCTCTGC- 991
QY 1165 ACGACTCTTCACTCTCCAGTGGGAGTGGCGGGAACAGGAGCTCTGCGGTTTGTGCT 1224
DB 992 -CCTCTTTGGGGTCTTCACTACTCAGACCAATAGCAATCTCTGGTCTGCACTCTGCGCT 1050
QY 1225 TCTCTCTCTGGACATTAAGCTGTCTTTAAGGGGAATACAAAGAGTTGAACAAAGAA 1284
DB 1051 TCTACCTAGATGACATTTGAACCTGGCTTTTGAAGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1110
QY 1285 CTTACGCTGGACTACT 1301
DB 1111 ATGGGGCTGGACTCT 1127

RESULT 11

US-09-976-594-632

; Sequence 632, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 632

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6673549 238322.6

; US-09-976-594-632

Query Match 2.4%; Score 84.2; DB 4; Length 4286;
Best Local Similarity 50.3%; Pred. No. 7.8e-13;
Matches 273; Conservative 0; Mismatches 253; Indels 17; Gaps 2;
QY 571 AGTGTTCACACTTCATCGGCTCTCTGTTTCTTACAAATGTACCCCACTCTTACACCTGCG 630
DB 611 AGTGTACAACTATATTCGTGTTCTTGTCTTCCCTGGGACTCCCAAGAGCTCTCTTGGCTGTG 670
QY 631 GCACCTTCGCTTCAGCCCTGTTGACCTTCACTTGAACCTTCAAGATTCTTACCTGTTCG 690
DB 671 GAAGAACTCATTCAGCCCTGTGTGCGGAGCTATGGAT-----AACTTCG 718

APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1953
US-08-835-268-59
Query Match 2.2%; Score 78.6; DB 1; Length 3560;
Best Local Similarity 49.2%; Pred. No. 2.5e-11;
Matches 358; Conservative 0; Mismatches 324; Indels 45; Gaps 4;
QY 711 ATGGAGGGAAGGCAAGCCCTTTGACCCCGCTCACAGCATACGGCTGCTTGGTG 770
DB 139 AAGAAGGACAGCGGGTGTGCCCTACGATCAAGTCAAACTCCACTCTGTCTGCC 198
QY 771 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCGAGTGACCCCATCTGATG 830
DB 199 GACAACGAACTGTAATTCGGGTACCGTGGCGATTTTCAGTGGCAGCATCCGATTATC--- 255
QY 831 CCGCACTGGATCCAGCCTGCTCTCAGACCGACAACTTCCTCCGCTGCTGCATCAT 890
DB 256 -----TACCGGAGCCCTTGCAGACCGAGCTAGCTAGCTAAGTCTCAAC 303
QY 891 GAGCGCTCTTTGTGGGACCATCCCTTCGACCCAGGTCGTCTACTTCTTTTCGAGAG 950
DB 304 GCACCGAACTTTGTGAGCTCAATTTACGCGAGGCGACTTTGTCTATTCTTTCTTCGGGAA 363
QY 951 ACAGCCAGGAGTTTGACTTCTTTGAGAGGCTCCACATCGCGGTGCTAGAGTCTGC 1010
DB 364 ACCGCGTGTGATTTATCACTGTGGCAAGGCGATTTATTCGCGGTGTCGCGGTCTGC 423
QY 1011 AAGAATGAGTGGGGGGGAAAGTGTGCGAAGAGAGTGGACACCATCTTCTGAAGGCC 1070
DB 424 AATGGGACAAAGTGGCCGCGATCGATTCCGCAACCGTGACATCTTCTCAAGTCC 483
QY 1071 CAGCTGCTTGACACCGCGGGGAGCTGCCCTTCAAGTCA-----TC 1115

484 GCCTCAACTGCTCATTCGCGGATATCTCTTACTTTAATGAATCAATCTGCC 543
1116 CGCACGCGGTCCTGCTCCCGCGGATTCCTCCACAGCTCCCACTACGAGTCTTC 1175
DB 544 AGCAATCTGGTGGAGGAGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGAGTCTTC 603
QY 1176 ACCTCCCACTGCGAGGTTGGGGGACACAGGAGCTCTGGGTTTCTGCTTCTCTCTCTG 1235
DB 604 AACAGCCGAGCAA-----CTCAATTCGCGCTCAGCGGTTTGTGCTTTGCCCTCCAG 657
QY 1236 GACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTG- 1294
DB 658 GACATTGCCGATACGTTTGAAGGCTCAGTTCAAGGAGCAGACTGGCATCAACTCCAACTGG 717
QY 1295 -----GACTACTTATAGGGGCGCTGAGACCAACCCCGCGAGGCGAGTTGCTCAGTG 1346
DB 718 CTGCCAGTGAACACGCGCAAGTACCCGATCTCTGACCCGCTTCTGTCAACAGGATTCG 777
QY 1347 GCGCCCTCTCTGTGATTAAGGCGCTGACCTTCATGAAGGACCATTTCTGATGATGAGCAA 1406
DB 778 AGAGCGCTTCGGATCCCACTGAACTTCAATCAAAACACATTCGCTAATGAGAGAGAT 837
QY 1407 GTGGTG 1413
DB 838 GTGCCGG 844

RESULT 14
US-09-060-692-59
Sequence 59, Application US/09060692
Patent No. 593585
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

```
FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1953
US-09-060-692-59

Query Match      2.2%; Score 78.6; DB 2; Length 3560;
Best Local Similarity 49.2%; Pred. No. 2.5e-11;
Matches 358; Conservative 0; Mismatches 324; Indels 45; Gaps 4;

QY 711 ATGAGGAAAGGCGGAAAGCCCTTTGACCCCTCACAAGCATACGGCTGTCTGGTG 770
Db 139 AAGAACGACAGCGGGTGTGCCCCCTAGCATCCAGTCCAACTCCAGCTGTCTGGTG 198
QY 771 GATGGATGCTCTATCTGTGTAATGAACAACCTTCTGGGCGAGTGAAGCCATCTGATG 830
Db 199 GACAAAGAACTGTATTCGGTACCGGTGCGGATTTTCAAGTGGCAGGATCCGATTATC 255
QY 831 CGCACACTGGGATCCAGCCTGTCTCAAGACCGCAACTTCTCGCTGGCTGCATCAT 890
Db 256 -----TACGGGAGCCCTGCGAGACCGAGTACGATAGCCTAAGTCTCAAC 303
QY 891 GAGCCTCTCTGTGGCAGCCATCCCTTCGACCCAGGTGCTACTTCTTTCGAGGAG 950
Db 304 GCACCGAACTTGTGAGCTCATTTACGCGGCGACTTTGTCTATTTCTTTCGGAA 363
QY 1071 CAGCTGCTCTGACCCAGCGGGGAGCTGCGCTTCAAGCTCA-----TC 1115
Db 484 CGCCTCACTGCTCCATTCCCGGCGATTATCTTCTTCTTCTTCAATGAATCAATCTGCC 543
QY 1116 CGCACGCGGTCTCTGCTCCCGCGATTTCTCCACAGCTCCCACTACGAGTCTTC 1175
Db 544 AGCAATCTGGTGGAGGAGATGATGGCTCGATGAGCTGAACTGATCTACGAGTCTTC 603
QY 1176 ACCTCCCAAGTGGAGGAGGAGGAGGAGTCTGCGGTTGTGCTTCTCTCTG 1235
Db 604 AACAGCGCGAGCA-----CTCAATCCCGCTCAGCGGTTGTGCTTTCGCTCCAG 657
QY 1236 GACATTGACGTTCTTTAAGGGGAATACAAAGATTGACAAAGAACTTCAAGCTG- 1294
Db 658 GACATTGCGGATACGTTTGGAGGTCAGTTCAAGGAGCAGACTGGCATCACTCCAATGG 717
QY 1295 -----GACTACTTATAGGGGCGCTGAGACCAACCCCGGCGAGGAGTTGCTCAGTG 1346
Db 718 CTGCCAGTGAAACAGCGCAAGTACCCGATCTCGACCGGTTCTGTCAACGATTGG 777
QY 1347 GCGCCTCTCTGATAGCGCTGACCTTCATGAGGAGCAATTCCTGATGGATGAGCAA 1406
Db 778 AGAGCGCTTCGGATCCCACTGAACCTTCATCAAAACACATTCGCTTAATGAGAGAT 837
QY 1407 GTGGTGG 1413
Db 838 GTGCCGG 844

RESULT 15
US-08-833-391-59
; Sequence 59, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Bentley, David
; APPLICANT: Matthes, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1953
; US-08-833-391-59

Query Match      2.2%; Score 78.6; DB 3; Length 3560;
Best Local Similarity 49.2%; Pred. No. 2.5e-11;
Matches 358; Conservative 0; Mismatches 324; Indels 45; Gaps 4;

QY 711 ATGAGGAAAGGCGGAAAGCCCTTTGACCCCTCACAAGCATACGGCTGTCTGGTG 770
Db 139 AAGAACGACAGCGGGTGTGCCCCCTAGCATCCAGTCCAACTCCAGCTGTCTGGTG 198
QY 771 GATGGATGCTCTATCTGTGTAATGAACAACCTTCTGGGCGAGTGAAGCCATCTGATG 830
Db 199 GACAAAGAACTGTATTCGGTACCGGTGCGGATTTTCAAGTGGCAGGATCCGATTATC 255
QY 831 CGCACACTGGGATCCAGCCTGTCTCAAGACCGCAACTTCTCGCTGGCTGCATCAT 890
Db 256 -----TACGGGAGCCCTGCGAGACCGAGTACGATAGCCTAAGTCTCAAC 303
QY 891 GAGCCTCTCTGTGGCAGCCATCCCTTCGACCCAGGTGCTACTTCTTTCGAGGAG 950
Db 304 GCACCGAACTTGTGAGCTCATTTACGCGGCGACTTTGTCTATTTCTTTCGGAA 363
QY 1071 CAGCTGCTCTGACCCAGCGGGGAGCTGCGCTTCAAGCTCA-----TC 1115
Db 484 CGCCTCACTGCTCCATTCCCGGCGATTATCTTCTTCTTCTTCAATGAATCAATCTGCC 543
QY 1116 CGCACGCGGTCTCTGCTCCCGCGATTTCTCCACAGCTCCCACTACGAGTCTTC 1175
Db 544 AGCAATCTGGTGGAGGAGATGATGGCTCGATGAGCTGAACTGATCTACGAGTCTTC 603
QY 1176 ACCTCCCAAGTGGAGGAGGAGGAGGAGTCTGCGGTTGTGCTTCTCTCTG 1235
Db 604 AACAGCGCGAGCA-----CTCAATCCCGCTCAGCGGTTGTGCTTTCGCTCCAG 657
QY 1236 GACATTGACGTTCTTTAAGGGGAATACAAAGATTGACAAAGAACTTCAAGCTG- 1294
Db 658 GACATTGCGGATACGTTTGGAGGTCAGTTCAAGGAGCAGACTGGCATCACTCCAATGG 717
QY 1295 -----GACTACTTATAGGGGCGCTGAGACCAACCCCGGCGAGGAGTTGCTCAGTG 1346
Db 718 CTGCCAGTGAAACAGCGCAAGTACCCGATCTCGACCGGTTCTGTCAACGATTGG 777
QY 1347 GCGCCTCTCTGATAGCGCTGACCTTCATGAGGAGCAATTCCTGATGGATGAGCAA 1406
Db 778 AGAGCGCTTCGGATCCCACTGAACCTTCATCAAAACACATTCGCTTAATGAGAGAT 837
QY 1407 GTGGTGG 1413
Db 838 GTGCCGG 844
```

Db	544	AGCAATCTGGTGGAGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC	603
Qy	1176	ACCTCCAGTGGCAGGTTGGCGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTCTG	1235
Db	604	AACAGCCGAGCAA-----CTCAATCCCGGCTCAGCGGTTGTGCTTGGCCCTCCAG	657
Qy	1236	GACATTGAACGTGTCTTTTAAGGGGAAATACAAAGAGTTGAAACAAAGAACTTCAAGCTG-	1294
Db	658	GACATTGCCGATACGTTTGAAGGTCAGTTCAAGGAGCAGACTGGCATCAACTCCAACTGG	717
Qy	1295	-----GACTACTTATAGGGCCCTGAGACCAACCCCGCCAGGCACTTGTCTAGTG	1346
Db	718	CTGCCAGTGAACAAGCCAGATACCGATCTCGACCCGGTTCTGTCAACAGATTCTG	777
Qy	1347	GGCCCCCTCTCTGATAAGGCCCTGACCTTTCATGAAGGACCAATTTCTGATGATGAGCAA	1406
Db	778	AGAGCGCTTCGGATCCCACTGAACCTTCATCAAAACACATTCGCTAATGGAGAGAAT	837
Qy	1407	GTGGTGG	1413
Db	838	GTGCCGG	844

Search completed: April 26, 2004, 02:10:54
Job time : 180.879 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:47:42 ; Search time 931.295 Seconds
(without alignments)
15988.422 Million cell updates/sec

Title: US-10-051-835-13
Perfect score: 3505
Sequence: 1 ggcttgccatgatgggac.....tttgggccaaccacaggttg 3505

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 337363 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002s.*
7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3060.8	87.3	3143	3 AAC58392	Human PRO
2	3060.8	87.3	3143	8 ACD68436	Novel hum
3	3060.8	87.3	3143	8 ACH04538	Human CDN
4	3060.8	87.3	3143	8 ACD68082	Novel hum
5	3060.8	87.3	3143	9 ADC18145	Human PRO
6	3060.8	87.3	3143	9 ADD70791	Human CDN
7	3060.8	87.3	3143	9 ADD33868	Human CDN
8	3060.8	87.3	3143	9 ADD70314	Human CDN
9	3060.8	87.3	3143	9 ADD38435	Human CDN
10	3060.8	87.3	3143	9 ADD33391	Human CDN
11	3060.8	87.3	3143	9 ADD33914	Human CDN
12	3060.8	87.3	3143	9 ADD40345	Human CDN
13	3060.8	87.3	3143	9 ADE50566	Human CDN
14	3060.8	87.3	3143	9 ADE20178	Human CDN
15	3060.8	87.3	3143	9 ADE50089	Human CDN
16	3060.8	87.3	3143	9 ADE21647	Human CDN
17	3060.8	87.0	3142	3 AAA37100	Human PRO
18	3043.8	86.8	3252	9 ADD67570	Human Ly6
19	3040.8	86.7	3042	4 AAK53428	Human pol
20	3038.4	86.7	3042	7 ABX13628	Human cyt
21	3031.6	86.5	3104	5 AAF45125	Human TAN
22	3031.6	86.5	3104	7 ABX94103	cDNA enco
23	3031.6	86.5	3104	7 ACD66780	Secreted

24	3031.4	86.5	3191	3 AAC69084	Human sec
25	3022.4	86.2	3146	7 ACC69002	Human neu
26	2998.8	85.6	3075	4 AAF54397	DNA enco
27	2682.2	76.5	2981	9 ADB62165	Human CDN
28	2642.8	75.4	2768	6 ABS64946	Human CDN
29	2435.4	69.5	2745	7 ACC68985	Human neu
30	2381.4	65.1	2283	5 AAF45126	Human TAN
31	2281.4	65.1	2283	7 ACD66781	Secreted
C	2279.4	65.0	2281	6 ADD28945	Human MOL
C	2279.4	65.0	2281	9 ADD18199	Human MOL
34	2226.8	63.5	2271	6 AAD28944	Human MOL
35	2226.8	63.5	2271	9 ADD18197	Human mol
36	2114.4	60.3	2238	7 ACC69003	Human neu
37	1838	52.4	1838	4 AAH15636	Human CDN
38	1726.8	49.3	3046	5 AAF45137	Murine se
39	1726.8	49.3	3046	5 AAF45140	Murine DN
40	1726.8	49.3	3046	7 ACD26369	Secreted
41	1726.8	49.3	3046	7 ACD26370	Secreted
C	1708.8	48.8	1901	4 AAK53434	Human pol
43	1187.8	33.9	1674	6 ABK94920	Human nov
44	918.4	26.2	1730	6 ABS54021	cDNA enco
45	698.2	19.9	775	4 AAH04875	Human CDN

ALIGNMENTS

RESULT 1
AAC58392
ID AAC58392 standard; cDNA; 3143 BP.
XX
AC AAC58392;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1317 nucleotide sequence SEQ ID NO:70.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumorigenesis; identification; cancer; cytostatic; KW
KW notoprotection; neuroprotective; antiinflammatory; immunosuppressive; KW
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; KW
KW neuronal disorder; glioma; astrocytic disorder; astrocytic disorder; angiogenic; KW
KW hypothalamic disorder; glandular disorder; macrophagal disorder; KW
KW epithelial disorder; adrenal disorder; immunologic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US000376.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 30-NOV-1999; 99WO-US028313.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
XX
(GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA; PI
PI Watanabe CK, Wood WT;
XX
DR WPI; 2000-572270/53.
DR P-PSDB; AAE24084.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the PT
PT treatment, diagnosis and prevention of cancer.

XX PS Claim 50; Fig 51; 286pp; English.

XX CC The present invention describes an isolated antibody that binds to one of

CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,

CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,

CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,

CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR

CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The

CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis

CC and prevention of cancer. The antibodies and other anti-tumour compounds

CC may be used to treat various conditions, including those characterised by

CC overexpression and/or activation of the amplified PRO genes. Exemplary

CC conditions or disorders to be treated with such antibodies and other

CC compounds include benign or malignant tumours (e.g., renal, liver,

CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,

CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, and

CC glioblastomas, and various head and neck tumours), leukaemias and

CC lymphoid malignancies, other disorders such as neuronal, glial,

CC astrocytic, hypothalamic and other glandular, macrophagal, epithelial,

CC stromal and blastocoeleic disorders, and inflammatory, angiogenic and

CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and

CC hybridisation probes used in the isolation of the human PRO sequences.

CC AAC58367 to AAC58396 and AAB24037 to AAB24089 represent human PRO

CC polynucleotide and protein sequences given in the exemplification of the

XX present invention

SQ Sequence 3143 BP; 656 A; 963 C; 828 G; 696 T; 0 U; 0 Other;

Query Match 87.3%; Score 3060.8; DB 3; Length 3143;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCCTGGTGAAGTCTGTGGTGTAGCATGGCCCTCCAGCCCTGGGCTGGAGCC 232

DB 74 AGAGTCCCTGGTGAAGTCTGTGGTGTAGCATGGCCCTCCAGCCCTGGGCTGGAGCC 133

QY 233 CTGGAGCTCTGGGCTTTCTCTTCCAACTGCTTCAGTCTGCTGCTGCGGACGAC 292

DB 134 CTGGAGCTCTGGGCTTTCTCTTCCAACTGCTTCAGTCTGCTGCTGCGGACGAC 193

QY 293 CGCGGGGGAGGGGGGAGGGGGCCATGCCAGGGTCAGATATGACAGGGGATGAAG 352

DB 194 CGCGGGGGAGGGGGGAGGGGGCCATGCCAGGGTCAGATATGACAGGGGATGAAG 253

QY 353 TAGGGCACTTAGCTTCTTCCACAGAGGGCTCCAGGATTTTGAACACTGCTGCTGAG 412

DB 254 TAGGGCACTTAGCTTCTTCCACAGAGGGCTCCAGGATTTTGAACACTGCTGCTGAG 313

QY 413 TGSTGATGGAATACTCTCTACCTGGGGCTCGAGAAGCCATTTCTGGCCTTGGATATCA 472

DB 314 TGSTGATGGAATACTCTCTACCTGGGGCTCGAGAAGCCATTTCTGGCCTTGGATATCA 373

QY 473 GGATCCAGGGGTCGCCAGGCTAAGAACATGATACCGTGGCCAGCCAGTGAAGAAAAA 532

DB 374 GGATCCAGGGGTCGCCAGGCTAAGAACATGATACCGTGGCCAGCCAGTGAAGAAAAA 433

QY 533 GAGTGAATGTGCTTTTAAAGAGAGAGCAATGAGACACAGTGTTCATCTTCCTGCT 592

DB 434 GAGTGAATGTGCTTTTAAAGAGAGAGCAATGAGACACAGTGTTCATCTTCCTGCT 493

QY 593 CTGGGTTCCTTAAATGTACCACTCTACACCTGGGACCTTCGCTTCAGCCCTCG 652

DB 494 CTGGGTTCCTTAAATGTACCACTCTACACCTGGGACCTTCGCTTCAGCCCTCG 553

QY 653 TTGTACCTTCATTTGAACCTCAAGATTCCTACCTGTTGCCATCTCGAGGAGCAAGTCA 712

DB 554 TTGTACCTTCATTTGAACCTCAAGATTCCTACCTGTTGCCATCTCGAGGAGCAAGTCA 613

QY 713 GGAGGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGAGCATACGGCTGTCTTGTTGA 772

DB 614 GGAGGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGAGCATACGGCTGTCTTGTTGA 673

QY 773 TGGGATGCTCTATTCTGTTACTATGAACAACCTTCTCGGCACTGAGCCCATCTGATGG 832

DB 674 TGGGATGCTCTATTCTGTTACTATGAACAACCTTCTCGGCACTGAGCCCATCTGATGG 733

QY 833 CACACTGGGATCCCGAGCTGCTCTCAAGAGCCGAACTTCTCGCTGGGTGATCATGA 892

DB 734 CACACTGGGATCCCGAGCTGCTCTCAAGAGCCGAACTTCTCGCTGGGTGATCATGA 793

QY 893 CGCTCTCTTTGTGGAGCATCTCCCTTCGACCCAGGTGCTTACTTCTTCTCGAGGAGAC 952

DB 794 CGCTCTCTTTGTGGAGCATCTCCCTTCGACCCAGGTGCTTACTTCTTCTCGAGGAGAC 853

QY 953 AGCCAGCGAGTTTCACTTCTTTAGAGGCTCCACACATCGGGGTGCTAGAGTCTCAA 1012

DB 854 AGCCAGCGAGTTTCACTTCTTTAGAGGCTCCACACATCGGGGTGCTAGAGTCTCAA 913

QY 1013 GAATGACGTGGGGCGGAAAGCTGCTGCAAGAGAGTGAACACCTTCTGTAAGGCCCA 1072

DB 914 GAATGACGTGGGGCGGAAAGCTGCTGCAAGAGAGTGAACACCTTCTGTAAGGCCCA 973

QY 1073 GCTGCTCTGCACCCAGCGGGGAGCTGCCCTTCAAGCTCATCGCCACCGCTCTGCT 1132

DB 974 GCTGCTCTGCACCCAGCGGGGAGCTGCCCTTCAAGCTCATCGCCACCGCTCTGCT 1033

QY 1133 CCCGCGCATTTCTCCACAGCTCCCACTACGAGTCTTCACTTCCAGTGGGAGGT 1192

DB 1034 CCCGCGCATTTCTCCACAGCTCCCACTACGAGTCTTCACTTCCAGTGGGAGGT 1093

QY 1193 TGGGGGACACGAGGAGCTGCGGTTTCTGCTTCTCTCTGAGACATTCGACGTGCTT 1252

DB 1094 TGGGGGACACGAGGAGCTGCGGTTTCTGCTTCTCTCTGAGACATTCGACGTGCTT 1153

QY 1253 TAAAGGAAATPACAAAGAGTTGAACAAAGAACTTCAAGCTGGAATACTTATAGGGGCC 1312

DB 1154 TAAAGGAAATPACAAAGAGTTGAACAAAGAACTTCAAGCTGGAATACTTATAGGGGCC 1213

QY 1313 TGAGACAAACCCCGGCGAGGAGTCTCAGTGGGCGCTCTCTCTCATTAAGGCCCTGAC 1372

DB 1214 TGAGACAAACCCCGGCGAGGAGTCTCAGTGGGCGCTCTCTCTCATTAAGGCCCTGAC 1273

QY 1373 CTTTATGAAGACCATTTTCTGATGAGATGAGCAAGTGGTGGGACGCGCTCTGCTGTGAA 1432

DB 1274 CTTTATGAAGACCATTTTCTGATGAGATGAGCAAGTGGTGGGACGCGCTCTGCTGTGAA 1333

QY 1433 ATCTGGGTGGAGTATACAGGCTTGCAGTGGAGACGCGGCGCTTGCATGGGACAG 1492

DB 1334 ATCTGGGTGGAGTATACAGGCTTGCAGTGGAGACGCGGCGCTTGCATGGGACAG 1393

QY 1493 CCATCTTTGTATGTACCTGGGAAACCAACACAGGGTCTCTCCCAAGGCTGTGTAAGTGG 1552

DB 1394 CCATCTTTGTATGTACCTGGGAAACCAACACAGGGTCTCTCCCAAGGCTGTGTAAGTGG 1453

QY 1553 GGACAGAGTCTCATCTGTTGGAGAGATTCAGTGTTCCTGACCTGAACTGTCTG 1612

DB 1454 GGACAGAGTCTCATCTGTTGGAGAGATTCAGTGTTCCTGACCTGAACTGTCTG 1513

QY 1613 CAACTGCACTGCGCCCGCCCGAGGCTGAGTGTGTTGTAGGCTTCTCAGAGGTGCTG 1672

DB 1514 CAACTGCACTGCGCCCGCCCGAGGCTGAGTGTGTTGTAGGCTTCTCAGAGGTGCTG 1573

QY 1673 GAGGGTCCCGAGCCCAACTGTGTATGAGAGCTGTGTGAGTGTGTCTTGTGCGCG 1732

DB 1574 GAGGGTCCCGAGCCCAACTGTGTATGAGAGCTGTGTGAGTGTGTCTTGTGCGCG 1633

QY 1733 GGACCCCACTGTGCTCGGACCTGAGTCCCGAACCTGTTGCTCTGCTGTGCCCCAA 1792

DB 1634 GGACCCCACTGTGCTCGGACCTGAGTCCCGAACCTGTTGCTCTGCTGTGCCCCAA 1693

QY 1793 CCTGAACTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGGCACTGTGCCAGTGG 1852

DB 1694 CCTGAACTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGGCACTGTGCCAGTGG 1753

QY 1853 CCCCATGAGCAGGAGCCTTCGGCTCAGAGCGCCCGCCCAATCATTAAGAGAGTCTCTGGC 1912

1754 Db CCCCATGAGCAGAGGCTTTCGGCTCAGAGCCGCCGCAATCATTTAAAGAGTCTCTGCG 1813
1913 QY TGTCCCTTACTCCTGAGCTCCCTGCCCCCACCCTGTGAGCTTGGCTCTTTATTA 1972
1814 Db TGTCCCACTCCTATCTGAGCTCCCTGCCCCCACCCTGTGAGCTTGGCTCTTTATTA 1873
1973 QY TTGGAGTCATGGCCAGCAGCAGTCCAGAGGCTTTTCCATCTTTCAATGGCTCCCT 2032
1874 Db TTGGAGTCATGGCCAGCAGCAGTCCAGAGGCTTTTCCATCTTTCAATGGCTCCCT 1933
2033 QY TTGTCTGATAGTCAGAGTGGGCTCTACAGCTGCTGGCAGTGGAGATGG 2092
1934 Db TTGTCTGATAGTCAGAGTGGGCTCTACAGCTGCTGGCAGTGGAGATGG 1993
2093 QY CTTTTCATACCTCTGATCTCTACTGCTGAGCAGCAGGACAGACCTGCCCCCTGGA 2152
1994 Db CTTTTCATACCTCTGATCTCTACTGCTGAGCAGCAGGACAGACCTGCCCCCTGGA 2053
2153 QY TCCTGAATCGGAGGATCCCGGGAGCATGTGAAGTCCGTTACAGGTCAGTGG 2212
2054 Db TCCTGAATCGGAGGATCCCGGGAGCATGTGAAGTCCGTTACAGGTCAGTGG 2113
2213 QY TGGGGCCGCTGCTGCTGCCAGAGTCTTACTGCCCCCACCCTTTGTCTCACTGTCTCT 2272
2114 Db TGGGGCCGCTGCTGCTGCCAGAGTCTTACTGCCCCCACCCTTTGTCTCACTGTCTCT 2173
2273 QY CTTTGGCTTATGCTTTTTCAGAGGCTTCATCTCTGCTGGCTCCCTTGGAGCAGT 2332
2174 Db CTTTGGCTTATGCTTTTTCAGAGGCTTCATCTCTGCTGGCTCCCTTGGAGCAGT 2233
2333 QY CCGGGCTCGGGGAAGGTTTCAGGCTGTGAGACCTTGGCCCTGGGGAGAGGCCCGTT 2392
2234 Db CCGGGCTCGGGGAAGGTTTCAGGCTGTGAGACCTTGGCCCTGGGGAGAGGCCCGTT 2293
2393 QY AAGCAGAGAGCAACCTCAGTCTCCAAAGGAATGACAGACCTTGGCAGTATGGA 2452
2294 Db AAGCAGAGAGCAACCTCAGTCTCCAAAGGAATGACAGACCTTGGCAGTATGGA 2353
2453 QY CGCTGACAACTGCTTAGGCTAGGTTAACTCTAGGACAGCCCGGGCTG 2512
2354 Db CGCTGACAACTGCTTAGGCTAGGTTAACTCTAGGACAGCCCGGGCTG 2413
2513 QY CGGTGACAGCACTTGGCTGCTGGCTGGCCGAGCAAGCAAGCCCTGATAGGATGAC 2572
2414 Db CGGTGACAGCACTTGGCTGCTGGCTGGCCGAGCAAGCAAGCCCTGATAGGATGAC 2473
2573 QY AGCAGCAAAAGACCACTTCTCCCTGAGAGGCTTCTGCTACTCTGATCACTGA 2632
2474 Db AGCAGCAAAAGACCACTTCTCCCTGAGAGGCTTCTGCTACTCTGATCACTGA 2533
2633 QY TGACACTCAGCAGGGTGATGACAGCAGTCTGCTCCCTATGGGACTCCCTTTTACCAA 2692
2534 Db TGACACTCAGCAGGGTGATGACAGCAGTCTGCTCCCTATGGGACTCCCTTTTACCAA 2593
2693 QY GCATGAGCTCTTAACAGGGTGGGGCTACCCGAGACCTGCTCTTACACTGATATG 2752
2594 Db GCATGAGCTCTTAACAGGGTGGGGCTACCCGAGACCTGCTCTTACACTGATATG 2653
2753 QY AAGAACCTGGAGAGGATCTTTCAGTCTTGGCCATTCAGGAGACCTCCAGAAACACAGTG 2812
2654 Db AAGAACCTGGAGAGGATCTTTCAGTCTTGGCCATTCAGGAGACCTCCAGAAACACAGTG 2713
2813 QY TTTTAAAGAGCCCTAAATAAATCTGCTGCCAGGACCTTATGTAATGACCAACA 2872
2714 Db TTTTAAAGAGCCCTAAATAAATCTGCTGCCAGGACCTTATGTAATGACCAACA 2773
2873 QY TCTAAACATCATATGCTAAATGCACTCTGGAACCTCCACTCTGAAGCTGCCGTTT 2932
2774 Db TCTAAACATCATATGCTAAATGCACTCTGGAACCTCCACTCTGAAGCTGCCGTTT 2833
2933 QY GGACACCAACACTCTCTTCTCCAGGTCATGAGGATCTGCTCCCTCTGCTTCCCTT 2992

2834 Db GGACACCAACACTCTCTTCTCCAGGGTCATGAGGATCTGCTCCCTCTGCTTCCCTT 2893
2993 QY ACCAGTCGTGACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTTCT 3052
2894 Db ACCAGTCGTGACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTTCT 2953
3053 QY TGCCTTCAGTTGGGCGAGACTCTGATCCCTTCTGCTCCGAGAAATGCGAGGGTAAATCTG 3112
2954 Db TGCCTTCAGTTGGGCGAGACTCTGATCCCTTCTGCTCCGAGAAATGCGAGGGTAAATCTG 3013
3113 QY AGCCTTCTTCACTCTTTTACCTAGTGAACCTTCACTCTCCCTCCCTTCTTCTTCTT 3172
3014 Db AGCCTTCTTCACTCTTTTACCTAGTGAACCTTCACTCTCCCTCCCTTCTTCTTCTT 3073
3173 QY GTTTCGGATTCAGAAACTGCTTCTCAGAGACTGTTTATTTTATTAATAATAAAGG 3232
3074 Db GTTTCGGATTCAGAAACTGCTTCTCAGAGACTGTTTATTTTATTAATAATAAAGG 3133
3233 QY CTTA 3236
3134 Db CTTA 3137

RESULT 2
ACD68436
ID ACD68436 standard; cDNA; 3143 BP.
XX ACD68436;
XX 17-SEP-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO1317 cDNA.
DE Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; cellac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
KW cartilage disorder; sports injury; arthritis; gene; ss.
XX Homo sapiens.
XX US2003073130-A1.
XX 17-APR-2003.
XX 11-DEC-2001; 2001US-00015869.
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 02-SEP-1998; 98US-0099536P.
XX 09-SEP-1998; 98US-0099596P.
XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 09-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98US-0099815P.
XX 10-SEP-1998; 98US-0099816P.

PR 15-SEP-1998;	98US-0100385P.	PR 28-OCT-1998;	98US-0106178P.
PR 15-SEP-1998;	98US-0100388P.	PR 29-OCT-1998;	98US-0106248P.
PR 15-SEP-1998;	98US-0100390P.	PR 29-OCT-1998;	98US-0106384P.
PR 15-SEP-1998;	98US-0100384P.	PR 30-OCT-1998;	98US-0108500P.
PR 16-SEP-1998;	98US-0100627P.	PR 30-OCT-1998;	98US-0106464P.
PR 16-SEP-1998;	98US-0100661P.	PR 03-NOV-1998;	98US-0106856P.
PR 16-SEP-1998;	98US-0100662P.	PR 03-NOV-1998;	98US-0106902P.
PR 16-SEP-1998;	98US-0100664P.	PR 03-NOV-1998;	98US-0106905P.
PR 17-SEP-1998;	98US-0100683P.	PR 03-NOV-1998;	98US-0106919P.
PR 17-SEP-1998;	98US-0100684P.	PR 03-NOV-1998;	98US-0106932P.
PR 17-SEP-1998;	98US-0100710P.	PR 10-NOV-1998;	98US-0107783P.
PR 17-SEP-1998;	98US-0100711P.	PR 17-NOV-1998;	98US-0108775P.
PR 17-SEP-1998;	98US-0100819P.	PR 17-NOV-1998;	98US-0108779P.
PR 17-SEP-1998;	98US-0100930P.	PR 17-NOV-1998;	98US-0108787P.
PR 17-SEP-1998;	98US-0100848P.	PR 17-NOV-1998;	98US-0108788P.
PR 18-SEP-1998;	98US-0100849P.	PR 17-NOV-1998;	98US-0108801P.
PR 18-SEP-1998;	98US-0101014P.	PR 17-NOV-1998;	98US-0108802P.
PR 18-SEP-1998;	98US-0101068P.	PR 17-NOV-1998;	98US-0108806P.
PR 18-SEP-1998;	98US-0101071P.	PR 17-NOV-1998;	98US-0108807P.
PR 22-SEP-1998;	98US-0101279P.	PR 17-NOV-1998;	98US-0108867P.
PR 23-SEP-1998;	98US-0101471P.	PR 17-NOV-1998;	98US-0108867P.
PR 23-SEP-1998;	98US-0101472P.	PR 17-NOV-1998;	98US-0108925P.
PR 23-SEP-1998;	98US-0101474P.	PR 18-NOV-1998;	98US-0108848P.
PR 23-SEP-1998;	98US-0101475P.	PR 18-NOV-1998;	98US-0108849P.
PR 23-SEP-1998;	98US-0101476P.	PR 18-NOV-1998;	98US-0108850P.
PR 23-SEP-1998;	98US-0101477P.	PR 18-NOV-1998;	98US-0108851P.
PR 23-SEP-1998;	98US-0101479P.	PR 18-NOV-1998;	98US-0108852P.
PR 24-SEP-1998;	98US-0101738P.	PR 18-NOV-1998;	98US-0108858P.
PR 24-SEP-1998;	98US-0101741P.	PR 18-NOV-1998;	98US-0108904P.
PR 24-SEP-1998;	98US-0101915P.	PR 22-DEC-1998;	98US-0113256P.
PR 24-SEP-1998;	98US-0101916P.	PR 30-DEC-1998;	98US-0114223P.
PR 29-SEP-1998;	98US-0102207P.	PR 05-JAN-1999;	99WO-US000106.
PR 29-SEP-1998;	98US-0102240P.	PR 16-APR-1999;	99US-0129674P.
PR 29-SEP-1998;	98US-0102307P.	PR 23-JUN-1999;	99US-0141037P.
PR 29-SEP-1998;	98US-0102330P.	PR 20-JUL-1999;	99US-0144758P.
PR 29-SEP-1998;	98US-0102331P.	PR 26-JUL-1999;	99US-0145698P.
PR 30-SEP-1998;	98US-0102487P.	PR 01-SEP-1999;	99WO-US020111.
PR 30-SEP-1998;	98US-0102487P.	PR 15-SEP-1999;	99WO-US021194.
PR 30-SEP-1998;	98US-0102570P.	PR 29-OCT-1999;	99US-0162506P.
PR 30-SEP-1998;	98US-0102571P.	PR 30-NOV-1999;	99WO-US028313.
PR 01-OCT-1998;	98US-0102684P.	PR 02-DEC-1999;	99WO-US028551.
PR 01-OCT-1998;	98US-0102687P.	PR 16-DEC-1999;	99WO-US030095.
PR 02-OCT-1998;	98US-0102965P.	PR 05-JAN-2000;	2000WO-US000219.
PR 06-OCT-1998;	98US-0103258P.	PR 06-JAN-2000;	2000WO-US000376.
PR 06-OCT-1998;	98US-0103449P.	PR 11-FEB-2000;	2000WO-US003565.
PR 07-OCT-1998;	98US-0103314P.	PR 18-FEB-2000;	2000WO-US004342.
PR 07-OCT-1998;	98US-0103328P.	PR 24-FEB-2000;	2000WO-US005004.
PR 07-OCT-1998;	98US-0103335P.	PR 02-MAR-2000;	2000WO-US005841.
PR 07-OCT-1998;	98US-0103335P.	PR 15-MAR-2000;	2000WO-US006884.
PR 07-OCT-1998;	98US-0103335P.	PR 17-MAY-2000;	2000WO-US013705.
PR 07-OCT-1998;	98US-0103335P.	PR 22-MAY-2000;	2000WO-US014042.
PR 07-OCT-1998;	98US-0103335P.	PR 30-MAY-2000;	2000WO-US014941.
PR 07-OCT-1998;	98US-0103335P.	PR 02-JUN-2000;	2000WO-US015284.
PR 08-OCT-1998;	98US-0103633P.	PR 23-AUG-2000;	2000WO-US023522.
PR 08-OCT-1998;	98US-0103678P.	PR 24-AUG-2000;	2000WO-US023328.
PR 08-OCT-1998;	98US-0103711P.	PR 08-NOV-2000;	2000WO-US030952.
PR 14-OCT-1998;	98US-0104257P.	PR 10-NOV-2000;	2000WO-US030873.
PR 20-OCT-1998;	98US-0104987P.	PR 01-DEC-2000;	2000WO-US032678.
PR 20-OCT-1998;	98US-0105000P.	PR 28-FEB-2001;	2001WO-US006520.
PR 20-OCT-1998;	98US-0105002P.	PR 01-MAR-2001;	2001WO-US006666.
PR 21-OCT-1998;	98US-0105104P.	PR 01-JUN-2001;	2001WO-US017800.
PR 22-OCT-1998;	98US-0105169P.	PR 20-JUN-2001;	2001WO-US019692.
PR 22-OCT-1998;	98US-0105266P.	PR 29-JUN-2001;	2001WO-US021066.
PR 26-OCT-1998;	98US-0105693P.	PR 09-JUL-2001;	2001WO-US021735.
PR 26-OCT-1998;	98US-0105694P.	PR 04-SEP-2001;	2001US-00946374.
PR 27-OCT-1998;	98US-0105807P.	XX (GETH) GENENTECH INC.	
PR 27-OCT-1998;	98US-0105881P.	XX PA	
PR 27-OCT-1998;	98US-0105882P.	XX PI	
PR 27-OCT-1998;	98US-0106062P.	XX PI	Baker KD, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PR 28-OCT-1998;	98US-0106023P.	XX PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ;
PR 28-OCT-1998;	98US-0106029P.	XX PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PR 28-OCT-1998;	98US-0106030P.	XX PI	Williams PM, Wood WL;
PR 28-OCT-1998;	98US-0106032P.	XX	
PR 28-OCT-1998;	98US-0106033P.	XX	

QY 2213 TGGGGCGCCCTGGCTGCGCCAGAGTCTTACTGGCCCACTTGTCTACTGTCTCACTGTCTCT 2272
Db 2114 TGGGGCGCCCTGGCTGCGCCAGAGTCTTACTGGCCCACTTGTCTACTGTCTCACTGTCTCT 2173
QY 2273 CTTTGGCTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGCTGGCCCTCCCACTTGTAGAGCACT 2332
Db 2174 CTTTGGCTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGCTGGCCCTCCCACTTGTAGAGCACT 2233
QY 2333 CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCTCGCGCTGGGGAGAAAGGCCCGCTT 2392
Db 2234 CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCTCGCGCTGGGGAGAAAGGCCCGCTT 2293
QY 2393 AAGCAGAGACAACCTTCAGTCTTCCAAAGGAATGAGAACCTCTGCCAGTGTATGTGA 2452
Db 2294 AAGCAGAGACAACCTTCAGTCTTCCAAAGGAATGAGAACCTCTGCCAGTGTATGTGA 2353
QY 2453 CGCTGACAAACCTTCAGTCTTCCAAAGGAATGAGAACCTCTGCCAGTGTATGTGA 2512
Db 2354 CGCTGACAAACCTTCAGTCTTCCAAAGGAATGAGAACCTCTGCCAGTGTATGTGA 2413
QY 2513 CGGTGAGGACCTTGGCCATCTGCTGGCTGGCGGCCCAAGCAGACAGCCCTGACTAGATGAC 2572
Db 2414 CGGTGAGGACCTTGGCCATCTGCTGGCTGGCGGCCCAAGCAGACAGCCCTGACTAGATGAC 2473
QY 2573 AGCAGACAAGAGACCACTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTCACTGA 2632
Db 2474 AGCAGACAAGAGACCACTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTCACTGA 2533
QY 2633 TGACACTCAGCAGGGTGATGACAGCAGTCTGCTTCCCTTATGGGACTCCCTTCTACCAA 2692
Db 2534 TGACACTCAGCAGGGTGATGACAGCAGTCTGCTTCCCTTATGGGACTCCCTTCTACCAA 2593
QY 2693 GCACATGAGTCTCTACAGGCTGGGGCTTACCCAGAGCTCTCTCTACACTGATGATG 2752
Db 2594 GCACATGAGTCTCTACAGGCTGGGGCTTACCCAGAGCTCTCTCTACACTGATGATG 2653
QY 2753 AAGAACCTGGAGAGGATCTTCTAGTCTTGGCCATTCAGGAGACCTTCCAGAAACACAGTG 2812
Db 2654 AAGAACCTGGAGAGGATCTTCTAGTCTTGGCCATTCAGGAGACCTTCCAGAAACACAGTG 2713
QY 2813 TTTTCAAGAGCCCTTAAAGACCTTCTCCAGGCTCATGAGGACCTTATGTAACACCAACA 2872
Db 2714 TTTTCAAGAGCCCTTAAAGACCTTCTCCAGGCTCATGAGGACCTTATGTAACACCAACA 2773
QY 2873 TCTAAACAATCATATGTAATGCACTGCACTCTCTGAAACTCCACTCTGAAGCTGCGCTT 2932
Db 2774 TCTAAACAATCATATGTAATGCACTGCACTCTCTGAAACTCCACTCTGAAGCTGCGCTT 2833
QY 2933 GGACACCAACTCTCTTCCAGGCTCATGAGGACCTTCTCTCTCTGCTTCCCTT 2992
Db 2834 GGACACCAACTCTCTTCCAGGCTCATGAGGACCTTCTCTCTCTGCTTCCCTT 2893
QY 2993 ACCAGTCTGTCAGCAGCTGACTTCCAGGAGTCTTCCCTGAGTCTGACACCTTCTTCT 3052
Db 2894 ACCAGTCTGTCAGCAGCTGACTTCCAGGAGTCTTCCCTGAGTCTGACACCTTCTTCT 2953
QY 3053 TGCTTCAAGTGGGACACTCTGATCTCTTCCAGGCTCATGAGGACCTTCTCTCTCTGCTTCCCTT 3112
Db 2954 TGCTTCAAGTGGGACACTCTGATCTCTTCCAGGCTCATGAGGACCTTCTCTCTCTGCTTCCCTT 3013
QY 3113 AGCTTCTTCACTCTTCTTACCTAGCTGACCCCTTCACTCTCTCCCTCTCTCTTCTCTT 3172
Db 3014 AGCTTCTTCACTCTTCTTACCTAGCTGACCCCTTCACTCTCTCCCTCTCTCTTCTCTT 3073
QY 3173 GTTTGGGATTCAGAAACTGCTTGTGAGAGACTGTTTATTTTATTAATAATAAGG 3232
Db 3074 GTTTGGGATTCAGAAACTGCTTGTGAGAGACTGTTTATTTTATTAATAATAATAAGG 3133
QY 3233 CTTA 3236
Db 3134 CTTA 3137

RESULT 3
ACH04538
ID ACH04538 standard; cDNA; 3143 BP.
XX ACH04538;
AC ACH04538;
XX
DT 01-OCT-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnary;
KW cardiac; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
KW adrenal cortical capillary; endothelial cell growth; wound healing;
KW stimulated T-lymphocyte proliferation; immune response suppression;
KW neonatal heart hypertrophy; cardiac insufficiency disorder;
KW vascular endothelial growth factor; inflammation; mononuclear cell;
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003044841-A1.
XX
PD 06-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006856.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099782P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.

PR	23-SEP-1998;	98US-0101476P.	PR	18-NOV-1998;	98US-0108849P.
PR	23-SEP-1998;	98US-0101477P.	PR	18-NOV-1998;	98US-0108850P.
PR	23-SEP-1998;	98US-0101479P.	PR	18-NOV-1998;	98US-0108851P.
PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	PR	22-DEC-1998;	98US-0113296P.
PR	24-SEP-1998;	98US-0101916P.	PR	30-DEC-1998;	98US-0114223P.
PR	24-SEP-1998;	98US-0102207P.	PR	05-JAN-1999;	98US-0114223P.
PR	24-SEP-1998;	98US-0102207P.	PR	16-APR-1999;	98US-0129674P.
PR	24-SEP-1998;	98US-0102240P.	PR	23-JUN-1999;	98US-0144037P.
PR	24-SEP-1998;	98US-0102307P.	PR	23-JUN-1999;	98US-0144758P.
PR	24-SEP-1998;	98US-0102330P.	PR	26-JUL-1999;	98US-0145698P.
PR	24-SEP-1998;	98US-0102331P.	PR	01-SEP-1999;	98US-0145698P.
PR	30-SEP-1998;	98US-0102484P.	PR	15-SEP-1999;	98US-0145698P.
PR	30-SEP-1998;	98US-0102487P.	PR	23-OCT-1999;	98US-0162506P.
PR	30-SEP-1998;	98US-0102570P.	PR	30-NOV-1999;	98US-0162506P.
PR	30-SEP-1998;	98US-0102571P.	PR	02-DEC-1999;	98US-0162506P.
PR	01-OCT-1998;	98US-0102684P.	PR	16-DEC-1999;	98US-0162506P.
PR	01-OCT-1998;	98US-0102687P.	PR	02-MAR-2000;	98US-0162506P.
PR	02-OCT-1998;	98US-0102965P.	PR	15-MAR-2000;	98US-0162506P.
PR	06-OCT-1998;	98US-0103258P.	PR	05-JAN-2000;	98US-0162506P.
PR	06-OCT-1998;	98US-0103449P.	PR	11-FEB-2000;	98US-0162506P.
PR	07-OCT-1998;	98US-0103314P.	PR	11-FEB-2000;	98US-0162506P.
PR	07-OCT-1998;	98US-0103315P.	PR	24-FEB-2000;	98US-0162506P.
PR	07-OCT-1998;	98US-0103328P.	PR	02-MAR-2000;	98US-0162506P.
PR	07-OCT-1998;	98US-0103395P.	PR	15-MAR-2000;	98US-0162506P.
PR	07-OCT-1998;	98US-0103396P.	PR	17-MAY-2000;	98US-0162506P.
PR	07-OCT-1998;	98US-0103401P.	PR	22-MAY-2000;	98US-0162506P.
PR	07-OCT-1998;	98US-0103401P.	PR	30-MAY-2000;	98US-0162506P.
PR	08-OCT-1998;	98US-0103633P.	PR	02-JUN-2000;	98US-0162506P.
PR	08-OCT-1998;	98US-0103678P.	PR	23-AUG-2000;	98US-0162506P.
PR	08-OCT-1998;	98US-0103679P.	PR	23-AUG-2000;	98US-0162506P.
PR	08-OCT-1998;	98US-0103711P.	PR	08-NOV-2000;	98US-0162506P.
PR	14-OCT-1998;	98US-0104257P.	PR	10-NOV-2000;	98US-0162506P.
PR	20-OCT-1998;	98US-0105007P.	PR	01-DEC-2000;	98US-0162506P.
PR	20-OCT-1998;	98US-0105002P.	PR	28-FEB-2001;	98US-0162506P.
PR	21-OCT-1998;	98US-0105104P.	PR	01-MAR-2001;	98US-0162506P.
PR	22-OCT-1998;	98US-0105169P.	PR	01-JUN-2001;	98US-0162506P.
PR	22-OCT-1998;	98US-0105266P.	PR	20-JUN-2001;	98US-0162506P.
PR	26-OCT-1998;	98US-0105693P.	PR	29-JUN-2001;	98US-0162506P.
PR	26-OCT-1998;	98US-0105694P.	PR	09-JUL-2001;	98US-0162506P.
PR	27-OCT-1998;	98US-0105807P.	PR	04-SEP-2001;	98US-0162506P.
PR	27-OCT-1998;	98US-0105881P.	XX		
PR	27-OCT-1998;	98US-0105882P.	XX		
PR	27-OCT-1998;	98US-0106062P.	XX		
PR	28-OCT-1998;	98US-0106023P.	XX		
PR	28-OCT-1998;	98US-0106029P.	XX		
PR	28-OCT-1998;	98US-0106030P.	XX		
PR	28-OCT-1998;	98US-0106032P.	XX		
PR	28-OCT-1998;	98US-0106033P.	XX		
PR	28-OCT-1998;	98US-0106178P.	XX		
PR	29-OCT-1998;	98US-0106248P.	XX		
PR	29-OCT-1998;	98US-0106384P.	XX		
PR	29-OCT-1998;	98US-0108500P.	XX		
PR	30-OCT-1998;	98US-0106464P.	XX		
PR	30-OCT-				

QY 353 TAGGCACTTAGCTTCTTCCACCAAGAGGGCTCCAGGATTTTGACACTCTGCTCCTGAG 412
DB 254 TAGGGCACTTAGCTTCTTCCACCAAGAGGGCTCCAGGATTTTGACACTCTGCTCCTGAG 313
QY 413 TGGTGATGGAAATACTCTCTACGTGGGGCTCGAAGAGCAATCTTGCCCTTGATATCCA 472
DB 314 TGGTGATGGAAATACTCTCTACGTGGGGCTCGAAGAGCAATCTTGCCCTTGATATCCA 373
QY 473 GGATCCAGGGGTCCCAAGGCTAAAGAAACATGATACCGTGGCCAGCCAGTGCAGAGAAAAA 532
DB 374 GGATCCAGGGGTCCCAAGGCTAAAGAAACATGATACCGTGGCCAGCCAGTGCAGAGAAAAA 433
QY 533 GAGTGAATGTGCTTTAAGAAAGAGCAATGAGACACAGTGTGTTTCAACTTCACTTCGTGT 592
DB 434 GAGTGAATGTGCTTTAAGAAAGAGCAATGAGACACAGTGTGTTTCAACTTCACTTCGTGT 493
QY 593 CCGTGTCTTACCAATGTACCCACTCTCTACACCTGGGCAACCTTCGCTTCAGCCCTGC 652
DB 494 CCGTGTCTTACCAATGTACCCACTCTCTACACCTGGGCAACCTTCGCTTCAGCCCTGC 553
QY 653 TTGTACCTTCATGAACTTCAAGATTCCTTACCTGCTGCTGCTCGAGGACAGGTGAT 712
DB 554 TTGTACCTTCATGAACTTCAAGATTCCTTACCTGCTGCTGCTCGAGGACAGGTGAT 613
QY 713 GGAGGAAAGGCAAGCCCTTTGACCCGCTCACAAGCATACGGCTGTCTTGGTGA 772
DB 614 GGAGGAAAGGCAAGCCCTTTGACCCGCTCACAAGCATACGGCTGTCTTGGTGA 673
QY 773 TGGGATGCTTATTTGCTACTATGAACAACCTTCTGGGCAAGTGGCCATTCCTGATGG 832
DB 674 TGGGATGCTTATTTGCTACTATGAACAACCTTCTGGGCAAGTGGCCATTCCTGATGG 733
QY 833 CACACTGGATCCAGCCGCTCTCAGACCGACAGTCTCTCCGCTGGCTGCAATCATGA 892
DB 734 CACACTGGATCCAGCCGCTCTCAGACCGACAGTCTCTCCGCTGGCTGCAATCATGA 793
QY 893 CGCTCTCTTTGGGAGCCATCCCTTCGACCCAGTCTGCTACTTCTTTCGAGGAGAC 952
DB 794 CGCTCTCTTTGGGAGCCATCCCTTCGACCCAGTCTGCTACTTCTTTCGAGGAGAC 853
QY 953 AGCCAGCAGATTTGATCTTTTGAGAGGCTCCACATCGGGGTGGCTAGTCTGCAA 1012
DB 854 AGCCAGCAGATTTGATCTTTTGAGAGGCTCCACATCGGGGTGGCTAGTCTGCAA 913
QY 1013 GAATGACCTGGGCGCGGAAAGCTCTGCAGAGAAAGTGACACCTTCTCTGAAGGCCA 1072
DB 914 GAATGACCTGGGCGCGGAAAGCTCTGCAGAGAAAGTGACACCTTCTCTGAAGGCCA 973
QY 1073 GCTGCTCTGCACCAAGCCGGGAGCTGCTCTTCAAGTCTATCCGCCACGGGTCTGCT 1132
DB 974 GCTGCTCTGCACCAAGCCGGGAGCTGCTCTTCAAGTCTATCCGCCACGGGTCTGCT 1033
QY 1133 CCCCAGCATCTCCACAGTCTCCACATCTAGCAGTCTTCACTCCAGTGGCAGGT 1192
DB 1034 CCCCAGCATCTCCACAGTCTCCACATCTAGCAGTCTTCACTCCAGTGGCAGGT 1093
QY 1193 TGGGCGGACCAAGAGCTCTGCGGTTTGGCTTCTCTCTCTTGACATGGAAGTGTCTT 1252
DB 1094 TGGGCGGACCAAGAGCTCTGCGGTTTGGCTTCTCTCTCTTGACATGGAAGTGTCTT 1153
QY 1253 TAAAGGGAATACAAAGAGTTGAACAAGAACTTCAAGCTGGACTACTTATAGGGGCC 1312
DB 1154 TAAAGGGAATACAAAGAGTTGAACAAGAACTTCAAGCTGGACTACTTATAGGGGCC 1213
QY 1313 TGAGACCAACCCCGGCGAGGAGTGTCTCAGTGGGCCCTCTCTCTGATAGGGCCCTGAC 1372
DB 1214 TGAGACCAACCCCGGCGAGGAGTGTCTCAGTGGGCCCTCTCTCTGATAGGGCCCTGAC 1273
QY 1373 CTTCTAGAGGACCAATTTCTCTGATGAGCAAGTGTGGGAGCCCTCTGCTGTTGAA 1432
DB 1274 CTTCTAGAGGACCAATTTCTCTGATGAGCAAGTGTGGGAGCCCTCTGCTGTTGAA 1333

QY 1433 ATCTGGCTGGAGTATACAGGCTTGCAGTGGAGACAGCCAGGCTTGTATGGGCACAG 1492
DB 1334 ATCTGGCTGGAGTATACAGGCTTGCAGTGGAGACAGCCAGGCTTGTATGGGCACAG 1393
QY 1493 CCATCTCTGTATGTACCTGGGAAACACCAAGGCTGCTCCACAAGGCTGTGTAAAGTG 1552
DB 1394 CCATCTCTGTATGTACCTGGGAAACCAACAAGGCTGCTCCACAAGGCTGTGTAAAGTG 1453
QY 1553 GGACAGCAGTGTCTATCTGTGTGGAGAGATTACAGTGTGTCTGACCTGAACTGTTCG 1612
DB 1454 GGACAGCAGTGTCTATCTGTGTGGAGAGATTACAGTGTGTCTGACCTGAACTGTTCG 1513
QY 1613 CAACTCTGAGCTGGGCCCCCAAGGCTGAGTGTGTGTAGGCTTCTCAGAGAGTGTCTG 1672
DB 1514 CAACTCTGAGCTGGGCCCCCAAGGCTGAGTGTGTGTAGGCTTCTCAGAGAGTGTCTG 1573
QY 1673 GAGGTGCCCCGAGCAAACTGTAGTGTATGAGAGCTGTGTGACCTGTGTCTTGCCTG 1732
DB 1574 GAGGTGCCCCGAGCAAACTGTAGTGTATGAGAGCTGTGTGACCTGTGTCTTGCCTG 1633
QY 1733 GGACCCCACTGTGCTGGGACCTGAGTCCCGAACTGTTCCTCTCTGCTGCCCCCAA 1792
DB 1634 GGACCCCACTGTGCTGGGACCTGAGTCCCGAACTGTTCCTCTCTGCTGCCCCCAA 1693
QY 1793 CTTGAATCTCTGGAAAGCAGGACATGAGCGGGGAAACCAAGAGTGGGATGTGCCAGTG 1852
DB 1694 CTTGAATCTCTGGAAAGCAGGACATGAGCGGGGAAACCAAGAGTGGGATGTGCCAGTG 1753
QY 1853 CCGCATGAGCAGGAGCTTCGGCTCAGAGCGGCGCGCAATCATTAAGAAAGTCTCTGC 1912
DB 1754 CCGCATGAGCAGGAGCTTCGGCTCAGAGCGGCGCGCAATCATTAAGAAAGTCTCTGC 1813
QY 1913 TGTCTCTAACTCCTCTGAGCTCCCTGCCCCCACTGTGAGCTTGGCTCTTTATTA 1972
DB 1814 TGTCTCTAACTCCTCTGAGCTCCCTGCCCCCACTGTGAGCTTGGCTCTTTATTA 1873
QY 1973 TTGGAGTCTATGCCCCAGCAGAGTCCAGAGGCTTCTCCAGTCTACAGTGGCTCCT 2032
DB 1874 TTGGAGTCTATGCCCCAGCAGAGTCCAGAGGCTTCTCCAGTCTACAGTGGCTCCT 1933
QY 2033 CTTGTCTGATGTGACAGGATGGAGTTGGGGGTCTCTACAGTGTCTGGGCACTGAGATGG 2092
DB 1934 CTTGTCTGATGTGACAGGATGGAGTTGGGGGTCTCTACAGTGTCTGGGCACTGAGATGG 1993
QY 2093 CTTTTCATACCTCTGATCTCTACTGGGTGAGCAGCAGGACAGACCTGCGCCCTGGA 2152
DB 1994 CTTTTCATACCTCTGATCTCTACTGGGTGAGCAGCAGGACAGACCTGCGCCCTGGA 2053
QY 2153 TCTGAACTGGCAGGCACTCCCCGGGAGCATGTGAAGGTCCCGTTGACCCAGGGTCAGTGG 2212
DB 2054 TCTGAACTGGCAGGCACTCCCCGGGAGCATGTGAAGGTCCCGTTGACCCAGGGTCAGTGG 2113
QY 2213 TGGGGCGCCCTGGCTGCCAGCAGTCTTA CTGGGCCCACTTTGTACCTGTCTCTCT 2272
DB 2114 TGGGGCGCCCTGGCTGCCAGCAGTCTTA CTGGGCCCACTTTGTACCTGTCTCTCT 2173
QY 2273 CTTTGTCTTAGTGTCTTTCAGAGGCTCTCATCTCTGCTGGCTCCCTCATTTGAGAGCACT 2332
DB 2174 CTTTGTCTTAGTGTCTTTCAGAGGCTCTCATCTCTGCTGGCTCCCTCATTTGAGAGCACT 2233
QY 2333 CGGGCTCGGGCAAGGTTTCAGGGCTGTGAGACCTTGGCCCTGGGGAGAGGCCCTGTT 2392
DB 2234 CGGGCTCGGGCAAGGTTTCAGGGCTGTGAGACCTTGGCCCTGGGGAGAGGCCCTGTT 2293
QY 2393 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAAATGACAGGCTCTGCGAGTGTGGA 2452
DB 2294 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAAATGACAGGCTCTGCGAGTGTGGA 2353
QY 2453 CGCTGCAACAACCTGCTTAGGCACTGAGTGTAACTCTAGGCAAGGCCGGGGCTG 2512
DB 2354 CGCTGCAACAACCTGCTTAGGCACTGAGTGTAACTCTAGGCAAGGCCGGGGCTG 2413
QY 2513 CGGTGCAAGCACTGCGGCACTGCTGGCTGGGGCGGCCCAAGCACAGCCCTGACTAGGATGAC 2572

Db	2414	CGGTGACGACCTGGCCATCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGAC	2473	PR	01-SEP-1998;	98US-0098716P.
				PR	01-SEP-1998;	98US-0098723P.
				PR	01-SEP-1998;	98US-0098749P.
Qy	2573	AGCAGCAAAAGAACCAACCTTTCTCCCTCTGAGAGGAGCTTCTGCTACTCTGCACTCACTGA	2632	PR	01-SEP-1998;	98US-0098750P.
				PR	02-SEP-1998;	98US-0098803P.
Db	2474	AGCAGCACAAAGAACCAACCTTTCTCCCTCTGAGAGGAGCTTCTGCTACTCTGCACTCACTGA	2533	PR	02-SEP-1998;	98US-0098821P.
				PR	02-SEP-1998;	98US-0098843P.
Qy	2633	TGACACTCAGCAGGGTGATGACAGCAGTGTGCTCTCCCTATGGGACTCCCTTCTACCAA	2692	PR	09-SEP-1998;	98US-0099536P.
				PR	09-SEP-1998;	98US-0099596P.
Db	2534	TGACACTCAGCAGGGTGATGACAGCAGTGTGCTCTCCCTATGGGACTCCCTTCTACCAA	2593	PR	09-SEP-1998;	98US-0099598P.
				PR	09-SEP-1998;	98US-0099602P.
Qy	2693	GCACATGAGCTCTTAACAGGGTGGGGCTACCCCCAGACCTGCTCTACACTGATATTG	2752	PR	09-SEP-1998;	98US-0099642P.
				PR	10-SEP-1998;	98US-0099741P.
Db	2594	GCACATGAGCTCTTAACAGGGTGGGGCTACCCCCAGACCTGCTCTACACTGATATTG	2653	PR	10-SEP-1998;	98US-0099754P.
				PR	10-SEP-1998;	98US-0099763P.
Qy	2753	AAGAACCTGGAGAGATCTCTTCACTTCTGGGCATTCAGGACCTCCAGAAACACAGTG	2812	PR	10-SEP-1998;	98US-0099792P.
				PR	10-SEP-1998;	98US-0099808P.
Db	2654	AAGAACCTGGAGAGATCTCTTCACTTCTGGGCATTCAGGACCTCCAGAAACACAGTG	2713	PR	10-SEP-1998;	98US-0099812P.
				PR	10-SEP-1998;	98US-0099815P.
Qy	2813	TTTCAAGAGACCTTAAACAACTGCTGTCCAGGACCTATGTAATGAACACCAACA	2872	PR	10-SEP-1998;	98US-0099816P.
				PR	15-SEP-1998;	98US-0100385P.
Db	2714	TTTCAAGAGACCTTAAACAACTGCTGTCCAGGACCTATGTAATGAACACCAACA	2773	PR	15-SEP-1998;	98US-0100388P.
				PR	15-SEP-1998;	98US-0100390P.
Qy	2873	TCTAAACAATCATATGCTTAAATGCACTCTGGAACCTCCACTCTGAAGCTGCCGCTTT	2932	PR	16-SEP-1998;	98US-0100584P.
				PR	16-SEP-1998;	98US-0100627P.
Db	2774	TCTAAACAATCATATGCTTAAATGCACTCTGGAACCTCCACTCTGAAGCTGCCGCTTT	2833	PR	16-SEP-1998;	98US-0100661P.
				PR	16-SEP-1998;	98US-0100662P.
Qy	2933	GGACACCAACTCCCTTCTCCAGGGTCATGCAAGGATCTGCTCCCTCTGCTTCCCTT	2992	PR	16-SEP-1998;	98US-0100664P.
				PR	17-SEP-1998;	98US-0100683P.
Db	2834	GGACACCAACTCCCTTCTCCAGGGTCATGCAAGGATCTGCTCCCTCTGCTTCCCTT	2893	PR	17-SEP-1998;	98US-0100684P.
				PR	17-SEP-1998;	98US-0100710P.
Qy	2993	ACCAGTCGTGACCGCTGACTCCAGGAAGTCTTCCCTGAAGTGTGACCACTTCTTCT	3052	PR	17-SEP-1998;	98US-0100711P.
				PR	17-SEP-1998;	98US-0100919P.
Db	2894	ACCAGTCGTGACCGCTGACTCCAGGAAGTCTTCCCTGAAGTGTGACCACTTCTTCT	2953	PR	17-SEP-1998;	98US-0100930P.
				PR	18-SEP-1998;	98US-0100849P.
Qy	3053	TGCTTCAGTTGGGCGAGACTGTATCCCTCTGCCGAGATGGCAGGGTAATCTG	3112	PR	18-SEP-1998;	98US-0101014P.
				PR	18-SEP-1998;	98US-0101068P.
Db	2954	TGCTTCAGTTGGGCGAGACTGTATCCCTCTGCCGAGATGGCAGGGTAATCTG	3013	PR	18-SEP-1998;	98US-0101071P.
				PR	22-SEP-1998;	98US-0101279P.
Qy	3113	AGCCCTTCTTCACTCTTACCTTAGCTGACCCCTTCACTCTGCCCTCCCTTCTTCT	3172	PR	22-SEP-1998;	98US-0101471P.
				PR	23-SEP-1998;	98US-0101472P.
Db	3014	AGCCCTTCTTCACTCTTACCTTAGCTGACCCCTTCACTCTGCCCTCCCTTCTTCT	3073	PR	23-SEP-1998;	98US-0101472P.
				PR	23-SEP-1998;	98US-0101474P.
Qy	3173	GTTTGGGATTGAGAAACTGCTGTGAGAGACTGTTATTTTATTAATAATATAGG	3232	PR	23-SEP-1998;	98US-0101475P.
				PR	23-SEP-1998;	98US-0101476P.
Db	3074	GTTTGGGATTGAGAAACTGCTGTGAGAGACTGTTATTTTATTAATAATATAGG	3133	PR	23-SEP-1998;	98US-0101477P.
				PR	23-SEP-1998;	98US-0101479P.
Qy	3233	CTTA 3236		PR	24-SEP-1998;	98US-0101738P.
				PR	24-SEP-1998;	98US-0101741P.
Db	3134	CITA 3137		PR	24-SEP-1998;	98US-0101743P.
				PR	24-SEP-1998;	98US-0101915P.
				PR	24-SEP-1998;	98US-0101916P.
				PR	29-SEP-1998;	98US-0102207P.
				PR	29-SEP-1998;	98US-0102307P.
				PR	29-SEP-1998;	98US-0102330P.
				PR	29-SEP-1998;	98US-0102331P.
				PR	30-SEP-1998;	98US-0102484P.
				PR	30-SEP-1998;	98US-0102487P.
				PR	30-SEP-1998;	98US-0102570P.
				PR	30-SEP-1998;	98US-0102571P.
				PR	01-OCT-1998;	98US-0102684P.
				PR	01-OCT-1998;	98US-0102687P.
				PR	01-OCT-1998;	98US-0102965P.
				PR	06-OCT-1998;	98US-0103258P.
				PR	06-OCT-1998;	98US-0103449P.
				PR	07-OCT-1998;	98US-0103314P.
				PR	07-OCT-1998;	98US-0103315P.
				PR	07-OCT-1998;	98US-0103328P.
				PR	07-OCT-1998;	98US-0103335P.
				PR	07-OCT-1998;	98US-0103396P.
				PR	07-OCT-1998;	98US-0103401P.
				PR	08-OCT-1998;	98US-0103633P.

RESULT 4
ACD68082
ID ACD68082 standard; cdna; 3143 BP.
XX
AC ACD68082;
XX
XX
XX 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1317 cdna.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW tissue typing; chromosome identification; vaccine; gene; ss.
XX Homo sapiens.
XX
PN US2003073129-A1.
XX
PD 17-APR-2003.
XX
PF 04-SEP-2001; 2001US-00946374.
XX

```
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106903P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108803P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0021851P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 98US-0000106.
PR 12-APR-1999; 98US-00284291.
PR 16-APR-1999; 98US-0129674P.
PR 23-JUN-1999; 98US-0141037P.
PR 26-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 01-SEP-1999; 98US-0020111.
PR 15-SEP-1999; 98US-0021194.
PR 18-OCT-1999; 98US-00403297.
PR 30-NOV-1999; 98US-0028313.
PR 02-DEC-1999; 98US-0028551.
PR 16-DEC-1999; 98US-0030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Fan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX
XX WBI: 2003-585292/55.
XX P-PSDB; ABO33537.
XX
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
XX preparation of a medicament for treating a condition responsive to PRO
XX polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 2; Fig 157; 561pp; English.
XX
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (1), having at least 80% sequence identity to a sequence
XX
Query Match 87.3%; Score 3060.8; DB 8; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 173 AGAGCTCCCTGGTGACAGCTCTGGCTGAGCATGCGCTCCAGCATGCGCTCCAGCGCTGGCGCTGGACCC 232
DB 74 AGAGCTCCCTGGTGACAGCTCTGGCTGAGCATGCGCTCCAGCATGCGCTCCAGCGCTGGCGCTGGACCC 133
QY 233 CTGGAGCTCTCTGGGCGCTTTTCTCTTCCAACTGCTTCAGCTGCTGCTGCCAGCAGCAGC 292
DB 134 CTGGAGCTCTCTGGGCGCTTTTCTCTTCCAACTGCTTCAGCTGCTGCTGCCAGCAGCAGC 193
QY 293 CGCGGGGGAGCGGGCGAGGGGCCCATGCCAGGCTCAGATCTATGACGGGATGAACG 352
DB 194 CGCGGGGGAGCGGGCGAGGGGCCCATGCCAGGCTCAGATCTATGACGGGATGAACG 253
QY 353 TAGGGCAGCTTAGCTTCTTCCACAGAGGGCGCTCCAGGATTTTGACACTCTGCTCTCTGAG 412
DB 254 TAGGGCAGCTTAGCTTCTTCCACAGAGGGCGCTCCAGGATTTTGACACTCTGCTCTCTGAG 313
QY 413 TGGTGATGGAATACTCTCTAGCTGGGGCTCGAAGAGCAATCTTGGCTTGGATATCA 472
DB 314 TGGTGATGGAATACTCTCTAGCTGGGGCTCGAAGAGCAATCTTGGCTTGGATATCA 373
QY 473 GGATCCAGGGGTCCCAGGCTAAAGAACATGATACCTGGCGCAGCAGTGACAGAAAAA 532
DB 374 GGATCCAGGGGTCCCAGGCTAAAGAACATGATACCTGGCGCAGCAGTGACAGAAAAA 433
QY 533 GAGTGAATGTGCTTTAAGAGAGAGCAATGAGACAGTGTTCATCTTCATCCGTGT 592
DB 434 GAGTGAATGTGCTTTAAGAGAGAGCAATGAGACAGTGTTCATCTTCATCCGTGT 493
QY 593 CTGTGTTTCTTACAATGTCAACCATCTCTACACCTGGCGCAGCTTCGGCTTCAGCCCTGC 652
DB 494 CTGTGTTTCTTACAATGTCAACCATCTCTACACCTGGCGCAGCTTCGGCTTCAGCCCTGC 553
QY 653 TTGTACCTTCAATTGAATTCATCAAGATTCCTTACCTGTGGCCATCTCGGAGGACAAAGTCA 712
```

554 TTGTACCTTCATTGAACCTTCAGATTCTCACTGTTCCTTCTCGGAGCAAGGTCAAT 613
713 GGAGGAAAAGCCAAAGCCCTTTGACCCCGCTCAACAGCATACGCGTCTCTTGTGGA 772
614 GGAGGAAAAGCCAAAGCCCTTTGACCCCGCTCAACAGCATACGCGTCTCTTGTGGA 673
773 TGGGATGCTCTATTCTGTGTACTATGAACAACTTCTGGGAGTGAAGCCCATCTCTGATGCG 832
674 TGGGATGCTCTATTCTGTGTACTATGAACAACTTCTGGGAGTGAAGCCCATCTCTGATGCG 733
833 CACACTGGGATCCGAGCCCTGTCTCAAGACCGACAACTTCTCTCGCTGGCTGTCATGA 892
734 CACACTGGGATCCGAGCCCTGTCTCAAGACCGACAACTTCTCTCGCTGGCTGTCATGA 793
893 CGCTCTCTTTGTGGCAGCATCCCTTTCAGCCAGTGTCTACTTCTTCTCGAGGAGAC 952
794 CGCTCTCTTTGTGGCAGCATCCCTTTCAGCCAGTGTCTACTTCTTCTTTCGAGGAGAC 853
953 AGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACATCGCGGTGCTAGGTCTGCAA 1012
854 AGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACATCGCGGTGCTAGGTCTGCAA 913
1013 GAAAGCACTGGCGCGGAAAGCTGCTCAGAGAGTGAACCACTTCTTGAAGGCCCA 1072
914 GAATGACGTGGCGCGGAAAGCTGCTCAGAGAGTGAACCACTTCTTGAAGGCCCA 973
1073 GCTGCTCTGACCCAGCGCGGAGCTGCTCCCTTCAACGTCTATCGGCCCAAGCGGTCTGCT 1132
974 GCTGCTCTGACCCAGCGCGGAGCTGCTCCCTTCAACGTCTATCGGCCCAAGCGGTCTGCT 1033
1133 CCCCAGCATCTCCCAAGTCCCACTCCCACTATGCGAGTCTTCACTCCCAAGTGGAGGT 1192
1034 CCCCAGCATCTCCCAAGTCCCACTCCCACTATGCGAGTCTTCACTCCCAAGTGGAGGT 1093
1193 TGGCGGAGCAGGAGCTCTGCGGTTTGTGCTTCTCTCTTTGGACATTTGAACGTGCTT 1252
1094 TGGCGGAGCAGGAGCTCTGCGGTTTGTGCTTCTCTCTTTGGACATTTGAAGGTGCTT 1153
1253 TAAGGGGAAATACAAAGATTGAACAAAGAACTTCACGCTGGACTATTATAGGGGCC 1312
1154 TAAGGGGAAATACAAAGATTGAACAAAGAACTTCACGCTGGACTATTATAGGGGCC 1213
1313 TGAGACCAACCCCGCCAGGAGTGTCTCAGTGGGCGCTCTCTGATAGGCGCTGAC 1372
1214 TGAGACCAACCCCGCCAGGAGTGTCTCAGTGGGCGCTCTCTGATAGGCGCTGAC 1273
1373 CTTGATGAAGGACCAATTTCTGATGGATGAAGCAAGTGTGGGAGCGCCCTGTCTGTTGAA 1432
1274 CTTGATGAAGGACCAATTTCTGATGGATGAAGCAAGTGTGGGAGCGCCCTGTCTGTTGAA 1333
1433 ATCTGGCGTGGAGTATACAGCGTTGCAAGTGGAGACAGCCAGGCGCTTGTATGGGACAG 1492
1334 ATCTGGCGTGGAGTATACAGCGTTGCAAGTGGAGACAGCCAGGCGCTTGTATGGGACAG 1393
1493 CCACTTGTATGTACCTTGGGAAACCAACAGGCTGCTTCAAGGCTGTTGTAAGTGG 1552
1394 CCACTTGTATGTACCTTGGGAAACCAACAGGCTGCTTCAAGGCTGTTGTAAGTGG 1453
1553 GGACAGAGTGTCTATCTGTGGAGAGATTGAGTGTCTTCTGACCTGACCTGACCTGTCTG 1612
1454 GGACAGAGTGTCTATCTGTGGGAAAGATTGAGTGTCTTCTGACCTGACCTGACCTGTCTG 1513
1613 CAACCTGACGTGGCGCCCAACCCAGGCTGCAAGTGTCTTGTAGGCTTCTCAGGAGGTCTG 1672
1514 CAACCTGACGTGGCGCCCAACCCAGGCTGCAAGTGTCTTGTAGGCTTCTCAGGAGGTCTG 1573
1673 GAGGCTGCCCGAGCAACTGAGTGTCTATGAGAGCTGTGAGCTGTGCTTCTGCTGCG 1732
1574 GAGGCTGCCCGAGCAACTGAGTGTCTATGAGAGCTGTGAGCTGTGCTTCTGCTGCG 1633
1733 GGACCCCACTGTGCTGGAGCCCTGAGTCCCGAACCTGTGCTCTCTGCTGCTGCTGCTGCTG 1792

1634 GGACCCCACTGTGCTGGGACCTTGAGTCCCGAACCTGTTCCTCTCTCTGCTGCTGCTGCTG 1693
1793 CTTGAACCTCTCTGAAAGCAGGACATGAGCGGGGAAACCCAGAGTGGCATGTGCCAGTGG 1852
1694 CTTGAACCTCTCTGAAAGCAGGACATGAGCGGGGAAACCCAGAGTGGCATGTGCCAGTGG 1753
1853 CCCCATGAGCAGGAGCCTTTCGGCTCTCAGAGCGCGCCGAAATCATTAAGAAAGTCTCTGCG 1912
1754 CCCCATGAGCAGGAGCCTTTCGGCTCTCAGAGCGCGCCGAAATCATTAAGAAAGTCTCTGCG 1813
1913 TGTCCCTACTCCATCTCGAGCTCCCTGCGCCCACTGTCTCAGCTTGGCTCTCTTATTA 1972
1814 TGTCCCAACTCCATCTCGAGCTCCCTGCGCCCACTGTCTCAGCTTGGCTCTCTTATTA 1873
1973 TTTGGAGTCAATGSCCCAGCAGCAGTCCCGAAGACCTTTCCTCACTGTCTCAATTTGGTCTCT 2032
1874 TTTGGAGTCAATGSCCCAGCAGCAGTCCCGAAGACCTTTCCTCACTGTCTCAATTTGGTCTCT 1933
2033 CTTGCTGATGAGTGAAGTGGGCTCTTACAGAGTCTGCGGCAACTGAGAAATGG 2092
1934 CTTGCTGATGAGTGAAGTGGGCTCTTACAGAGTCTGCGGCAACTGAGAAATGG 1993
2093 CTTTTCATACCTGTGATCTCTACTTGGGTGACAGCCAGGACCCCTGCGCTCTGGA 2152
1994 CTTTTCATACCTGTGATCTCTACTTGGGTGACAGCCAGGACCCCTGCGCTCTGGA 2053
2153 TCTGMACTGGCAGGACATCCCGGAGCATGTGAAGTCCCGTTGACAGAGGTCTGAGTGG 2212
2054 TCTGMACTGGCAGGACATCCCGGAGCATGTGAAGTCCCGTTGACAGAGGTCTGAGTGG 2113
2213 TGGGGCGGCTGCTGCTGCGCAGCAGTCTCTACTTGGGCGCCACTTTGTCACTGTCTCTCT 2272
2114 TGGGGCGGCTGCTGCTGCGCAGCAGTCTCTACTTGGGCGCCACTTTGTCACTGTCTCTCT 2173
2273 CTTTGTCTTGTGCTTTTCAAGAGCCTCATCATCTCTGCGCTCTCCCACTTGGAGCACT 2332
2174 CTTTGTCTTGTGCTTTTCAAGAGCCTCATCATCTCTGCGCTCTCCCACTTGGAGCACT 2233
2333 CCGGGCTCGGGGCAAGTTTCAAGAGCCTCTGAGACCTTGGCGCTTGGGAGAAAGCCCGTT 2392
2234 CCGGGCTCGGGGCAAGTTTCAAGAGCCTCTGAGACCTTGGCGCTTGGGAGAAAGCCCGTT 2293
2393 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAAATGACAGGACCTCTGCGAGTGTGGA 2452
2294 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAAATGACAGGACCTCTGCGAGTGTGGA 2353
2453 CGCTGACACAACTGCTAGGACCTGAGTGTCTTAACTCTAGGACAGGCGCGGGCTG 2512
2354 CGCTGACACAACTGCTAGGACCTGAGTGTCTTAACTCTAGGACAGGCGCGGGCTG 2413
2513 CGGTGAGGACCACTGCGCTGCGCGCCCAAGCAGCAGCCTGACTGAGATGAC 2572
2414 CGGTGAGGACCACTGCGCTGCGCGCCCAAGCAGCAGCCTGACTGAGATGAC 2473
2573 AGCAGCAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGACTCTGACTCTG 2632
2474 AGCAGCAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGACTCTGACTCTG 2533
2633 TGACACTCAGCAGGAGTGTGCAAGCAGTCTGCTCTCCCTATGGGACTCTCTTCTACCAA 2692
2534 TGACACTCAGCAGGAGTGTGCAAGCAGTCTGCTCTCCCTATGGGACTCTCTTCTACCAA 2593
2693 GCACATGAGCTCTTAACAGGAGTGTGCAAGCAGTCTGCTCTCTCTCTCTCTCTCTCTCT 2752
2594 GCACATGAGCTCTTAACAGGAGTGTGCAAGCAGTCTGCTCTCTCTCTCTCTCTCTCTCT 2653
2753 AAGAACTCGAGAGGATCTTCAAGTGTGGCGCAATTCAGGAGCCCTCCAGAAACACAGTGG 2812
2654 AAGAACTCGAGAGGATCTTCAAGTGTGGCGCAATTCAGGAGCCCTCCAGAAACACAGTGG 2713
2813 TTTCAAGAGACCTTAAGAAACCTGCTGCTCCAGGACCTCTATGAGTGTGAAACACCAAA 2872
2714 TTTCAAGAGACCTTAAGAAACCTGCTGCTCCAGGACCTCTATGAGTGTGAAACACCAAA 2773

QY	2873	TCTAACAATCATATGCTAACATGCACTCCCTGGAACCTCCACTCTGAAAGCTGCGCTTT	2932	PR	15-SEP-1998;	98US-0100390P.
Db	2774	TCTAACAATCATATGCTAACATGCACTCCCTGGAACCTCCACTCTGAAAGCTGCGCTTT	2833	PR	16-SEP-1998;	98US-0100584P.
QY	2933	GGACACACACTCCCTTCTCCAGGGTATGAGGATCTGCTCCCTCTGCTTCCCTTT	2992	PR	16-SEP-1998;	98US-0100627P.
Db	2834	GGACACACACTCCCTTCTCCAGGGTATGAGGATCTGCTCCCTCTGCTTCCCTTT	2893	PR	16-SEP-1998;	98US-0100661P.
QY	2993	ACAGTCTGTCACCGCTGACTCCAGGAACTCTTCCCTGAAGTCTGACCACTTCTTCT	3052	PR	16-SEP-1998;	98US-0100662P.
Db	2894	ACAGTCTGTCACCGCTGACTCCAGGAACTCTTCCCTGAAGTCTGACCACTTCTTCT	2953	PR	17-SEP-1998;	98US-0100683P.
QY	3053	TGCTTCAGTTGGGGGAGACTCTGATCCCTTCTGCTCCCTGAGGAAAGGAGGATCTG	3112	PR	17-SEP-1998;	98US-0100710P.
Db	2954	TGCTTCAGTTGGGGGAGACTCTGATCCCTTCTGCTCCCTGAGGAAAGGAGGATCTG	3013	PR	17-SEP-1998;	98US-0100711P.
QY	3113	AGCTTCTTCACTCCCTTACCTTAGCTGACCCCTTCACTCTCCCTCCCTTTCCTTT	3172	PR	17-SEP-1998;	98US-0100919P.
Db	3014	AGCTTCTTCACTCCCTTACCTTAGCTGACCCCTTCACTCTCCCTCCCTTTCCTTT	3073	PR	17-SEP-1998;	98US-0100930P.
QY	3173	GTTTGGGATCGAAGAACTGCTTGTGTCAGAGCTGTTTATTTTATTAATAATAAGG	3232	PR	18-SEP-1998;	98US-0100948P.
Db	3074	GTTTGGGATCGAAGAACTGCTTGTGTCAGAGCTGTTTATTTTATTAATAATAAGG	3133	PR	18-SEP-1998;	98US-0100949P.
QY	3233	CTTA 3236		PR	18-SEP-1998;	98US-0101014P.
Db	3134	CTTA 3137		PR	18-SEP-1998;	98US-0101014P.
RESULT 5						
ID	ADCl8145	ADCl8145 standard; cDNA; 3143 BP.				
XX	ADCl8145;					
DT	18-DEC-2003 (first entry)					
XX	Human PRO polynucleotide #79.					
XX	Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;					
KW	gene mapping; genetic disorder.					
XX	Homo sapiens.					
OS	US2003064925-A1.					
XX	03-APR-2003.					
XX	10-DEC-2001; 2001US-00013907.					
PR	01-SEP-1998;	98US-0098716P.				
PR	01-SEP-1998;	98US-0098723P.				
PR	01-SEP-1998;	98US-0098749P.				
PR	01-SEP-1998;	98US-0098750P.				
PR	02-SEP-1998;	98US-0098803P.				
PR	02-SEP-1998;	98US-0098821P.				
PR	02-SEP-1998;	98US-0098843P.				
PR	09-SEP-1998;	98US-0099536P.				
PR	09-SEP-1998;	98US-0099598P.				
PR	09-SEP-1998;	98US-0099602P.				
PR	09-SEP-1998;	98US-0099642P.				
PR	10-SEP-1998;	98US-0099741P.				
PR	10-SEP-1998;	98US-0099754P.				
PR	10-SEP-1998;	98US-0099763P.				
PR	10-SEP-1998;	98US-0099792P.				
PR	10-SEP-1998;	98US-0099808P.				
PR	10-SEP-1998;	98US-0099812P.				
PR	10-SEP-1998;	98US-0099815P.				
PR	15-SEP-1998;	98US-0100385P.				
PR	15-SEP-1998;	98US-0100388P.				

1013 GAAATGACGTGGCGCGGAGAAAGCTGCTGCAGAGAGAGTGGACCAACCTTCTCTGAAGGCCCA 1072
Db |||||
914 GAAATGACGTGGCGCGGAGAAAGCTGCTGCAGAGAGAGTGGACCAACCTTCTCTGAAGGCCCA 973
Qy |||||
1073 GCTGCTCTGCACCCAGAGCCGGGCGAGCTGCCCTTCAAGCTCATCCGCCACCGCGTCTGTCT 1132
Db |||||
974 GCTGCTCTGCACCCAGAGCCGGGCGAGCTGCCCTTCAAGCTCATCCGCCACCGCGTCTGTCT 1033
Qy |||||
1133 CCCCAGCGATTTCTCCCAAGCTCCCAATCTAGCGAGTCTTCACTCTCCAGTGGAGGT 1192
Db |||||
1034 CCCCAGCGATTTCTCCCAAGCTCCCAATCTAGCGAGTCTTCACTCTCCAGTGGAGGT 1093
Qy |||||
1193 TGGCGGACCAAGAGCTCTCGGCTTGTGCTTCTCTCTCTGCAATTTGAAGTGTCTT 1252
Db |||||
1094 TGGCGGACCAAGAGCTCTCGGCTTGTGCTTCTCTCTCTGCAATTTGAAGTGTCTT 1153
Qy |||||
1253 TAAGGGGAAATACAAAGATTGAAACAAAGAAATTCACGCTGAGTACTTATAGGGGCC 1312
Db |||||
1154 TAAGGGGAAATACAAAGATTGAAACAAAGAAATTCACGCTGAGTACTTATAGGGGCC 1213
Qy |||||
1313 TGAGACCAACCCCGGCGAGGAGTGTCTCAGTGGGCCCTCTCTGTGATAGGCCCTGAC 1372
Db |||||
1214 TGAGACCAACCCCGGCGAGGAGTGTCTCAGTGGGCCCTCTCTGTGATAGGCCCTGAC 1273
Qy |||||
1373 CTTTATGAGGACCAATTTCTGATGATGAGTGAAGTGGGACGCGCTGTGTGTGAA 1432
Db |||||
1274 CTTTATGAGGACCAATTTCTGATGATGAGTGAAGTGGGACGCGCTGTGTGTGAA 1333
Qy |||||
1433 ATCTGGCGTGGAGTATACAGGCTTGCAGTGGGAGACAGCCAGGCTTGTGATGGGCACAG 1492
Db |||||
1334 ATCTGGCGTGGAGTATACAGGCTTGCAGTGGGAGACAGCCAGGCTTGTGATGGGCACAG 1393
Qy |||||
1493 CCATCTTGTGATGATGAGTGAAGTGGGACGCGCTGTGTGTGAA 1552
Db |||||
1394 CCATCTTGTGATGATGAGTGAAGTGGGACGCGCTGTGTGTGAA 1453
Qy |||||
1553 GGACAGCAGTGTCTCATCTGTGTGAAGATTCAGCTGTTCCTGACCCAGGCTTGTGATGGGCACAG 1612
Db |||||
1454 GGACAGCAGTGTCTCATCTGTGTGAAGATTCAGCTGTTCCTGACCCAGGCTTGTGATGGGCACAG 1513
Qy |||||
1613 CAACCTGACGTGGCCCAACCCAGGCTGAGTGTGTGTGAGGCTTCTCAGGAGTGTCTG 1672
Db |||||
1514 CAACCTGACGTGGCCCAACCCAGGCTGAGTGTGTGTGAGGCTTCTCAGGAGTGTCTG 1573
Qy |||||
1673 GAGGTCGCCCGAGCCCAACCCAGGCTGAGTGTGTGTGAGGCTTCTCAGGAGTGTCTG 1732
Db |||||
1574 GAGGTCGCCCGAGCCCAACCCAGGCTGAGTGTGTGTGAGGCTTCTCAGGAGTGTCTG 1633
Qy |||||
1733 GGAACCCCACTGTGCTGGGACCTGAGTCCGAACTGTGCTCTCTGCTGCCCCCA 1792
Db |||||
1634 GGAACCCCACTGTGCTGGGACCTGAGTCCGAACTGTGCTCTCTGCTGCCCCCA 1693
Qy |||||
1793 CTTGACCTCTGGAAGCAGACATGGAGCGGGGGAACCCAGAGTGGGATGTGCCAGTGG 1852
Db |||||
1694 CTTGACCTCTGGAAGCAGACATGGAGCGGGGGAACCCAGAGTGGGATGTGCCAGTGG 1753
Qy |||||
1853 CCCCATGAGCAGGAGCTTCTGGGCTCAGAGCCCGCGCAAACTATTAAGAGTCTTGGC 1912
Db |||||
1754 CCCCATGAGCAGGAGCTTCTGGGCTCAGAGCCCGCGCAAACTATTAAGAGTCTTGGC 1813
Qy |||||
1913 TGTCCCTTAATCTCTGAGCTCCCTGCGCCCACTGTGAGCTTGGCTCTTTATTA 1972
Db |||||
1814 TGTCCCACTCTCATCTGGAGTCCCTGCGCCCACTGTGAGCTTGGCTCTTTATTA 1873
Qy |||||
1973 TTGGAGTCAATGGCCAGCAGCTCCCAAGAGCTCTTCACTGTCTCAATGGCTCCCT 2032
Db |||||
1874 TTGGAGTCAATGGCCAGCAGCTCCCAAGAGCTCTTCACTGTCTCAATGGCTCCCT 1933
Qy |||||
2033 CTTTGTGATGATGAGTGGAGTGGGGTCTTACAGTGTGGGCACTGAGATGG 2092
Db |||||
1934 CTTTGTGATGATGAGTGGAGTGGGGTCTTACAGTGTGGGCACTGAGATGG 1993

2093 CTTTTCATACCTCTGTGATCTCTTACTGGTGGACAGCCAGACCCCTGGCCCTGGA 2152
Db |||||
1994 CTTTTCATACCTCTGTGATCTCTTACTGGTGGACAGCCAGACCCCTGGCCCTGGA 2053
Qy |||||
2153 TCCTGAACTGCGAGGCAATCCCGCGGAGCATGTGAAGTCCCGTGTGACAGGTCAGTGG 2212
Db |||||
2054 TCCTGAACTGCGAGGCAATCCCGCGGAGCATGTGAAGTCCCGTGTGACAGGTCAGTGG 2113
Qy |||||
2213 TGGGCGCCCTGGCTGCGGAGCATCTACTGCGCCCACTTTTGTCACTGTCTCTCT 2272
Db |||||
2114 TGGGCGCCCTGGCTGCGGAGCATCTACTGCGCCCACTTTTGTCACTGTCTCTCT 2173
Qy |||||
2273 CTTTGGCTTGTGCTTTTCAGGAGCCCTCATCTCTGTCGTCCTCCCATTTGAGAGCACT 2332
Db |||||
2174 CTTTGGCTTGTGCTTTTCAGGAGCCCTCATCTCTGTCGTCCTCCCATTTGAGAGCACT 2233
Qy |||||
2333 CCGGCTCGGCGCAAGGTTTCAGGCTGTGAGACCTCTGCGCCCTGGGAGAGGCGCCGCTT 2392
Db |||||
2234 CCGGCTCGGCGCAAGGTTTCAGGCTGTGAGACCTCTGCGCCCTGGGAGAGGCGCCGCTT 2293
Qy |||||
2393 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGAGGACCTCTGCCAGTGTGGA 2452
Db |||||
2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGAGGACCTCTGCCAGTGTGGA 2353
Qy |||||
2453 CGCTGACAACTGCTTAGGCACTGAGTAGCTTAACTCTAGGCAAGGCGCGGCTG 2512
Db |||||
2354 CGCTGACAACTGCTTAGGCACTGAGTAGCTTAACTCTAGGCAAGGCGCGGCTG 2413
Qy |||||
2513 CGGTCAGGCACTGGCCATGCTGGCTGGGCGGCCAAGCAGACCCCTGACTAGGATGAC 2572
Db |||||
2414 CGGTCAGGCACTGGCCATGCTGGCTGGGCGGCCAAGCAGACCCCTGACTAGGATGAC 2473
Qy |||||
2573 AGCAGCAAAAGAGCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTACTGA 2632
Db |||||
2474 AGCAGCAAAAGAGCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTACTGA 2533
Qy |||||
2633 TGAACCTGAGAGGATGATGAGAGCTGTCCTTCCCTCTATGGAGTCTCCCTTACCAA 2692
Db |||||
2534 TGAACCTGAGAGGATGATGAGAGCTGTCCTTCCCTCTATGGAGTCTCCCTTACCAA 2593
Qy |||||
2693 GCACATGAGCTCTCTAAACAGGCTGGGCTTACCCAGGAGCTGCTCTTACATGATATG 2752
Db |||||
2594 GCACATGAGCTCTCTAAACAGGCTGGGCTTACCCAGGAGCTGCTCTTACATGATATG 2653
Qy |||||
2753 AAGAACCTGAGAGGATGCTTCACTTGGCAATCCAGGAGCCCTCCAGAAACACAGTG 2812
Db |||||
2654 AAGAACCTGAGAGGATGCTTCACTTGGCAATCCAGGAGCCCTCCAGAAACACAGTG 2713
Qy |||||
2813 TTTCAAGAGAGCCCTAAAAAACCTGCTGCTCCAGGAGCCCTATGGTAATGAACACCAACA 2872
Db |||||
2714 TTTCAAGAGAGCCCTAAAAAACCTGCTGCTCCAGGAGCCCTATGGTAATGAACACCAACA 2773
Qy |||||
2873 TCTTAAACATATATGCTTAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2932
Db |||||
2774 TCTTAAACATATATGCTTAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2833
Qy |||||
2933 GGACACCAACATCTCCCTTCTCCAGGAGTATGAGGAGTCTGCTCCCTCTGCTGCTGCT 2992
Db |||||
2834 GGACACCAACATCTCCCTTCTCCAGGAGTATGAGGAGTCTGCTCCCTCTGCTGCTGCT 2893
Qy |||||
2993 ACCAGTGTGACCGCTGACTCCAGGAGTCTTCCCTGAGTCTGACCACTTCTTCTTCT 3052
Db |||||
2894 ACCAGTGTGACCGCTGACTCCAGGAGTCTTCCCTGAGTCTGACCACTTCTTCTTCT 2953
Qy |||||
3053 TGTCTTCAAGTGGGCGAGCTCTGATCCCTTCTGCTGCGGAGATGGCAGGCTTAACTG 3112
Db |||||
2954 TGTCTTCAAGTGGGCGAGCTCTGATCCCTTCTGCTGCGGAGATGGCAGGCTTAACTG 3013
Qy |||||
3113 AGCCTTCTTCACTCTTCTTACCTAGTGTGACCCCTTCACTCTCCCTCTCCCTTCTTCT 3172
Db |||||
3014 AGCCTTCTTCACTCTTCTTACCTAGTGTGACCCCTTCACTCTCCCTCTCCCTTCTTCT 3073
Qy |||||
3173 GTTTTGGGATTCAGAAACCTGCTTGTGTCAGAGACTGTTTATTTTATTAATAAATAGG 3232

```
Db      3074 GTTTGGATTTCAGAAACTGCTGTGCAGAGACTGTTATTTTATATAAATAAAGG 3133
Qv      3233 CTTA 3236
Db      3134 CTTA 3137

RESULT 6
ADD70791
ID      ADD70791 standard; cDNA; 3143 BP.
AC      ADD70791;
XX
XX
XX      15-JAN-2004 (first entry)
XX
XX      Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
XX      Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
XX      immune response; cardiac insufficiency disorder; calcium flux;
XX      umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX      arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX      Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX      dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
XX      Homo sapiens.
XX
XX      US2003099625-A1.
XX
XX      29-MAY-2003.
XX
XX
XX      12-DEC-2001; 2001US-00015386.
XX
XX      01-SEP-1998; 98US-0098716P.
XX      01-SEP-1998; 98US-0098723P.
XX      01-SEP-1998; 98US-0098749P.
XX      01-SEP-1998; 98US-0098750P.
XX      02-SEP-1998; 98US-0098803P.
XX      02-SEP-1998; 98US-0098821P.
XX      02-SEP-1998; 98US-0098843P.
XX      09-SEP-1998; 98US-0099536P.
XX      09-SEP-1998; 98US-0099596P.
XX      09-SEP-1998; 98US-0099598P.
XX      09-SEP-1998; 98US-0099602P.
XX      09-SEP-1998; 98US-0099642P.
XX      10-SEP-1998; 98US-0099741P.
XX      10-SEP-1998; 98US-0099754P.
XX      10-SEP-1998; 98US-0099763P.
XX      10-SEP-1998; 98US-0099792P.
XX      10-SEP-1998; 98US-0099808P.
XX      10-SEP-1998; 98US-0099812P.
XX      10-SEP-1998; 98US-0099815P.
XX      15-SEP-1998; 98US-0099816P.
XX      15-SEP-1998; 98US-0100385P.
XX      15-SEP-1998; 98US-0100388P.
XX      15-SEP-1998; 98US-0100390P.
XX      16-SEP-1998; 98US-0100584P.
XX      16-SEP-1998; 98US-0100627P.
XX      16-SEP-1998; 98US-0100661P.
XX      16-SEP-1998; 98US-0100662P.
XX      16-SEP-1998; 98US-0100664P.
XX      17-SEP-1998; 98US-0100683P.
XX      17-SEP-1998; 98US-0100684P.
XX      17-SEP-1998; 98US-0100710P.
XX      17-SEP-1998; 98US-0100711P.
XX      17-SEP-1998; 98US-0100913P.
XX      17-SEP-1998; 98US-0100930P.
XX      18-SEP-1998; 98US-0100848P.
XX      18-SEP-1998; 98US-0100849P.
XX      18-SEP-1998; 98US-0101014P.
XX      18-SEP-1998; 98US-0101068P.
XX      18-SEP-1998; 98US-0101071P.
XX      22-SEP-1998; 98US-0101279P.
PR      23-SEP-1998; 98US-0101471P.
PR      23-SEP-1998; 98US-0101472P.
PR      23-SEP-1998; 98US-0101474P.
PR      23-SEP-1998; 98US-0101475P.
PR      23-SEP-1998; 98US-0101476P.
PR      23-SEP-1998; 98US-0101477P.
PR      23-SEP-1998; 98US-0101479P.
PR      24-SEP-1998; 98US-0101738P.
PR      24-SEP-1998; 98US-0101741P.
PR      24-SEP-1998; 98US-0101743P.
PR      24-SEP-1998; 98US-0101915P.
PR      24-SEP-1998; 98US-0101916P.
PR      29-SEP-1998; 98US-0102079P.
PR      29-SEP-1998; 98US-0102240P.
PR      29-SEP-1998; 98US-0102307P.
PR      29-SEP-1998; 98US-0102330P.
PR      29-SEP-1998; 98US-0102331P.
PR      30-SEP-1998; 98US-0102484P.
PR      30-SEP-1998; 98US-0102487P.
PR      30-SEP-1998; 98US-0102570P.
PR      30-SEP-1998; 98US-0102571P.
PR      01-OCT-1998; 98US-0102684P.
PR      01-OCT-1998; 98US-0102687P.
PR      02-OCT-1998; 98US-0102965P.
PR      06-OCT-1998; 98US-0103258P.
PR      06-OCT-1998; 98US-0103449P.
PR      07-OCT-1998; 98US-0103314P.
PR      07-OCT-1998; 98US-0103315P.
PR      07-OCT-1998; 98US-0103328P.
PR      07-OCT-1998; 98US-0103355P.
PR      07-OCT-1998; 98US-0103396P.
PR      07-OCT-1998; 98US-0103401P.
PR      08-OCT-1998; 98US-0103633P.
PR      08-OCT-1998; 98US-0103678P.
PR      08-OCT-1998; 98US-0103679P.
PR      08-OCT-1998; 98US-0103711P.
PR      14-OCT-1998; 98US-0104257P.
PR      20-OCT-1998; 98US-0105000P.
PR      20-OCT-1998; 98US-0105002P.
PR      21-OCT-1998; 98US-0105104P.
PR      22-OCT-1998; 98US-0105169P.
PR      22-OCT-1998; 98US-0105266P.
PR      26-OCT-1998; 98US-0105693P.
PR      26-OCT-1998; 98US-0105694P.
PR      27-OCT-1998; 98US-0105807P.
PR      27-OCT-1998; 98US-0105811P.
PR      27-OCT-1998; 98US-0105882P.
PR      27-OCT-1998; 98US-0106062P.
PR      28-OCT-1998; 98US-0106023P.
PR      28-OCT-1998; 98US-0106029P.
PR      28-OCT-1998; 98US-0106030P.
PR      28-OCT-1998; 98US-0106032P.
PR      28-OCT-1998; 98US-0106033P.
PR      28-OCT-1998; 98US-0106178P.
PR      29-OCT-1998; 98US-0106248P.
PR      29-OCT-1998; 98US-0106384P.
PR      29-OCT-1998; 98US-0108500P.
PR      30-OCT-1998; 98US-0108464P.
PR      03-NOV-1998; 98US-0108566P.
PR      03-NOV-1998; 98US-0108567P.
PR      03-NOV-1998; 98US-0108505P.
PR      03-NOV-1998; 98US-0108519P.
PR      03-NOV-1998; 98US-0108532P.
PR      03-NOV-1998; 98US-0108534P.
PR      10-NOV-1998; 98US-0107782P.
PR      17-NOV-1998; 98US-0108775P.
PR      17-NOV-1998; 98US-0108779P.
PR      17-NOV-1998; 98US-0108787P.
PR      17-NOV-1998; 98US-0108788P.
PR      17-NOV-1998; 98US-0108801P.
PR      17-NOV-1998; 98US-0108802P.
PR      17-NOV-1998; 98US-0108806P.
```


Db 1214 TGAGACCAACCCCGGCGAGGAGTGGTCTCAGTGGGCCCCCTCTCTGATAAGGCCCTGAC 1273
Qy 1373 CTTTCATGAAGGACCAATTTCTGATGAGATGAGCAAGTGGTGGGACCGCCCTGCTGTGAA 1432
Db 1274 CTTTCATGAAGGACCAATTTCTGATGAGATGAGCAAGTGGTGGGACCGCCCTGCTGTGAA 1333
Qy 1433 ATCTGGCGTGAAGTATACAGGCTTGAGTGGAGACAGCCAGGCGCTTGATGGGCACAG 1492
Db 1334 ATCTGGCGTGAAGTATACAGGCTTGAGTGGAGACAGCCAGGCGCTTGATGGGCACAG 1393
Qy 1493 CCATCTTGTGATGATACCTGGGAACCAACAGGGTGGCTCCACAGGCTGTGTAAAGTGG 1552
Db 1394 CCATCTTGTGATGATACCTGGGAACCAACAGGGTGGCTCCACAGGCTGTGTAAAGTGG 1453
Qy 1553 GGACAGAGTCTCATCTGGTGGGAAGATTCAGCTGTTCCTGACCCCTGAACCTGTCG 1612
Db 1454 GGACAGAGTCTCATCTGGTGGGAAGATTCAGCTGTTCCTGACCCCTGAACCTGTCG 1513
Qy 1613 CAACCTGAGTGGCCCCCAACCCAGGCTGCAAGTGTGTTGTAGGCTTCTCAGAGGTGCTG 1672
Db 1514 CAACCTGAGTGGCCCCCAACCCAGGCTGCAAGTGTGTTGTAGGCTTCTCAGAGGTGCTG 1573
Qy 1673 GAGGGTGGCCGAGCACTGTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTGCCCG 1732
Db 1574 GAGGGTGGCCGAGCACTGTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTGCCCG 1633
Qy 1733 GGAACCCCACTGTGCTGGGACCCCTGATCCGACCTGTGTCTCTGCTGCCCCCAA 1792
Db 1634 GGAACCCCACTGTGCTGGGACCCCTGATCCGACCTGTGTCTCTGCTGCCCCCAA 1693
Qy 1793 CTTGAACTCTGGAGAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1852
Db 1694 CTTGAACTCTGGAGAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1753
Qy 1853 CCCCATGAGCAGGAGGCTTCGGCTCCTCAGAGCGCGCGCAATCATTAAGAGTCTTGGC 1912
Db 1754 CCCCATGAGCAGGAGGCTTCGGCTCCTCAGAGCGCGCGCAATCATTAAGAGTCTTGGC 1813
Qy 1913 TGTCCCTAACTCCATCTGGAGTCCCTGCTGCGCCACCTGTGAGCTTGGCTCTTATTA 1972
Db 1814 TGTCCCTAACTCCATCTGGAGTCCCTGCTGCGCCACCTGTGAGCTTGGCTCTTATTA 1873
Qy 1973 TTGGAGTCAATGGCCAGCAGCAGTCCAGAGAGCTCTTCCACTGTCTACAAATGGCTCCCT 2032
Db 1874 TTGGAGTCAATGGCCAGCAGCAGTCCAGAGAGCTCTTCCACTGTCTACAAATGGCTCCCT 1933
Qy 2033 CTTGCTGATGAGCAGGATGAGTGGGGTCTCTACAGTGTCTGGGCAACTGAGATGG 2092
Db 1934 CTTGCTGATGAGCAGGATGAGTGGGGTCTCTACAGTGTCTGGGCAACTGAGATGG 1993
Qy 2093 CTTTTCATACCTGTGATCTCTACTGGTGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2152
Db 1994 CTTTTCATACCTGTGATCTCTACTGGTGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2053
Qy 2153 TCTGAACCTGGCAGGATCCCGGGAGATGTGAAGTTCGGTTCGACAGGGTCAAGTGG 2212
Db 2054 TCTGAACCTGGCAGGATCCCGGGAGATGTGAAGTTCGGTTCGACAGGGTCAAGTGG 2113
Qy 2213 TGGGGCGCCCTGGCTGGCCAGCAGTCTTACTGGCCCGCCACCTTGTGCTGCTGCTGCT 2272
Db 2114 TGGGGCGCCCTGGCTGGCCAGCAGTCTTACTGGCCCGCCACCTTGTGCTGCTGCTGCTGCT 2173
Qy 2273 CTTTGGCTTGTGCTTTCAGGAGCCCTCATCATCTCTGCTGGCTCCCATTTGAGAGCACT 2332
Db 2174 CTTTGGCTTGTGCTTTCAGGAGCCCTCATCATCTCTGCTGGCTCCCATTTGAGAGCACT 2233
Qy 2333 CCGGGCTCGGGCAGGTTTCAGGGCTGTGAGACCTGGCCCTGGGGAGAGGCCCGCTT 2392
Db 2234 CCGGGCTCGGGCAGGTTTCAGGGCTGTGAGACCTGGCCCTGGGGAGAGGCCCGCTT 2293
Qy 2393 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGTGGA 2452

Db 2294 AAGCAGAGAGCAACACCTCAGTCTCCCAAGAAATGACAGGACCTCTGCCAGTGTGGA 2353
Qy 2453 CGCTGACAAACCTAGCTAGGCACTGAGGTAGCTTAAATCTTAGGCAAGCCGCGGCTG 2512
Db 2354 CGCTGACAAACCTAGCTAGGCACTGAGGTAGCTTAAATCTTAGGCAAGCCGCGGCTG 2413
Qy 2513 CGCTGACAGCACTGGCCATCTGCTGGTGGGGCCCAAGCAGCAGCCTGATAGGATGAC 2572
Db 2414 CGCTGACAGCACTGGCCATCTGCTGGTGGGGCCCAAGCAGCAGCCTGATAGGATGAC 2473
Qy 2573 AGCAGCACAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGCTACTCTGATCACTGA 2632
Db 2474 AGCAGCACAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGCTACTCTGATCACTGA 2533
Qy 2633 TGACACTCAGAGGATGATGACAGCAGTCTGCTCCCTGATGGACTCCCTTCTACCAA 2692
Db 2534 TGACACTCAGAGGATGATGACAGCAGTCTGCTCCCTGATGGACTCCCTTCTACCAA 2593
Qy 2693 GCACATGAGCTCTTAAACAGGGTGGGGCTACCCCGACACCTGCTCTACACTGATATTG 2752
Db 2594 GCACATGAGCTCTTAAACAGGGTGGGGCTACCCCGACACCTGCTCTACACTGATATTG 2653
Qy 2753 AAGAACCTGGAGAGATCTTCACTGCTGGCATTTCCAGGAGCCCTCCAGAAACACAGTGG 2812
Db 2654 AAGAACCTGGAGAGATCTTCACTGCTGGCATTTCCAGGAGCCCTCCAGAAACACAGTGG 2713
Qy 2813 TTTCAGAGACCTTAAACCTGCTGCTCCAGGACCTATGTAATGAACACCAACA 2872
Db 2714 TTTCAGAGACCTTAAACCTGCTGCTCCAGGACCTATGTAATGAACACCAACA 2773
Qy 2873 TCTAAACATCATATGCTAAACATGCTCTGCGAACTTCCACTCTGAGAGCTGCGCTTT 2932
Db 2774 TCTAAACATCATATGCTAAACATGCTCTGCGAACTTCCACTCTGAGAGCTGCGCTTT 2833
Qy 2933 GGACACCACTCTCTCTCCAGGCTCATGAGGATCTGCTCCCTGCTCTCCCTT 2992
Db 2834 GGACACCACTCTCTCTCCAGGCTCATGAGGATCTGCTCCCTGCTCTCCCTT 2893
Qy 2993 ACCAGTCTGCTACCGCTGACTCCAGGAACTCTTCCCTGGAAGTCTGACACCTTTCTTCT 3052
Db 2894 ACCAGTCTGCTACCGCTGACTCCAGGAACTCTTCCCTGGAAGTCTGACACCTTTCTTCT 2953
Qy 3053 TGCTTCACTGGGAGACTCTGATCCCTTCTGCTCCAGGATCTGCTCCCTGCTCTCCCTT 3112
Db 2954 TGCTTCACTGGGAGACTCTGATCCCTTCTGCTCCAGGATCTGCTCCCTGCTCTCCCTT 3013
Qy 3113 AGCTTCTTCACTCTCTTACCTTAGCTGACCCCTTCACTCTCCCTGCTCTCCCTT 3172
Db 3014 AGCTTCTTCACTCTCTTACCTTAGCTGACCCCTTCACTCTCCCTGCTCTCCCTT 3073
Qy 3173 GTTTTGGGATTCAGAAACCTGCTTGTGAGAGCTGTTTATTTTATTTTAAATAAAG 3232
Db 3074 GTTTTGGGATTCAGAAACCTGCTTGTGAGAGCTGTTTATTTTATTTTAAATAAAG 3133
Qy 3233 CTTA 3236
Db 3134 CTTA 3137

RESULT 7

ADD39868
ID ADD39868 standard; cDNA; 3143 BP.

XX ADD39868;

DT 15-JAN-2004 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO1317.

XX Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX Homo sapiens.
XX US2003083462-A1.
XX 01-MAY-2003.
XX 10-DEC-2001; 2001US-00013913.
XX 05-JAN-1999; 99WO-US000106.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-755122/71.
DR P-PSDB; ADD39869.
XX New secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.
XX Claim 2; SEQ ID NO 276; 557pp; English.
PS The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. PRO is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410

CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
CC disease. PRO1478, PRO1465, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence encodes a PRO protein of the invention.
XX
SQ Sequence 3143 BP; 656 A; 963 C; 828 G; 696 T; 0 U; 0 Other;

Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 173 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGAGCC 232
DB 74 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGAGCC 133
QY 233 CTGGAGCTCTCTGGGCTTTTCCCTTCCACTCTTCAGCTGCTGCTGCCGAGAGCAGC 292
DB 134 CTGGAGCTCTCTGGGCTTTTCCCTTCCACTCTTCAGCTGCTGCTGCCGAGAGCAGC 193
QY 293 CGCGGGGGAGCGGGCGAGGGGCCCATGCCAGGCTCAGATACTATGACGGGGATGAACG 352
DB 194 CGCGGGGGAGCGGGCGAGGGGCCCATGCCAGGCTCAGATACTATGACGGGGATGAACG 253
QY 353 TAGGGCACTTAGCTTTTCCACGAGAGGGGCTCCAGATTTTGACACTCTGCTCTCTGAG 412
DB 254 TAGGGCACTTAGCTTTTCCACGAGAGGGGCTCCAGATTTTGACACTCTGCTCTCTGAG 313
QY 413 TGGTGATGGAATACTCTCTAGCTGGGGCTCGAGAGCCATTTCTGGCTTTGGATATCCA 472
DB 314 TGGTGATGGAATACTCTCTAGCTGGGGCTCGAGAGCCATTTCTGGCTTTGGATATCCA 373
QY 473 GGATCAGGGTCCCGGCTTAAGAACATGATATACCTGGCCAGCCAGTGACAGAAAAA 532
DB 374 GGATCAGGGTCCCGGCTTAAGAACATGATATACCTGGCCAGCCAGTGACAGAAAAA 433
QY 533 GAGTCAATGTGCTTTAAGAGAGAGCAATGAGACACAGTGTGTTCAACTTTCATCCGTGT 592
DB 434 GAGTCAATGTGCTTTAAGAGAGAGCAATGAGACACAGTGTGTTCAACTTTCATCCGTGT 493
QY 593 CTGTGTTCTTACAAATGACCCATCTCTACCTGGGGACCTTCGCCCTTCAGCCCTGC 652
DB 494 CTGTGTTCTTACAAATGACCCATCTCTACCTGGGGACCTTCGCCCTTCAGCCCTGC 553
QY 653 TTGTACCTTCATTGAACTTCAAGATTCTCTACTGTGGCCATCTCGAGAGGCAAGGTGAT 712
DB 554 TTGTACCTTCATTGAACTTCAAGATTCTCTACTGTGGCCATCTCGAGAGGCAAGGTGAT 613
QY 713 GGAGGAAAAAGCCAAAGCCCTTTTGACCCGCTCAAGCATAGCGGTGTCTTGTTGGA 772
DB 614 GGAGGAAAAAGCCAAAGCCCTTTTGACCCGCTCAAGCATAGCGGTGTCTTGTTGGA 673
QY 773 TGGGATGCTCTATTCTGTGTACTATGAACAACCTTCTGGGCGAGTGAGCCCATCTCATCG 832
DB 674 TGGGATGCTCTATTCTGTGTACTATGAACAACCTTCTGGGCGAGTGAGCCCATCTCATCG 733
QY 833 CACACTGGGATCCAGCTGTCTCTCAAGACCGACAACTTCTCCGCTGGGTGCATCATGA 892
DB 734 CACACTGGGATCCAGCTGTCTCTCAAGACCGACAACTTCTCCGCTGGGTGCATCATGA 793
QY 893 CGCCTCTTTGGGAGAGCATCCCTTCGACCCAGTCTCTACTTCTTCTTCGAGGAGAC 952
DB 794 CGCCTCTTTGGGAGAGCATCCCTTCGACCCAGTCTCTACTTCTTCTTTCGAGGAGAC 853

QY 953 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGGGTGGCTAGAGTCTGCAG 1012
DB 854 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGGGTGGCTAGAGTCTGCAG 913
QY 1013 GAATGACGTGGCGCGGAGAAAGCTGCTGCGAGAGAGTGGACCACTTCTTGAAGGCCCA 1072
DB 914 GAATGACGTGGCGCGGAGAAAGCTGCTGCGAGAGAGTGGACCACTTCTTGAAGGCCCA 973
QY 1073 GCTGCTGACACCGCGGGGAGCTGCCCTTCAACGTCATCGCCGACGCGGTCTGTCT 1132
DB 974 GCTGCTGACACCGCGGGGAGCTGCCCTTCAACGTCATCGCCGACGCGGTCTGTCT 1033
QY 1133 CCCGCGGATCTTCCACAGCTCCCAATCTACGAGTCTTACCTCCAGTGGCAGGT 1192
DB 1034 CCCGCGGATCTTCCACAGCTCCCAATCTACGAGTCTTACCTCCAGTGGCAGGT 1093
QY 1193 TGGCGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTAAGAGTGTCTT 1252
DB 1094 TGGCGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTAAGAGTGTCTT 1153
QY 1253 TAAGGGGAATPACAAAGAGTTGAACAAAGAAATTCACGCTGGACTATTTATAGGGGCC 1312
DB 1154 TAAGGGGAATPACAAAGAGTTGAACAAAGAAATTCACGCTGGACTATTTATAGGGGCC 1213
QY 1313 TGAGACCAACCCCGCGGAGGAGTGTGCTAGTGGGCGCTCTCTCTGATTAAGGCGCTGAC 1372
DB 1214 TGAGACCAACCCCGCGGAGGAGTGTGCTAGTGGGCGCTCTCTCTGATTAAGGCGCTGAC 1273
QY 1373 CTTTCAATGAAGACCAATTTCTGATGAGTGAAGTGGTGGGAGCGCCCTGCTGTGTGAA 1432
DB 1274 CTTTCAATGAAGACCAATTTCTGATGAGTGAAGTGGTGGGAGCGCCCTGCTGTGTGAA 1333
QY 1433 ATCTGGGCTGAGATATACAGGCTTGCAGTGGAGACAGCCAGGCGCTTGAATGGGACAG 1492
DB 1334 ATCTGGGCTGAGATATACAGGCTTGCAGTGGAGACAGCCAGGCGCTTGAATGGGACAG 1393
QY 1493 CCATCTTGTGATGATGAGTGGAGAACCAACAGAGGTGCTCCACAGGCTGCTGTAAGTGG 1552
DB 1394 CCATCTTGTGATGAGTGGAGAACCAACAGAGGTGCTCCACAGGCTGCTGTAAGTGG 1453
QY 1553 GGACAGAGTCTCATCTGTTGGAAGAGATTCAGCTGTTCCCTGAGACCTGAACTGTTCG 1612
DB 1454 GGACAGAGTCTCATCTGTTGGAAGAGATTCAGCTGTTCCCTGAGACCTGAACTGTTCG 1513
QY 1613 CAACCTGAGCTGCCCCACCCAGGCTGAGTGTGTTGTAAGGCTTCTCAGAGGTGCTG 1672
DB 1514 CAACCTGAGCTGCCCCACCCAGGCTGAGTGTGTTGTAAGGCTTCTCAGAGGTGCTG 1573
QY 1673 GAGGTTGCCCGAGCCAACTGATGTCTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1732
DB 1574 GAGGTTGCCCGAGCCAACTGATGTCTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1633
QY 1733 GGACCCCACTGCTGGGACCTGAGTCCCGAACCTGTGCTCTGCTGCTGCTGCCCA 1792
DB 1634 GGACCCCACTGCTGGGACCTGAGTCCCGAACCTGTGCTCTGCTGCTGCTGCCCA 1693
QY 1793 CTTGAATCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGCATGTGCCAGTGG 1852
DB 1694 CTTGAATCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGCATGTGCCAGTGG 1753
QY 1853 CCCCATGAGCAGGAGCTTGGGCTTCAGAGCGCGCGCCCAATCATTAAGAGTCTGGC 1912
DB 1754 CCCCATGAGCAGGAGCTTGGGCTTCAGAGCGCGCGCCCAATCATTAAGAGTCTGGC 1813
QY 1913 TGTCTTAACTCTCTGAGCTCCCCCTGCGCCCACTGCTCAGCTTGGCCTCTTATTA 1972
DB 1814 TGTCTTAACTCTCTGAGCTCCCCCTGCGCCCACTGCTCAGCTTGGCCTCTTATTA 1873
QY 1973 TTGAGTCTATGGCCAGCAGGAGCTTCCAGAGGCTTCTCAGTCTCTACATGCTCTCCT 2032
DB 1874 TTGAGTCTATGGCCAGCAGGAGCTTCCAGAGGCTTCTCAGTCTCTACATGCTCTCCT 1933
QY 2033 CTTGCTGATAGTGAGGATGGATTGGGGTCTCTACCAAGTGTGGGCACTGAGAGTGG 2092

DB 1934 CTTGCTGATAGTGAGGATGGATTGGGGTCTCTACCAAGTCTGGCAACTGAGAAATGG 1993
QY 2093 CTTTTCATACCTCTGTGATCTCTACTGGTGGAGAGCCAGGACAGACCTGGCCCTGGA 2152
DB 1994 CTTTTCATACCTCTGTGATCTCTACTGGTGGAGAGCCAGGACAGACCTGGCCCTGGA 2053
QY 2153 TCTCTAACTGGCAGGACATCCCCCGGAGCATGTGAAGGTCTCCGTTGACACAGGTCAGTGG 2212
DB 2054 TCTCTAACTGGCAGGACATCCCCCGGAGCATGTGAAGGTCTCCGTTGACACAGGTCAGTGG 2113
QY 2213 TGGGCGCGCTGGCTGGCTGCCAGCAGTCTTACTTGGGCGCCACTTGTCACTGTCACTGTCT 2272
DB 2114 TGGGCGCGCTGGCTGGCTGCCAGCAGTCTTACTTGGGCGCCACTTGTCACTGTCACTGTCT 2173
QY 2273 CTTTGGCTTGTGCTTTTTCAGGAGCCCTCATCATCTCTGCTGGCCTCCCATTTAGAGAGCACT 2332
DB 2174 CTTTGGCTTGTGCTTTTTCAGGAGCCCTCATCATCTCTGCTGGCCTCCCATTTAGAGAGCACT 2233
QY 2333 CGGGCTCGGGGCAAGGTTTCAGGCTGTGAGACCTCGCTGGGCTTGGGAGAGAGGCGCGT 2392
DB 2234 CGGGCTCGGGGCAAGGTTTCAGGCTGTGAGACCTCGCTGGGCTTGGGAGAGAGGCGCGT 2293
QY 2393 AAGCAGAGAGCAACACCTTCCAGTCTCCAAAGATGACAGGACCTCTGCCAGTGAATGGA 2452
DB 2294 AAGCAGAGAGCAACACCTTCCAGTCTCCAAAGATGACAGGACCTCTGCCAGTGAATGGA 2353
QY 2453 CGCTGAACAACTGCCCTAGGCACTGAGGTAGCTTAACTCTTAGGCAACAGGCGGGGCTG 2512
DB 2354 CGCTGAACAACTGCCCTAGGCACTGAGGTAGCTTAACTCTTAGGCAACAGGCGGGGCTG 2413
QY 2513 CGGTGAGGACCTGGCCATGCTGGCGGCGCCAAAGCAGACAGCCCTGACTAGGATGAC 2572
DB 2414 CGGTGAGGACCTGGCCATGCTGGCGGCGCCAAAGCAGACAGCCCTGACTAGGATGAC 2473
QY 2573 AGCAGCACAAAGACCACTTTCTCCCTGAGAGAGCTTCTGTACTCTGCATCACTGA 2632
DB 2474 AGCAGCACAAAGACCACTTTCTCCCTGAGAGAGCTTCTGTACTCTGCATCACTGA 2533
QY 2633 TGACACTGAGGAGGTGATGACAGAGTCTGCTCCCTTATGGACCTCCCTTCTACCAA 2692
DB 2534 TGACACTGAGGAGGTGATGACAGAGTCTGCTCCCTTATGGACCTCCCTTCTACCAA 2593
QY 2693 GCACATGAGCTCTTAAACAGGGTGGGGCTACCCCGCAGACCTGTCTTACACTGATATG 2752
DB 2594 GCACATGAGCTCTTAAACAGGGTGGGGCTACCCCGCAGACCTGTCTTACACTGATATG 2653
QY 2753 AAGAACCTGGAGAGATCTTTCAGTCTGGCCATTTCCAGGACCTCTCCAGAACAGAGT 2812
DB 2654 AAGAACCTGGAGAGATCTTTCAGTCTGGCCATTTCCAGGACCTCTCCAGAACAGAGT 2713
QY 2813 TTTTCAAGAGACCTTAAACAACTGCTGTCCAGGACCTTATGGTAATGAACACCAACA 2872
DB 2714 TTTTCAAGAGACCTTAAACAACTGCTGTCCAGGACCTTATGGTAATGAACACCAACA 2773
QY 2873 TCTAAACATATGCTTAAACATGCACTCTTGGAACTCTCACTCTGAAGCTGGCGCTT 2932
DB 2774 TCTAAACATATGCTTAAACATGCACTCTTGGAACTCTCACTCTGAAGCTGGCGCTT 2833
QY 2933 GGACACCAACACTCTCTTCCAGGCTCATGAGGATCTGCTCCCTCTGCTTCCCTT 2992
DB 2834 GGACACCAACACTCTCTTCCAGGCTCATGAGGATCTGCTCCCTCTGCTTCCCTT 2893
QY 2993 ACCAGTCTGCACTCTGCTGCTCCAGGAGTCTTCCCTGAAGTCTGACCCACTTCTCT 3052
DB 2894 ACCAGTCTGCACTCTGCTGCTCCAGGAGTCTTCTTCTGAAGTCTGACCCACTTCTCT 2953
QY 3053 TGTCTTCAAGTGGGAGCTCTGATCTTCTGCTCCAGGATCTGCTCCCTCTGCTTCCCTT 3112
DB 2954 TGTCTTCAAGTGGGAGCTCTGATCTTCTGCTCCAGGATCTGCTCCCTCTGCTTCCCTT 3013
QY 3113 AGCTTCTTCACTCTCTTACCTTAGCTGACCTCTTCACTCTCCCTCTCTCTTCTTCTT 3172

Db	1154	TAAGGGGAATAACAAGAGTTGAACAAGAACTTTCACGCTGGACTACTTATTAGGGGGCCC	1213
Qy	1313	TGAGACCAACCCCCGGCCAGGCACTTGCTCAGTGGGGCCCTCTCTCTGATTAAGGCCCTGAC	1372
Db	1214	TGAGACCAACCCCCGGCCAGGCACTTGCTCAGTGGGGCCCTCTCTCTGATTAAGGCCCTGAC	1273
Qy	1373	CTTCATGAAGGACCAATTTCCCTGATGAGTGAAGCAAGTGGTGGGACGCCCCCTGCTGGTGAA	1432
Db	1274	CTTCATGAAGGACCAATTTCCCTGATGAGTGAAGCAAGTGGTGGGACGCCCCCTGCTGGTGAA	1333
Qy	1433	ATCTGGCGTGGAGTATACAGGCTTCAGTGGAGACAGCCGACGGCCCTTGATGGGCACAG	1492
Db	1334	ATCTGGCGTGGAGTATACAGGCTTCAGTGGAGACAGCCGACGGCCCTTGATGGGCACAG	1393
Qy	1493	CCATCTGTCATGTACTCTGGGAAACACACAGGCTCGCTCCACAAGGCTGTGGTAAGTGG	1552
Db	1394	CCATCTGTCATGTACTCTGGGAAACACACAGGCTCGCTCCACAAGGCTGTGGTAAGTGG	1453
Qy	1553	GGACAGCAGTGCTCATCTGCTGGAGAGATTACAGCTGTTCCCTGACCCCTGAACTGTTCTG	1612
Db	1454	GGACAGCAGTGCTCATCTGCTGGAGAGATTACAGCTGTTCCCTGACCCCTGAACTGTTCTG	1513
Qy	1613	CAACCTGCAGCTGGCCCCCACCACAGGCTGCAAGTCTTTGTAGGCTTCTCAGGAGTGTCTG	1672
Db	1514	CAACCTGCAGCTGGCCCCCACCACAGGCTGCAAGTCTTTGTAGGCTTCTCAGGAGTGTCTG	1573
Qy	1673	GAGGGTGGCCCCGAGCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGCCCCG	1732
Db	1574	GAGGGTGGCCCCGAGCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGCCCCG	1633
Qy	1733	GGACCCCCACCTGTGCTGGGACCCCTGAGTCCCGAACCTGTTGCTCTCTGCTGCGCCCAA	1792
Db	1634	GGACCCCCACCTGTGCTGGGACCCCTGAGTCCCGAACCTGTTGCTCTCTGCTGCGCCCAA	1693
Qy	1793	CCTGAATCTCTGGAGCAGGACATGAGCGGGGGAACCCAGAGTGGGCACTGTGCCAGTGG	1852
Db	1694	CCTGAATCTCTGGAGCAGGACATGAGCGGGGGAACCCAGAGTGGGCACTGTGCCAGTGG	1753
Qy	1853	CCCCATGAGCAGGAGCCCTTCGGCCCTCAGAGCGCGCCGCAATCAATTAAGAAAGTCTCTGGC	1912
Db	1754	CCCCATGAGCAGGAGCCCTTCGGCCCTCAGAGCGCGCCGCAATCAATTAAGAAAGTCTCTGGC	1813
Qy	1913	TGTCCTTAACCTCCATCTGGAGCTCCCCGCCCCCAGCTGTCAAGCTTGCCCTCTTATTA	1972
Db	1814	TGTCCTTAACCTCCATCTGGAGCTCCCCGCCCCCAGCTGTCAAGCTTGCCCTCTTATTA	1873
Qy	1973	TTGGAGTCATGGCCCGCAGCAGTCCAGAGCCCTCTTCCACTGTCTACAATGGCTCCCT	2032
Db	1874	TTGGAGTCATGGCCCGCAGCAGTCCAGAGCCCTCTTCCACTGTCTACAATGGCTCCCT	1933
Qy	2033	CTTGCTGATGTGAGGATGAGTGGGGTCTCTACAGTGTCTGGGCACTGAGATGG	2092
Db	1934	CTTGCTGATGTGAGGATGAGTGGGGTCTCTACAGTGTCTGGGCACTGAGATGG	1993
Qy	2093	CTTTTTCATACCCTGTGATCTCCTACTGGGTTGGAGCAGCAGGACCCAGACCCTGGCCCTGGGA	2152
Db	1994	CTTTTTCATACCCTGTGATCTCCTACTGGGTTGGAGCAGCAGGACCCAGACCCTGGCCCTGGGA	2053
Qy	2153	TCCTGACTGGCAGGCACTCCCCCGGAGCATGTGAAGTCCGCTTGACCGAGGTCAGTGG	2212
Db	2054	TCCTGACTGGCAGGCACTCCCCCGGAGCATGTGAAGTCCGCTTGACCGAGGTCAGTGG	2113
Qy	2213	TGGGGCCCTTGCTGCTGCCAGCATCTACTGTGCCCCCACTTTGTCACTGTCACTGTCTCT	2272
Db	2114	TGGGGCCCTTGCTGCTGCCAGCATCTACTGTGCCCCCACTTTGTCACTGTCACTGTCTCT	2173
Qy	2273	CTTTGCTCTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTGSCCTCCCCATTTGAGAGCACT	2332
Db	2174	CTTTGCTCTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTGSCCTCCCCATTTGAGAGCACT	2233
Qy	2333	CCGGGCTCGGGCAAGTTCAAGGCTGTGAGACCCCTGCGCCCTGGGAGAGGCCCTGTT	2392
Db	2234	CCGGGCTCGGGCAAGTTCAAGGCTGTGAGACCCCTGCGCCCTGGGAGAGGCCCTGTT	2293

QY	2393	AAGCAGAGAGCAACACCTCCAGTCTCTCCAAAGATGACGAGACCTCTGCAGTGTATGGA	2455
DB	2394	AAGCAGAGAGCAACACCTCCAGTCTCTCCAAAGATGACGAGACCTCTGCAGTGTATGGA	2353
QY	2453	CGCTGACAAACAACCTGCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGCCGGGGCTG	2512
DB	2354	CGCTGACAAACAACCTGCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGCCGGGGCTG	2413
QY	2513	CGGTGCAGGCACCTGGCCATGCTGGCTGGGGGGCCCAAGCACACGACCTGACTAGGATGAC	2572
DB	2414	CGGTGCAGGCACCTGGCCATGCTGGCTGGGGGGCCCAAGCACACGACCTGACTAGGATGAC	2473
QY	2573	AGCAGCACAAAAGACCACTTTCTCCCTCAGAGGAGCTTCTGCTACTCTGCATCACTGA	2632
DB	2474	AGCAGCACAAAAGACCACTTTCTCCCTCAGAGGAGCTTCTGCTACTCTGCATCACTGA	2533
QY	2633	TGACACTCAGCAGGAGTATGACACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAA	2692
DB	2534	TGACACTCAGCAGGAGTATGACACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAA	2593
QY	2693	GCAATAGAGTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTGCTCTACACTGATATG	2752
DB	2594	GCAATAGAGTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTGCTCTACACTGATATG	2653
QY	2753	AAGAACTTGGAGAGGATCTCTCAGTCTTGCCCATCTCCAGGAGCCCTCCAGAAAAACACAGTG	2812
DB	2654	AAGAACTTGGAGAGGATCTCTCAGTCTTGCCCATCTCCAGGAGCCCTCCAGAAAAACACAGTG	2713
QY	2813	TTTCAAGGAGACCTTAAAAACCTGCCTGTCACGAGACCTATGGTATGAAACACCAACA	2872
DB	2714	TTTCAAGGAGACCTTAAAAACCTGCCTGTCACGAGACCTATGGTATGAAACACCAACA	2773
QY	2873	TCTAAACAATCATATGCTTAAACATGCCACTCCTCGAAAACTCCACCTCTGAAGCTGCGCCTTT	2933
DB	2774	TCTAAACAATCATATGCTTAAACATGCCACTCCTCGAAAACTCCACCTCTGAAGCTGCGCCTTT	2833
QY	2933	GGACACCAACTCCTTCTTCCAGGGTCATGACGGGATCTGCTCCCTCCCTGCTTCCCTTT	2999
DB	2834	GGACACCAACTCCTTCTTCCAGGGTCATGACGGGATCTGCTCCCTCCCTGCTTCCCTTT	2899
QY	2993	ACCAAGTCGTGACCGCTGACTCCCAAGGAAGTCTTCCCTGGAAGTCTGACCACTTTCTCT	3052
DB	2894	ACCAAGTCGTGACCGCTGACTCCCAAGGAAGTCTTCTGGAAGTCTGACCACTTTCTCTCT	2953
QY	3053	TGCTTCAGTTGGGGCAGACTCTGATCCCTCTGCGCTGGCAGATGGCAGGGTAAATCTG	3112
DB	2954	TGCTTCAGTTGGGGCAGACTCTGATCCCTCTGCGCTGGCAGATGGCAGGGTAAATCTG	3013
QY	3113	AGCCTTCTTCACTCCTTTACCCCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCCCTTT	3172
DB	3014	AGCCTTCTTCACTCCTTTACCCCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCCCTTT	3073
QY	3173	GTTTTGGGATTCAGAAAACCTGTTGTGAGAGACTGTTTTATTTTTTATTTAAATATAGG	3232
DB	3074	GTTTTGGGATTCAGAAAACCTGTTGTGAGAGACTGTTTTATTTTTTATTTAAATATAGG	3133
QY	3233	CTTA 3236	
DB	3134	CTTA 3137	

RESULT 9
ADD38435
ID ADD38435 standard: cDNA; 3143 BP.

XX
AC
ADD38435;

DT 15-JAN-2004 (first entry)

XX DE Human cDNA encoding secreted/transmembrane protein PRO1317.

Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schönlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.

XX Homo sapiens.

XX US2003096955-A1.

XX 22-MAY-2003.

XX 07-DEC-2001; 2003US-00012755.

PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 23-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 30-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.

PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 14-OCT-1998; 98US-0103711P.
PR 20-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 28-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113236P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0123674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.

1613 CAACCTGAGCTGGCCGCCACCCAGGCTGAGTGTTCGTAGGCTTCTCAGAGGTGTCTG 1672
1514 CAACCTGAGCTGGCCGCCACCCAGGCTGAGTGTTCGTAGGCTTCTCAGAGGTGTCTG 1573
1673 GAGGTGGCCGCCAGCCAACTGTAGTGTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1732
1574 GAGGTGGCCGCCAGCCAACTGTAGTGTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1633
1733 GGACCCCACTGTGCTGGGACCTTGTAGTGTCCGGAACCTGTGTCCCTGTGTGCCCCAA 1792
1634 GGACCCCACTGTGCTGGGACCTTGTAGTGTCCGGAACCTGTGTCCCTGTGTGCCCCAA 1693
1793 CTTGAACCTCTTGAAGCAGGACATGAGAGCGGGGAACCCAGAGTGGGCAATGTGCGAGTGG 1852
1694 CTTGAACCTCTTGAAGCAGGACATGAGAGCGGGGAACCCAGAGTGGGCAATGTGCGAGTGG 1753
1853 CCCCATGAGCAGGAGCTTGGGCTTCCAGAGCGCCCGCAATCATTAAGAAGTCTTGGC 1912
1754 CCCCATGAGCAGGAGCTTGGGCTTCCAGAGCGCCCGCAATCATTAAGAAGTCTTGGC 1813
1913 TGTCCCTAACTCCATCTTGGAGCTCCCTTGGCCCTCCACCTGTGAGCTTGGCTCTTATTA 1972
1814 TGTCCCTAACTCCATCTTGGAGCTCCCTTGGCCCTCCACCTGTGAGCTTGGCTCTTATTA 1873
1973 TTGGAGTATGAGCCAGCAGAGCTCCAGAGGCTTCCAGCTTCCAGCTTCAATGGCTCCCT 2032
1874 TTGGAGTATGAGCCAGCAGAGCTCCAGAGGCTTCCAGCTTCCAGCTTCAATGGCTCCCT 1933
2033 CTTTGTGATGAGTGCAGAGTGGAGTGGGGTCTCTACAGTGTCTGGGCAACTGAGAAATGG 2092
1934 CTTTGTGATGAGTGCAGAGTGGAGTGGGGTCTCTACAGTGTCTGGGCAACTGAGAAATGG 1993
2093 CTTTTCATACCTGTGATCTCTACTGTGGTGAGCAGCAGGACCGAGCTTGGCCCTGGA 2152
1994 CTTTTCATACCTGTGATCTCTACTGTGGTGAGCAGCAGGACCGAGCTTGGCCCTGGA 2053
2153 TCTGAACCTGGCAGGACATCCCGGAGCATGTGAGGTCTCCGTTGACAGAGTCACTGG 2212
2054 TCTGAACCTGGCAGGACATCCCGGAGCATGTGAGGTCTCCGTTGACAGAGTCACTGG 2113
2213 TGGGGCCGCTGGCTGCGCAGGCTCTACTGTGGCCCACTTTGTGCTCACTGTCTGTCT 2272
2114 TGGGGCCGCTGGCTGCGCAGGCTCTACTGTGGCCCACTTTGTGCTCACTGTCTGTCT 2173
2273 CTTTGTCTAGTGTCTTACAGGAGCTCTATCTCTGCTGCTCCCACTTGTGCTCACTGTCT 2332
2174 CTTTGTCTAGTGTCTTACAGGAGCTCTATCTCTGCTGCTCCCACTTGTGCTCACTGTCT 2233
2333 CCGGGCTCGGGCAAGGTTCAAGGCTGTGAGACCTTGCCTGCTGGGAGAGGCCCCGTT 2392
2234 CCGGGCTCGGGCAAGGTTCAAGGCTGTGAGACCTTGCCTGCTGGGAGAGGCCCCGTT 2293
2393 AAGCAGAGCAGACCTCCAGTCTCCAGGAATGACAGGCTCTGCGAGTGTGGA 2452
2294 AAGCAGAGCAGACCTCCAGTCTCCAGGAATGACAGGCTCTGCGAGTGTGGA 2353
2453 CGTGTGACCAACTGCTAGGCTAGGCTAGGCTTAACTCTAGGACAGGCGCGGGCTG 2512
2354 CGTGTGACCAACTGCTAGGCTAGGCTTAACTCTAGGACAGGCGCGGGCTG 2413
2513 CGTGTGAGGACCTTGGCAGCTGTGGCTGGCGGCCCAAGCAGCAGCTTACCTAGGATGAC 2572
2414 CGTGTGAGGACCTTGGCAGCTGTGGCTGGCGGCCCAAGCAGCAGCTTACCTAGGATGAC 2473
2573 AGCAGACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCTCACTGA 2632
2474 AGCAGACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCTCACTGA 2533
2633 TGAACCTCAGCAGGGTGTGACAGCAGTGTGCTCCCTATGGAGCTCTCCCTTCTACCAA 2692
2534 TGAACCTCAGCAGGGTGTGACAGCAGTGTGCTCCCTATGGAGCTCTCCCTTCTACCAA 2593
2693 GCACATGAGCTCTTAACAGGTTGGGGCTTACCCCCAGAGCTTCTCTCTACACTGATATTG 2752

2594 GCACATGAGCTCTTAACAGGTTGGGGCTACCCCCAGACCTGCTCTACACTGATATTG 2653
2753 AAGAACTGGAGAGGATCTTCACTTCTGGCCATTCAGGACCTCCAGGAAACACAGTG 2812
2654 AAGAACTGGAGAGGATCTTCACTTCTGGCCATTCAGGACCTCCAGGAAACACAGTG 2713
2813 TTTTCAAGAGACCCCTAAAAAACCCTGCTGCCAGGACCTATGGTAAATGAACACCAACA 2872
2714 TTTTCAAGAGACCCCTAAAAAACCCTGCTGCCAGGACCTATGGTAAATGAACACCAACA 2773
2873 TCTTAACATCATATCTTAACATGCCACTCTCTGGAACTCCCACTCTGAAGCTGCCCTTT 2932
2774 TCTTAACATCATATCTTAACATGCCACTCTCTGGAACTCCCACTCTGAAGCTGCCCTTT 2833
2933 GGACACAAACACTCCCTTCTCCAGGAGTCTGCTGCCAGGATCTGCTCCCTCTGCTTCCCTT 2992
2834 GGACACAAACACTCCCTTCTCCAGGAGTCTGCTGCCAGGATCTGCTCCCTCTGCTTCCCTT 2893
2993 ACCAGTGTGCACCGCTGACTCCAGGAGTCTTCCCTGAAGTCTGACCACTTCTTCT 3052
2894 ACCAGTGTGCACCGCTGACTCCAGGAGTCTTCCCTGAAGTCTGACCACTTCTTCT 2953
3053 TGCTTCAAGTTGGGCGAGACTCTGATCCCTTCTGCTGCGAGAAATGCGAGGGTAAATCTG 3112
2954 TGCTTCAAGTTGGGCGAGACTCTGATCCCTTCTGCTGCGAGAAATGCGAGGGTAAATCTG 3013
3113 AGCCTTCTTCACTCTTACCTTAGCTAGTCCCTTCACTTCCCTTCCCTTCCCTTCTTCT 3172
3014 AGCCTTCTTCACTCTTACCTTAGCTAGTCCCTTCACTTCCCTTCCCTTCCCTTCTTCT 3073
3173 GTTTTGGGATTCAGAAACCTGTTGTCAGAGACTGTTTATTTTATTTAAATAATAAGG 3232
3074 GTTTTGGGATTCAGAAACCTGTTGTCAGAGACTGTTTATTTTATTTAAATAATAAGG 3133
3233 CTTA 3236
3134 CTTA 3137

RESULT 10
ADD39391
ID ADD39391 standard; cDNA; 3143 BP.
XX
AC ADD39391;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003096954-A1.
XX
PD 22-MAY-2003.
XX
PF 07-DEC-2001; 2001US-00011671.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102571P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103335P.
PR 07-OCT-1998; 98US-0103336P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 14-OCT-1998; 98US-0103711P.
PR 20-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 21-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105633P.
PR 26-OCT-1998; 98US-0105694P.
PR 26-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0105882P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0106500P.
PR 30-OCT-1998; 98US-0106484P.
PR 30-OCT-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108856P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006584.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.

1814 TGTCCTCCCAATCCATCTCTGAGGTCCCTGCTCCCTCCCTCCCTGCTGAGCTTGGCTCTTATTA 1873
1973 TTGGAGTCATGGCCAGCAGCAGTCCAGAAAGCTCTTCCACTGTCTAACAATGGCTCCCT 2032
1874 TTGGAGTCATGGCCAGCAGCAGTCCAGAAAGCTCTTCCACTGTCTAACAATGGCTCCCT 1933
2033 CTTTGTGATAGTCAGAGTGGAGTGGGGTCTTACCAAGTCTGGCACTGAGATGG 2092
1934 CTTTGTGATAGTCAGAGTGGAGTGGGGTCTTACCAAGTCTGGCACTGAGATGG 1993
2093 CTTTTCATACCTGTGATCTCTTACTGGGTGGACAGCAGGACCAACCTCGCCCTGGA 2152
1994 CTTTTCATACCTGTGATCTCTTACTGGGTGGACAGCAGGACCAACCTCGCCCTGGA 2053
2153 TCCTGACTGGCAGGACCTCCCGGGGAGTGTGAAGTCCGTTGACAGGTCAGTG 2212
2054 TCCTGACTGGCAGGACCTCCCGGGGAGTGTGAAGTCCGTTGACAGGTCAGTG 2113
2213 TGGGGCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2272
2114 TGGGGCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2173
2273 CTTTGTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2332
2174 CTTTGTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2233
2333 CCGGGCTCGGGCAAGGTTGAGGCTGTGAGACCTGCGCCCTGGGGAGAAAGCCCGTT 2392
2234 CCGGGCTCGGGCAAGGTTGAGGCTGTGAGACCTGCGCCCTGGGGAGAAAGCCCGTT 2293
2393 AAGCAGAGCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2452
2294 AAGCAGAGCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2353
2453 CGCTGCAACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2512
2354 CGCTGCAACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2413
2513 CGCTGCAACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2572
2414 CGGTGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2473
2573 AGCAGCAACAAAGACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2632
2474 AGCAGCAACAAAGACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2533
2633 TGACATCAGCAGGCTGATGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2692
2534 TGACATCAGCAGGCTGATGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2593
2693 GCACATGAGCTCTTAACAGGCTGGGGCTACCCCGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2752
2594 GCACATGAGCTCTTAACAGGCTGGGGCTACCCCGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2653
2753 AGAACCTGGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2812
2654 AGAACCTGGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2713
2813 TTTTCAGAGACCTTAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2872
2714 TTTTCAGAGACCTTAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2773
2873 TCTAAACATCATATGCTAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2932
2774 TCTAAACATCATATGCTAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2833
2933 GGCACCAACACTCTTCTTCCAGGGTCACTGAGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2992
2834 GGCACCAACACTCTTCTTCCAGGGTCACTGAGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2893
2993 ACCAGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3052
2894 ACCAGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2953

QY 3053 TGCTTCAGTTGGGCGAGACTCTGATCCCTTCTGCTTGGCGAGAAATGGCAGGGTAAATCTG 3112
Db 2954 TGCTTCAGTTGGGCGAGACTCTGATCCCTTCTGCTTGGCGAGAAATGGCAGGGTAAATCTG 3013
QY 3113 AGCCTTCTTCACTCTCTTACCTAGCTGAGCCCTTCACTCTCCCTCCCTTCTTCTTCTT 3172
Db 3014 AGCCTTCTTCACTCTCTTACCTAGCTGAGCCCTTCACTCTCCCTCCCTTCTTCTTCTT 3073
QY 3173 GTTTTGGGATTTCAGAAACTGCTTGTTCAGAGACTGTTTATTTTATTTAAATAATAAGG 3232
Db 3074 GTTTTGGGATTTCAGAAACTGCTTGTTCAGAGACTGTTTATTTTATTTAAATAATAAGG 3133
QY 3233 CTTTA 3236
Db 3134 CTTA 3137
RESULT 11
ADD38914
ID ADD38914 standard; cDNA; 3143 BP.
XX
AC ADD38914;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schönlain-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003092061-A1.
XX
PD 15-MAY-2003.
XX
PF 06-DEC-2001; 2001US-00007194.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 02-SEP-1998; 98US-0098956P.
PR 02-SEP-1998; 98US-0098956P.
PR 09-SEP-1998; 98US-0098958P.
PR 09-SEP-1998; 98US-0098960P.
PR 09-SEP-1998; 98US-0098962P.
PR 10-SEP-1998; 98US-0098974P.
PR 10-SEP-1998; 98US-0098975P.
PR 10-SEP-1998; 98US-0098976P.
PR 10-SEP-1998; 98US-0098979P.
PR 10-SEP-1998; 98US-0098980P.
PR 10-SEP-1998; 98US-0098981P.
PR 10-SEP-1998; 98US-0098981P.
PR 10-SEP-1998; 98US-0098981P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100662P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.

PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100819P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 18-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0104712P.
 PR 23-SEP-1998; 98US-0104722P.
 PR 23-SEP-1998; 98US-0104742P.
 PR 23-SEP-1998; 98US-0104752P.
 PR 23-SEP-1998; 98US-0104762P.
 PR 23-SEP-1998; 98US-0104772P.
 PR 23-SEP-1998; 98US-0104792P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
 PR 07-OCT-1998; 98US-0103315P.
 PR 07-OCT-1998; 98US-0103328P.
 PR 07-OCT-1998; 98US-0103395P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 08-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103679P.
 PR 08-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 22-OCT-1998; 98US-0105269P.
 PR 26-OCT-1998; 98US-0105833P.
 PR 26-OCT-1998; 98US-0105894P.
 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105881P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108825P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145898P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-OCT-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 14-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030952.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030952.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006566.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Bak W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2003-765477/72.
 DR P-PSDB; ADD38915.
 XX New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,
 PT PRO1244, PRO1246, useful for treating cancerous tumors, cardiac
 PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.
 XX Claim 2; SEQ ID NO 276; 555pp; English.
 PS
 XX

CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTCGGACCC 232
DB 74 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTCGGACCC 133

QY 233 CTGGAGCCTCTGGGCCCTTTCTCTTCCAACTGCTTCAGCTGCTGCTGCGACGAC 292
DB 134 CTGGAGCCTCTGGGCCCTTTCTCTTCCAACTGCTTCAGCTGCTGCTGCGACGAC 193

QY 293 CGCGGGGGAGGGGGGAGGGGGCCCATGCGAGGGTCAAGTATATGAGGGGATGAAG 352
DB 194 CGCGGGGGAGGGGGGAGGGGGCCCATGCGAGGGTCAAGTATATGAGGGGATGAAG 253

QY 353 TAGGGCACTTACGTTCTTCCACGAAAGGGGCTCCAGGATTTTGAACACTTGTCTGAG 412
DB 254 TAGGGCACTTACGTTCTTCCACGAAAGGGGCTCCAGGATTTTGAACACTTGTCTGAG 313

QY 413 TGGTGATGGAATACTCTTACGTGGGGGCTCGAGAGGCAATTTCTGGCCCTTGGATATCA 472
DB 314 TGGTGATGGAATACTCTTACGTGGGGGCTCGAGAGGCAATTTCTGGCCCTTGGATATCA 373

QY 473 GGAATCCAGGGGTCCCAAGGCTTAAGAAATGATATACCGTGGCCAGCCAGTACAGAAATA 532
DB 374 GGAATCCAGGGGTCCCAAGGCTTAAGAAATGATATACCGTGGCCAGCCAGTACAGAAATA 433

QY 533 GAGTGAATGTCCCTTTAAGAAAGAGAGCAATGACACAGTGTTCAACTTCACTCCGTGT 592
DB 434 GAGTGAATGTCCCTTTAAGAAAGAGAGCAATGACACAGTGTTCAACTTCACTCCGTGT 493

QY 593 CCTGGTTCTTACAAATGTCACCAATCTTACACCTGGGCACTTGGCCCTTCAGCCCTGC 652
DB 494 CCTGGTTCTTACAAATGTCACCAATCTTACACCTGGGCACTTGGCCCTTCAGCCCTGC 553

QY 653 TTGTACCTTCAATGAACTTCAAGATTCCTACTGTTGCCATCTCGGAGGACAAAGTTCAT 712
DB 554 TTGTACCTTCAATGAACTTCAAGATTCCTACTGTTGCCATCTCGGAGGACAAAGTTCAT 613

QY 713 GGAGGAAAGGCGCAAGCCCTTTGACCCCGCTCAACGATACAGGCTGTCTTGTGTGA 772
DB 614 GGAGGAAAGGCGCAAGCCCTTTGACCCCGCTCAACGATACAGGCTGTCTTGTGTGA 673

QY 773 TGGGATGCTTATTTGTGTAATGAAACAATCTTGGGAGTGAGCCCATCTGTATGCG 832
DB 674 TGGGATGCTTATTTGTGTAATGAAACAATCTTGGGAGTGAGCCCATCTGTATGCG 733

QY 833 CACACTGGGATCCAGCCCTGCTCAAGACCGCAACTTCTCCGCTGGCTGCAATCA 892
DB 734 CACACTGGGATCCAGCCCTGCTCAAGACCGCAACTTCTCCGCTGGCTGCAATCA 793

QY 893 CGCCTCTTTTGGGAGGCACTCCCTTCAGCCAGGTGCTACTTCTTTCGAGGAGAC 952
DB 794 CGCCTCTTTTGGGAGGCACTCCCTTCAGCCAGGTGCTACTTCTTTCGAGGAGAC 853

QY 953 AGCCAGCAGATTTGACTTTCTTGGAGGCTCCACACATCGCGGTGGCTAGAGTCTGCAA 1012
DB 854 AGCCAGCAGATTTGACTTTCTTGGAGGCTCCACACATCGCGGTGGCTAGAGTCTGCAA 913

QY 1013 GAATGACGTGGGCGGCGAAAGTCTGTCAGAAAGTGGACCACTTCTTGAAGGCCCA 1072
DB 914 GAATGACGTGGGCGGCGAAAGTCTGTCAGAAAGTGGACCACTTCTTGAAGGCCCA 973

QY 1073 GCTGCTCTGACCCAGCGGGGAGCTGCTTCAACGTCATCCGCCACGCGGTCTTGTCT 1132
DB 974 GCTGCTCTGACCCAGCGGGGAGCTGCTTCAACGTCATCCGCCACGCGGTCTTGTCT 1033

QY 1133 CCCCAGCAATTCACAGCTTCCCAATCTACAGAGTCTTACCTCCAGTGGAGGT 1192
DB 1034 CCCCAGCAATTCACAGCTTCCCAATCTACAGAGTCTTACCTCCAGTGGAGGT 1093

QY 1193 TGGCGGACACAGGAGCTCTGGGTTTGTGCTTCTCTCTCTTGACATTTGAACGTGTCTT 1252
DB 1094 TGGCGGACACAGGAGCTCTGGGTTTGTGCTTCTCTCTCTTGACATTTGAACGTGTCTT 1153

QY 1253 TAAGGGGAAATACAAAGAGTTGAAACAAAGAACTTCAACGTGGACTTACTATAGGGGCC 1312
DB 1154 TAAGGGGAAATACAAAGAGTTGAAACAAAGAACTTCAACGTGGACTTACTATAGGGGCC 1213

QY 1313 TGAGACCAACCCCGGCGAGGCACTGCTCAGTGGGGCCCTCTCTCTCATAGGCGCTTGAC 1372
DB 1214 TGAGACCAACCCCGGCGAGGCACTGCTCAGTGGGGCCCTCTCTCTCATAGGCGCTTGAC 1273

QY 1373 CTTTCAATGAAGCACTTCTCTGATGAGCAAGTGGTGGAGCGCCCTCTGCTGTGTA 1432
DB 1274 CTTTCAATGAAGCACTTCTCTGATGAGCAAGTGGTGGAGCGCCCTCTGCTGTGTA 1333

QY 1433 ATCTGGCGTGGAGTATACACGGCTTTCAGTGGAGACAGCCAGGGCTTCTGATGGGACAG 1492
DB 1334 ATCTGGCGTGGAGTATACACGGCTTTCAGTGGAGACAGCCAGGGCTTCTGATGGGACAG 1393

QY 1493 CCATCTTGTCTATGTAACCTGGGAAACACACAGGCTGCTCCACAAAGGCTGTGTAAGTG 1552
DB 1394 CCATCTTGTCTATGTAACCTGGGAAACACACAGGCTGCTCCACAAAGGCTGTGTAAGTG 1453

QY 1553 GGACAGAGTGTCTCATCTGTTGGAGAGATTCAGCTGTTCCCTGACCTGAACTGTTCG 1612
DB 1454 GGACAGAGTGTCTCATCTGTTGGAGAGATTCAGCTGTTCCCTGACCTGAACTGTTCG 1513

QY 1613 CAACTGTGAGCTGGGCCCCACCCAGGGTGCAGTGTGTTAGGCTTCTCAGAGGTGTCTG 1672
DB 1514 CAACTGTGAGCTGGGCCCCACCCAGGGTGCAGTGTGTTAGGCTTCTCAGAGGTGTCTG 1573

QY 1673 GAGGTTGCCCGGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTGTGCCG 1732
DB 1574 GAGGTTGCCCGGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTGTGCCG 1633

QY 1733 GGACCCCACTGTGTGCTGGGACCCCTGAGTCCCGAACCTGTTGCTCTGCTGTGCCCCAA 1792
DB 1634 GGACCCCACTGTGTGCTGGGACCCCTGAGTCCCGAACCTGTTGCTCTGCTGTGCCCCAA 1693

QY 1793 CTTGAACTCTTGGAGAGGACATGAGGGGGGAGCCAGAGTGGGATGTCAGCTGGG 1852
DB 1694 CTTGAACTCTTGGAGAGGACATGAGGGGGGAGCCAGAGTGGGATGTCAGCTGGG 1753

QY 1853 CCCCCTGAGCAGGAGCCTTTCGGCCTTCAGAGCGCCCGCAATCATTAAGAAAGTCTCTGGC 1912
DB 1754 CCCCCTGAGCAGGAGCCTTTCGGCCTTCAGAGCGCCCGCAATCATTAAGAAAGTCTCTGGC 1813

QY 1913 TGTCCCTTAACTCTCATCTCTGAGCTCCCTGCCCCCAGCTGTGAGCTTGGCTCTTATTA 1972
DB 1814 TGTCCCTTAACTCTCATCTCTGAGCTCCCTGCCCCCAGCTGTGAGCTTGGCTCTTATTA 1873

QY 1973 TTGGAGTCAATGCGCCAGCAGCAGTCCAGAAAGCCTTCTTCCACTGTCTACAATGGCTCCCT 2032
DB 1874 TTGGAGTCAATGCGCCAGCAGCAGTCCAGAAAGCCTTCTTCCACTGTCTACAATGGCTCCCT 1933

QY 2033 CTTTGTGATGAGTGGAGTGGGGTCTTACAGTGTCTTACAGTGTGGGCACTGAGAAATGG 2092
DB 1934 CTTTGTGATGAGTGGAGTGGGGTCTTACAGTGTCTTACAGTGTGGGCACTGAGAAATGG 1993

QY 2093 CTTTTCATACCTGTGATCTCTTCTGAGTGGGAGCAGGACCCAGAGCCCTGGCCCTGGA 2152
DB 1994 CTTTTCATACCTGTGATCTCTTCTGAGTGGGAGCAGGACCCAGAGCCCTGGCCCTGGA 2053

QY 2153 TCTGAATCTGGGAGGATCCCGGGGAGCATGTGAAGGTCCGTTGACAGGCTCAGTGG 2212
DB 2054 TCTGAATCTGGGAGGATCCCGGGGAGCATGTGAAGGTCCGTTGACAGGCTCAGTGG 2113

QY 2213 TGGGGCGGCTGGCTGCGGAGCAGTCTTACCTGGGCCCACTTGTCACTGTCACTGTCTCT 2272
DB 2114 TGGGGCGGCTGGCTGCGGAGCAGTCTTACCTGGGCCCACTTGTCACTGTCACTGTCTCT 2173


```
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 07-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103335P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 14-OCT-1998; 98US-0103711P.
PR 20-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105633P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106484P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108859P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.

PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-755104/71.
DR P-PSDB; ADD40346.
XX
XX New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT insufficiency disorders.
XX Claim 2; SEQ ID NO 276; 550pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
CC Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGCTCCCTGGTGACACTGTGTGGCTGAGATGCCCTCCAGCCCTGGCCCTGGACCC 232
DB 74 AGAGCTCCCTGGTGACACTGTGTGGCTGAGATGCCCTCCAGCCCTGGCCCTGGACCC 133
QY 233 CTGGAGCCTCTGGGSCCTTTCTTCCAACTGTTCCAGTGTCTGCTGCCGACGACGAC 292
DB 134 CTGGAGCCTCTGGGSCCTTTCTTCCAACTGTTCCAGTGTCTGCTGCCGACGACGAC 193
QY 293 CGCGGGGGAGCGCGGCGAGGGGCCCATGCCAGGGTCAAGTACTATGAGGGGATGAACG 352
DB 194 CGCGGGGGAGCGCGGCGAGGGGCCCATGCCAGGGTCAAGTACTATGAGGGGATGAACG 253
QY 353 TAGGGCACTTAGCTTCTTCCACCAAGGGCTCCAGGATTTTGACACTCTGCTCTGAG 412
DB 254 TAGGGCACTTAGCTTCTTCCACCAAGGGCTCCAGGATTTTGACACTCTGCTCTGAG 313
```

QY 413 TGGTGAATGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCCTTGGATATCCA 472
DB 314 TGGTGAATGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCCTTGGATATCCA 373
QY 473 GGATCCAGGGGTCCCAGAGCTAAAGAAACATGATACCGTGGCCAGCCAGTGAAGAAAAA 532
DB 374 GGATCCAGGGGTCCCAGAGCTAAAGAAACATGATACCGTGGCCAGCCAGTGAAGAAAAA 433
QY 533 GAGTGAATGTGCTTTTAAAGAGAGCAATGAGACACAGTGTTCCTCACTTCATCCGTGT 592
DB 434 GAGTGAATGTGCTTTTAAAGAGAGCAATGAGACACAGTGTTCCTCACTTCATCCGTGT 493
QY 593 CTTGGTTTCTTAAATGTACCCATCTCTACACCTCGCGCACCTTCGCCCTTCAGGCCCTGC 652
DB 494 CTTGGTTTCTTAAATGTACCCATCTCTACACCTCGCGCACCTTCGCCCTTCAGGCCCTGC 553
QY 653 TTGTACTTTCAATGAATTCAGATTTCTACCTGTGCTTGGCCATCTCGGAGGACAAAGTCAAT 712
DB 554 TTGTACTTTCAATGAATTCAGATTTCTACCTGTGCTTGGCCATCTCGGAGGACAAAGTCAAT 613
QY 713 GGAGGAAAGGCAAGGCCCTTTGACCCCGCTTCAAGAGCATACCGCTGTCTTGGTGA 772
DB 614 GGAGGAAAGGCAAGGCCCTTTGACCCCGCTTCAAGAGCATACCGCTGTCTTGGTGA 673
QY 773 TGGATGTCTATTTCTGGTACTATGAACAACTTCTCGGGAGTGAGCCCATCTGATGCG 832
DB 674 TGGATGTCTATTTCTGGTACTATGAACAACTTCTCGGGAGTGAGCCCATCTGATGCG 733
QY 833 CACACTGGGATCCAGCGCTGTCTCAAGACCGCAACTTCTCCGCTGCTGCATCATGA 892
DB 734 CACACTGGGATCCAGCGCTGTCTCAAGACCGCAACTTCTCCGCTGCTGCATCATGA 793
QY 893 CGCCTCTTTTGGGAGCCATCCCTTTGACCCAGGTCGTCTACTTTCTTCGAGGAGAC 952
DB 794 CGCCTCTTTTGGGAGCCATCCCTTTGACCCAGGTCGTCTACTTTCTTCGAGGAGAC 853
QY 953 AGCCAGCGAGTTTGAATTTCTTCAGAGGCTCCACATCGCGGTGGCTAGAGTCTGCA 1012
DB 854 AGCCAGCGAGTTTGAATTTCTTCAGAGGCTCCACATCGCGGTGGCTAGAGTCTGCA 913
QY 1013 GAATGAGCTGGGGGGGAAAGTGTCTGAGAGAAAGTGAACACCTTCTGAAAGGCCCA 1072
DB 914 GAATGAGCTGGGGGGGAAAGTGTCTGAGAGAAAGTGAACACCTTCTGAAAGGCCCA 973
QY 1073 GCTGCTCTGACCGCGGGGAGCTGCGCTTCAAGGTCATCCGCGAGCGGTCTGCT 1132
DB 974 GCTGCTCTGACCGCGGGGAGCTGCGCTTCAAGGTCATCCGCGAGCGGTCTGCT 1033
QY 1133 CCGCGCGAATTTCTCCACAGCTCCCAACATCTACGAGTCTTCACTCCAGTGGCAGGT 1192
DB 1034 CCGCGCGAATTTCTCCACAGCTCCCAACATCTACGAGTCTTCACTCCAGTGGCAGGT 1093
QY 1193 TGGGGGACCGAGAGCTCTCGGTTTGTGCTTCTCTCTTGGACATTTGAAGTGTCTT 1252
DB 1094 TGGGGGACCGAGAGCTCTCGGTTTGTGCTTCTCTCTTGGACATTTGAAGTGTCTT 1153
QY 1253 TAAGGGGAAATACAAAGATTGAACAAAGAACTTCAAGTGTGACTACTTATAGGGGGCCC 1312
DB 1154 TAAGGGGAAATACAAAGATTGAACAAAGAACTTCAAGTGTGACTACTTATAGGGGGCCC 1213
QY 1313 TGAGACCAACCCCGGCGGAGGAGTGTCTCAGTGGGCCCTCTCTGATTAAGGCCCTGAC 1372
DB 1214 TGAGACCAACCCCGGCGGAGGAGTGTCTCAGTGGGCCCTCTCTGATTAAGGCCCTGAC 1273
QY 1373 CTTTCATGAAGGACATTTCTGATGATGAGCAAGTGTGGGACCGCCCTGCTGCTGAA 1432
DB 1274 CTTTCATGAAGGACATTTCTGATGATGAGCAAGTGTGGGACCGCCCTGCTGCTGAA 1333
QY 1433 ATCTGGCGTGGAGTATACCGGCTTGCAGTGGAGACAGCCAGGCGCTTGAATGGGACAG 1492
DB 1334 ATCTGGCGTGGAGTATACCGGCTTGCAGTGGAGACAGCCAGGCGCTTGAATGGGACAG 1393
QY 1493 CCATCTGTCTATCTGCGGAGCCACCAAGGCTGCTCCACAAAGGCTGTGTAAGTGG 1552

DB 1394 CCATCTGTCTATGTACTTGGAAACCAACAGGGTGGCTCCACAAAGGCTGTGTAAGTGG 1453
QY 1553 GGACAGCAGTGTCTATCTGTGGAAGAGATTACGTGTTCCTCTGACCCCTGAACCTGTTCG 1612
DB 1454 GGACAGCAGTGTCTATCTGTGGAAGAGATTACGTGTTCCTCTGACCCCTGAACCTGTTCG 1513
QY 1613 CAACCTCAGCTGGCCCCCACCAGGGTGCAGTGTGTAGGCTTCTCAGGAGGTGTCTG 1672
DB 1514 CAACCTCAGCTGGCCCCCACCAGGGTGCAGTGTGTAGGCTTCTCAGGAGGTGTCTG 1573
QY 1673 GAGGGTCCCCGAGCAACCTGTATGTCTATGAGAGCTGTGTGAGCTGTCTTGGCCG 1732
DB 1574 GAGGGTCCCCGAGCAACCTGTATGTCTATGAGAGCTGTGTGAGCTGTCTTGGCCG 1633
QY 1733 GGACCCCACTGTGCTGGGACCTGAGTCCCAACCTGTGTGCTCTCTGTCTGCCCCCA 1792
DB 1634 GGACCCCACTGTGCTGGGACCTGAGTCCCAACCTGTGTGCTCTCTGTCTGCCCCCA 1693
QY 1793 CCTGAACTCTCGAAGCAGACATGGAGCGGGGAAACCCAGAGTGGGCATGTGCAAGTGG 1852
DB 1694 CCTGAACTCTCGAAGCAGACATGGAGCGGGGAAACCCAGAGTGGGCATGTGCAAGTGG 1753
QY 1853 CCCCATGAGCAGGAGCCTTCGGCTCAGAGCGCCCGCAATCATTTAAAGAAAGTCTGGC 1912
DB 1754 CCCCATGAGCAGGAGCCTTCGGCTCAGAGCGCCCGCAATCATTTAAAGAAAGTCTGGC 1813
QY 1913 TGTCCCTAACTCTCGAGCTCCCTGCCCCACCTGTCTGAGCCTTGGCCTCTTATTA 1972
DB 1814 TGTCCCAACTCTCGAGCTCCCTGCCCCACCTGTCTGAGCCTTGGCCTCTTATTA 1873
QY 1973 TTGAGTATGCCCCAGCAGCAGTCCCAAGAGCTCTTCCACTGTCTACATGAGTCCCT 2032
DB 1874 TTGAGTATGCCCCAGCAGCAGTCCCAAGAGCTCTTCCACTGTCTACATGAGTCCCT 1933
QY 2033 CTTGCTATGATGAGGATGGAGTTGGGGTCTCTACAGTGTCTGGGCAACTGAGAAATGG 2092
DB 1934 CTTGCTATGATGAGGATGGAGTTGGGGTCTCTACAGTGTCTGGGCAACTGAGAAATGG 1993
QY 2093 CTTTTCATACCTGTGATCTCTACTGGTGGAGCAGCAGGACCCAGACCTTGGCCCTGGA 2152
DB 1994 CTTTTCATACCTGTGATCTCTACTGGTGGAGCAGCAGGACCCAGACCTTGGCCCTGGA 2053
QY 2153 TCCTGAACTGGCAGGCACTCCCGCGGAGCATGTGAAGGTCCCGTTGACAGGGTCAAGTGG 2212
DB 2054 TCCTGAACTGGCAGGCACTCCCGCGGAGCATGTGAAGGTCCCGTTGACAGGGTCAAGTGG 2113
QY 2213 TGGGGCGCCTGGCTGCCCCAGCAGTCTCTACTGGCCCCACTTTGTCTACTGTCACTGTCT 2272
DB 2114 TGGGGCGCCTGGCTGCCCCAGCAGTCTCTACTGGCCCCACTTTGTCTACTGTCACTGTCT 2173
QY 2273 CTTTGGCCTTAGTGTCTTTCAGGAGCCCTCATCTCTGCTGGCCTCCCATTTGAGAGCACT 2332
DB 2174 CTTTGGCCTTAGTGTCTTTCAGGAGCCCTCATCTCTGCTGGCCTCCCATTTGAGAGCACT 2233
QY 2333 CCGGGCTCGGGCAAGTTCAGGGCTGTGAGACCCCTGCGCTGGGAGAGAGGCCCGCTT 2392
DB 2234 CCGGGCTCGGGCAAGTTCAGGGCTGTGAGACCCCTGCGCTGGGAGAGAGGCCCGCTT 2293
QY 2393 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGAGGACCTCTGCAAGTGTGGA 2452
DB 2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGAGGACCTCTGCAAGTGTGGA 2353
QY 2453 CGCTGACAACTGCTTAGGCACTGAGGTAGCTTAACTCTTAGGCAAGCCCGGGGCTG 2512
DB 2354 CGCTGACAACTGCTTAGGCACTGAGGTAGCTTAACTCTTAGGCAAGCCCGGGGCTG 2413
QY 2513 CGGTGAGGACCTGTGGCCATGCTGGGCGCCCAAGCAGACCCCTGCTAGGATGAC 2572
DB 2414 CGGTGAGGACCTGTGGCCATGCTGGGCGCCCAAGCAGACCCCTGCTAGGATGAC 2473
QY 2573 AGCAGCAGAAAGACCACTTCTCCCTGAGAGAGGCTTCTGCTACTCTGCTCACTGA 2632

Db	2474	AGCAGCAGCAAAAGACACACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGA	2533	98US-0098723P.
QY	2633	TGACACTCAGCAGGGTGATGCACAGCAGTCTGCTCCCTCATGGGACTCCCTTCTACCAA	2692	98US-0098749P.
Db	2534	TGACACTCAGCAGGGTGATGCACAGCAGTCTGCTCCCTCATGGGACTCCCTTCTACCAA	2593	98US-0098803P.
QY	2693	GCACATGAGTCTCTTAACAGGGTGGGGGTACCCCCAGACCTGCTCTTACATGATATTG	2752	98US-0098821P.
Db	2594	GCACATGAGTCTCTTAACAGGGTGGGGGTACCCCCAGACCTGCTCTTACATGATATTG	2653	98US-0098843P.
QY	2753	AAGAACCTGGAGAGGATCCTTCTAGTTCTGGCCATTCAGGGACCTTCCAGAAACACAGTG	2812	98US-0099536P.
Db	2654	AAGAACCTGGAGAGGATCCTTCTAGTTCTGGCCATTCAGGGACCTTCCAGAAACACAGTG	2713	98US-0099559P.
QY	2813	TTTCAAGAGACCTTAAACACCTGCTGCTCCAGGACCTTATGTAATGAAACACAAACA	2872	98US-0099602P.
Db	2714	TTTCAAGAGACCTTAAACACCTGCTGCTCCAGGACCTTATGTAATGAAACACAAACA	2773	98US-0099741P.
QY	2873	TCTAAACATCATATGTAACATGCAATGCACTCTGGAACCTCCACTCTGAAGCTGCGCTTT	2932	98US-0099754P.
Db	2774	TCTAAACATCATATGTAACATGCAATGCACTCTGGAACCTCCACTCTGAAGCTGCGCTTT	2833	98US-0099763P.
QY	2933	GGACACCAACACTCCCTTCTCCAGGGTCATGACGGATCTGCTCCTCTCTCCCTT	2992	98US-0099792P.
Db	2834	GGACACCAACACTCCCTTCTCCAGGGTCATGACGGATCTGCTCCTCTCTCCCTT	2893	98US-0099808P.
QY	2993	ACAGTCTGTCACCGCTGACTCCAGGAGTCTTCCCTGAAGTCTGACCACTTCTTCT	3052	98US-0099812P.
Db	2894	ACAGTCTGTCACCGCTGACTCCAGGAGTCTTCCCTGAAGTCTGACCACTTCTTCT	2953	98US-0099815P.
QY	3053	TGCTTCAAGTGGGAGACTCTGATCCCTTCTGCGGATGATGAGGAGTGAATCTG	3112	98US-0099816P.
Db	2954	TGCTTCAAGTGGGAGACTCTGATCCCTTCTGCGGATGATGAGGAGTGAATCTG	3013	98US-0099816P.
QY	3113	AGCTTCTTCACTCCCTTACCTTAGCTGACCTTCACTCTCCCTCCCTTCTTCTT	3172	98US-0100385P.
Db	3014	AGCTTCTTCACTCCCTTACCTTAGCTGACCTTCACTCTCCCTCCCTTCTTCTT	3073	98US-0100388P.
QY	3173	GTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTATTTTATTTAAATATAAGG	3232	98US-0100642P.
Db	3074	GTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTATTTTATTTAAATATAAGG	3133	98US-0100644P.
QY	3233	CTTA 3236		98US-0100661P.
Db	3134	CTTA 3137		98US-0100662P.
RESULT 13				
ADE50566				
ID	ADE50566 standard; cDNA; 3143 BP.			
AC	ADE50566;			
DT	29-JAN-2004 (first entry)			
XX	Human cDNA encoding secreted/transmembrane protein PRO1317.			
DE	Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;			
XX	immune response; cardiac insufficiency disorder; calcium flux;			
XX	umbilical vein endothelial cell; bone disorder; cartilage disorder;			
KW	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;			
KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;			
KW	dermatitis; herpeticiformis; Crohn's disease; thalassemia.			
XX	Homo sapiens.			
OS	US2003069179-A1.			
XX	10-APR-2003.			
XX	11-DEC-2001; 2001US-00015393.			
XX	01-SEP-1998; 98US-0098716P.			
PR				

Db 614 GGAGGGAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGACATACCGGCTGTCTTGATGGA 673
Qy 773 TGGGATGCTCTATTCTGGTACTATGAACAACTTCTGGGAGTGAAGCCATCTGATGG 832
Db 674 TGGGATGCTCTATTCTGGTACTATGAACAACTTCTGGGAGTGAAGCCATCTGATGG 733
Qy 833 CACACTGGGATCCAGGCTGTCTCAAGAGGGAACACTTCTCGGCTGGCTGATCATGA 892
Db 734 CACACTGGGATCCAGGCTGTCTCAAGAGGGAACACTTCTCGGCTGGCTGATCATGA 793
Qy 893 CGCTCTCTTTGTGGCAGCCATCCCTTCGACCCAGGTGCTCTACTTTCTTTCAGGAGAC 952
Db 794 CGCTCTCTTTGTGGCAGCCATCCCTTCGACCCAGGTGCTCTACTTTCTTTCAGGAGAC 853
Qy 953 AGCCAGGAGTTGACATCTTTGAGAGCTTCAACATCCGCGGTGCTAGATCTGCAA 1012
Db 854 AGCCAGGAGTTGACATCTTTGAGAGCTTCAACATCCGCGGTGCTAGATCTGCAA 913
Qy 1013 GAATGAGCTGGGCGGCGAAAGTGTCTGAGAGAGTGAACACCTTCTGAAAGGCCCA 1072
Db 914 GAATGAGCTGGGCGGCGAAAGTGTCTGAGAGAGTGAACACCTTCTGAAAGGCCCA 973
Qy 1073 GCTGCTGTGACCCAGCCGGGAGCTGCCCTTCAAGCTCATTCGGCAAGCGGTCTGCT 1132
Db 974 GCTGCTGTGACCCAGCCGGGAGCTGCCCTTCAAGCTCATTCGGCAAGCGGTCTGCT 1033
Qy 1133 CCCCAGGATTTCTCCACAGCTCCCAATCTAGCAGTCTTCACTCTCCAGTGGCAGGT 1192
Db 1034 CCCCAGGATTTCTCCACAGCTCCCAATCTAGCAGTCTTCACTCTCCAGTGGCAGGT 1093
Qy 1193 TGGCGGACCGAGTCTCGGTTTGTGCTTCTCTCTTGGACATTTGAAGCTGTCTT 1252
Db 1094 TGGCGGACCGAGGAGCTCTCGGTTTGTGCTTCTCTCTTGGACATTTGAAGCTGTCTT 1153
Qy 1253 TAAAGGGAATACAAAGAGTTGAACAAAGAACTTACGCTGGACTACTTATAGGGGCC 1312
Db 1154 TAAAGGGAATACAAAGAGTTGAACAAAGAACTTACGCTGGACTACTTATAGGGGCC 1213
Qy 1313 TGAGACCAACCCCGGCGAGGAGTGTCTCAGTGGGCCCCCTCTCTGATGAAGCCCTGAC 1372
Db 1214 TGAGACCAACCCCGGCGAGGAGTGTCTCAGTGGGCCCCCTCTCTGATGAAGCCCTGAC 1273
Qy 1373 CTTCATGAAGGACCATTTCTGATGATGAGCAAGTGGTGGGAGCCGCTGTGTGTGA 1432
Db 1274 CTTCATGAAGGACCATTTCTGATGATGAGCAAGTGGTGGGAGCCGCTGTGTGTGA 1333
Qy 1433 ATCTGGCGTGGATATACAGGCTTGAGTGGAGACAGCCAGGCGCTTGAATGGGACAG 1492
Db 1334 ATCTGGCGTGGATATACAGGCTTGAGTGGAGACAGCCAGGCGCTTGAATGGGACAG 1393
Qy 1493 CCATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1552
Db 1394 CCATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1453
Qy 1553 GGACAGAGTGTCTCATCTGGTGGAGAGATTCAAGTGTTCCTTGAACCTGTGTCG 1612
Db 1454 GGACAGAGTGTCTCATCTGGTGGAGAGATTCAAGTGTTCCTTGAACCTGTGTCG 1513
Qy 1613 CAACCTGAGTGGGCCCCCAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1672
Db 1514 CAACCTGAGTGGGCCCCCAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1573
Qy 1673 GAGGAGTGGGCCCCCAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1732
Db 1574 GAGGAGTGGGCCCCCAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1633
Qy 1733 GGAACCCGATGCTGGGACCCCTGAGTCCGACCTGTTGCTCTGCTGCTGCTGCTGCTGCT 1792
Db 1634 GGAACCCGATGCTGGGACCCCTGAGTCCGACCTGTTGCTCTGCTGCTGCTGCTGCTGCT 1693
Qy 1793 CCTGAATCTCTGGAGAGGACATGGAGCGGGGGAACCCAGAGTGGGACATGTCAGTGG 1852
Db 1694 CCTGAATCTCTGGAGAGGACATGGAGCGGGGGAACCCAGAGTGGGACATGTCAGTGG 1753

Qy 1853 CCCATGAGCAGGAGCCTTCCGCTCAGAGCCGCGCCCAATCAATTAAGAAGTCTCTGGC 1912
Db 1754 CCCATGAGCAGGAGCCTTCCGCTCAGAGCCGCGCCCAATCAATTAAGAAGTCTCTGGC 1813
Qy 1913 TGTCCCTAACTCCATCTCGAGCTCCCTGCGCCCACTGTCAAGCTTGGCTCTTATTA 1972
Db 1814 TGTCCCACTCCATCTCGAGCTCCCTGCGCCCACTGTCAAGCTTGGCTCTTATTA 1873
Qy 1973 TTGAGATCATGGCCAGCAGCAGTCCAGAGCTCTTCCACTGTCTACAAATGCTCCCT 2032
Db 1874 TTGAGATCATGGCCAGCAGCAGTCCAGAGCTCTTCCACTGTCTACAAATGCTCCCT 1933
Qy 2033 CTTGCTGATGTCAGAGATGGAGTTGGGCTCTACAGTGTCTGGGCAACTGAGATGG 2092
Db 1934 CTTGCTGATGTCAGAGATGGAGTTGGGCTCTCTACAGTGTCTGGGCAACTGAGATGG 1993
Qy 2093 CTTTTCATACCCCTGTGATCTCTACTGGTGGACAGCCAGGACAGACCTTGGCCCTGGA 2152
Db 1994 CTTTTCATACCCCTGTGATCTCTACTGGTGGACAGCCAGGACAGACCTTGGCCCTGGA 2053
Qy 2153 TCCTGAATCTGGCAGGACATCCCGCGGAGCATGTGAAGTCCCGTTGACAGGCTCAGTGG 2212
Db 2054 TCCTGAATCTGGCAGGACATCCCGCGGAGCATGTGAAGTCCCGTTGACAGGCTCAGTGG 2113
Qy 2213 TGGGCGCCCTGGCTGCCAGCAGTCTACTGTGCCCACTTTGTCACTGTCACTGTCTCT 2272
Db 2114 TGGGCGCCCTGGCTGCCAGCAGTCTACTGTGCCCACTTTGTCACTGTCACTGTCTCT 2173
Qy 2273 CTTTGGCTTGTGCTTTTTCAGAGCCCTCATCATCTGTGGCTCCCTCATTTGAGAGACT 2332
Db 2174 CTTTGGCTTGTGCTTTTTCAGAGCCCTCATCATCTGTGGCTCCCTCATTTGAGAGACT 2233
Qy 2333 CCGGCTCGGGGCAAGGTTTCAAGGCTGTGAGACCTCGGCCCTGGGAGAGGCCCTGTT 2392
Db 2234 CCGGCTCGGGGCAAGGTTTCAAGGCTGTGAGACCTCGGCCCTGGGAGAGGCCCTGTT 2293
Qy 2393 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAATGACAGACCTTCCAGTGTATGGA 2452
Db 2294 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAATGACAGACCTTCTGCACTGTATGGA 2353
Qy 2453 CGCTGACAACTCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 2512
Db 2354 CGCTGACAACTCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 2413
Qy 2513 CGGTGAGGACCTGGCCATGCTGGTGGGCGGCCAAGCAGACCTTGTAGATGATGAC 2572
Db 2414 CGGTGAGGACCTGGCCATGCTGGTGGGCGGCCAAGCAGACCTTGTAGATGATGAC 2473
Qy 2573 AGCAGCAAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGCACTCACTGA 2632
Db 2474 AGCAGCAAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGCACTCACTGA 2533
Qy 2633 TGACACTCAGCAGGCTGATGACAGAGTCTGCTCCCTATGGAGCTCCCTTCTACAA 2692
Db 2534 TGACACTCAGCAGGCTGATGACAGAGTCTGCTCCCTATGGGACTCCCTTCTACAA 2593
Qy 2693 GCACATGAGCTCTTAAACAGGCTGGGCTACCCCGCAGACCTGCTCTACACTATATG 2752
Db 2594 GCACATGAGCTCTTAAACAGGCTGGGCTACCCCGCAGACCTGCTCTACACTATATG 2653
Qy 2753 AAGAACTGGAGAGATCCCTTTCAGTCTGGCCATTCAGGAGCCCTCCAGAAACACAGTG 2812
Db 2654 AAGAACTGGAGAGATCCCTTTCAGTCTGGCCATTCAGGAGCCCTCCAGAAACACAGTG 2713
Qy 2813 TTTCAAGAGACCTTAAACAACTGCTGTCCAGAGCCCTATGTAATGAACACCAACA 2872
Db 2714 TTTCAAGAGACCTTAAACAACTGCTGTCCAGAGCCCTATGTAATGAACACCAACA 2773
Qy 2873 TCTAAACATCATATGCTAAACATGCCACTCTCTGAAAATCTCCACTCTGAAAGTCCGCTTT 2932
Db 2774 TCTAAACATCATATGCTAAACATGCCACTCTCTGAAAATCTCCACTCTGAAAGTCCGCTTT 2833

```
QY 2933 GGACACCAACTCCCTTCTCCAGGGTCATGACAGGATCTGCTCCCTCTCTCCCTT 2992
DB 2834 GGACACCAACTCCCTTCTCCAGGGTCATGACAGGATCTGCTCCCTCTCTCCCTT 2893
QY 2993 ACCAGTCGTCACCGTGTGCTCCAGGAGTCTTCCCTGAGTCTGACACCTTCTCTCT 3052
DB 2894 ACCAGTCGTCACCGTGTGCTCCAGGAGTCTTCCCTGAGTCTGACACCTTCTCTCT 2953
QY 3053 TGCTTCAGTTGGGGAGACTCTGATCCCTTCTGCCCTGGCAGAAATGGCAGGGGTAATCTG 3112
DB 2954 TGCTTCAGTTGGGGAGACTCTGATCCCTTCTGCCCTGGCAGAAATGGCAGGGGTAATCTG 3013
QY 3113 AGCTTCTTCACTCTCTTACCTAGTACCCCTGACCTCTCCCTCCCTCTCTCTCTCTCT 3172
DB 3014 AGCTTCTTCACTCTCTTACCTAGTACCCCTGACCTCTCCCTCCCTCTCTCTCTCTCT 3073
QY 3173 GTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTATTTTATTTAAATAATAAGG 3232
DB 3074 GTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTATTTTATTTAAATAATAAGG 3133
QY 3233 CTTA 3236
DB 3134 CTTA 3137

RESULT 14
ADE20178
ID ADE20178 standard; cDNA; 3143 BP.
XX
AC ADE20178;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein. PRO1317.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX
OS Homo sapiens.
XX
XX US2003092883-A1.
XX
XX 15-MAY-2003.
XX
PF 10-DEC-2001; 2001US-00013430.
XX
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 02-OCT-1998; 98US-0102968P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103388P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 08-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 21-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 22-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
```


Db 3134 CTTA 3137

RESULT 15
ADE50089
ID ADE50089 standard; cDNA; 3143 BP.
XX AC ADE50089;
XX DT 29-JAN-2004 (first entry)
XX DE Human cDNA encoding secreted/transmembrane protein PRO1317.
XX KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX OS Homo sapiens.
XX FN US2003082626-A1.
XX PD 01-MAY-2003.
XX PF 06-DEC-2001; 2001US-00006116.
XX PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101044P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101913P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102077P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102454P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 14-OCT-1998; 98US-0103711P.
PR 20-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-01061178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 30-NOV-1998; 98US-0106856P.
PR 30-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106939P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108849P.

```
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 18-OCT-1999; 99US-00403297.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US021522.
PR 24-AUG-2000; 2000WO-US021328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00892636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski P, Grimaldi JC, Gurney AL, Hillan KJ;
XX Fan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PW, Wood WI;
XX
XX WPI; 2003-765413/72.
XX
XX P-PSDB; ADE50090.
XX
XX Novel isolated PRO polypeptides useful for tissue typing, modulating
XX biological activity of cell, as molecular weight markers in protein
XX Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 173 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 232
XX 74 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 133
XX
XX 233 CTGGAGCCCTCCGGGCTTTTCTCTTCCTCAACTGCTTCAAGTGTGCTGCCGACGAC 292
XX 134 CTGGAGCCCTCCGGGCTTTTCTCTTCCTCAACTGCTTCAAGTGTGCTGCCGACGAC 193
XX
XX 293 CGCGGGGGAGCGGGCGAGGGGCCCATGCCAGGGGTTCAGATATGTCGCGGGATGAACG 352
```

```
Db 194 CGCGGGGGAGCGGGCGAGGGGCCCATGCGCCAGGGTTCAGATATGTCGAGGGGATGAACG 253
Qy 353 TAGGGCACTTAGCTTCTTCCACAGAAAGGCTCCAGAGATTTTGACACTCTCTCTGAG 412
Db 254 TAGGGCACTTAGCTTCTTCCACAGAAAGGCTCCAGGATTTTGACACTCTCTCTGAG 313
Qy 413 TGGTATGGAATATCTCTTAAGTGGGGCTCGAAGGCAATCTGGCCCTGGATATCCA 472
Db 314 TGGTATGGAATATCTCTTAAGTGGGGCTCGAAGGCAATCTGGCCCTGGATATCCA 373
Qy 473 GGATCCAGGGGTCCCGAGGCTAAAGAAATGATACCGTGGCCAGCCAGTGACAGAAAAA 532
Db 374 GGATCCAGGGGTCCCGAGGCTAAAGAAATGATACCGTGGCCAGCCAGTGACAGAAAAA 433
Qy 533 GAGTGAATGTGCTTTAAGAAAGAGCAATGAGACAGTGTGTTCAATTCATCGGTGT 592
Db 434 GAGTGAATGTGCTTTAAGAAAGAGCAATGAGACAGTGTGTTCAATTCATCGGTGT 493
Qy 593 CTTGGTTTCTTCAATGTCAACCATCTCTACACCTGCGGCACCTTCGCTTCAGCCCTGC 652
Db 494 CTTGGTTTCTTCAATGTCAACCATCTCTACACCTGCGGCACCTTCGCTTCAGCCCTGC 553
Qy 653 TTGTACTCTTCAATGAATCTTCAAGATCTTCACTGTTGCCCCATCTCGAGGACAAGTCA 712
Db 554 TTGTACTCTTCAATGAATCTTCAAGATCTTCACTGTTGCCCCATCTCGAGGACAAGTCA 613
Qy 713 GGAGGAAAGGCGCAAGGCCCTTTGACCCGCTCAAGCATATCGGCTGTCTGGTGA 772
Db 614 GGAGGAAAGGCGCAAGGCCCTTTGACCCGCTCAAGCATATCGGCTGTCTGGTGA 673
Qy 773 TGGGATGCTCTAATTTCTGTATATGAACAACTTCTCGGCGAGTGCATCTGATGCG 832
Db 674 TGGGATGCTCTAATTTCTGTACTATGAACAACTTCTCGGCGAGTGCATCTGATGCG 733
Qy 833 CACACTGGGATCCAGGCTGCTCTCAAGACCGACACACTTCTCGCTGGCTGCATCATGA 892
Db 734 CACACTGGGATCCAGGCTGCTCTCAAGACCGACACACTTCTCGCTGGCTGCATCATGA 793
Qy 893 CGCTCTCTTTGTGGCGAGCCATCCCTTTCGACCCAGTGTCTACTTCTTTCGAGGAGAC 952
Db 794 CGCTCTCTTTGTGGCGAGCCATCCCTTTCGACCCAGTGTCTACTTCTTTCGAGGAGAC 853
Qy 953 AGCAGGAGTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGCTAGAGTTCGAA 1012
Db 854 AGCAGGAGTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGCTAGAGTTCGAA 913
Qy 1013 GAATGACGTGGGCGGAAAAAGCTGCTGCAGAAAGTGGACACCTTCTGAAAGGCCCA 1072
Db 914 GAATGACGTGGGCGGCGAAAAAGCTGCTGCAGAAAGTGGACACCTTCTGAAAGGCCCA 973
Qy 1073 GCTGCTCTGACCCAGCGGGGAGCTGCGCTTCAACGTCATCGGCCAGCGGCTCTGCT 1132
Db 974 GCTGCTCTGACCCAGCGGGGAGCTGCGCTTCAACGTCATCGGCCAGCGGCTCTGCT 1033
Qy 1133 CCGCGCGATTCTCCACAGCTCCCGACATCTACGAGTCTTCCACCTCCAGTGGCAGGT 1192
Db 1034 CCGCGCGATTCTCCACAGCTCCCGACATCTACGAGTCTTCCACCTCCAGTGGCAGGT 1093
Qy 1193 TGGCGGACAGGAGCTGCGGTTTGTGCTTCTCTCTCTGGAATGGAACGCTGCTT 1252
Db 1094 TGGCGGACAGGAGCTGCGGTTTGTGCTTCTCTCTCTGGAATGGAACGCTGCTT 1153
Qy 1253 TAAGGGGAATACAAAGAGTTGAACAAAGAACTTCAAGTGGACTACTTATAGGGGCC 1312
Db 1154 TAAGGGGAATACAAAGAGTTGAACAAAGAACTTCAAGTGGACTACTTATAGGGGCC 1213
Qy 1313 TGAGACCAACCCCGCGGCGAGGCTTGTGCTGAGTGGGCCCTCTCTGTATAAGGCCCTGAC 1372
Db 1214 TGAGACCAACCCCGCGGCGAGGCTTGTGCTGAGTGGGCCCTCTCTGTATAAGGCCCTGAC 1273
Qy 1373 CTTTCATGAAGGACCATTTCTCTGATGATGAGGAGTGGGGAGCGCCCTGCTGCTGGA 1432
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:54:27 ; Search time 9229.41 Seconds
(without alignments)
16460.143 Million cell updates/sec

Title: US-10-051-835-13
Perfect score: 3505
Sequence: 1 ggccttgccatgatggccac.....tttggggccacacacaggttg 3505

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.man.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3288.4	92.1	3257	9	BC020974	Homo sapi
2	3060.8	87.3	3143	6	AX697208	Sequence
3	3060.8	87.3	3143	9	AY358531	Homo sapi
4	3043.8	86.8	3252	9	AB029394	Homo sapi
5	3031.4	86.5	3191	6	BD249136	27 human
6	3008.8	85.8	3151	9	HSM807023	Homo sapi
7	2682.2	76.5	2981	6	AX746784	Sequence
8	2682.2	76.5	2981	9	AK091127	Homo sapi
9	2642.8	75.4	2768	6	AX512887	Sequence
10	2279.4	65.0	2281	6	AX528271	Sequence
11	2226.8	63.5	2271	6	AX528269	Sequence
12	1838	52.4	1838	6	AX879068	Sequence
13	1838	52.4	1838	6	BD157628	Primer fo
14	1838	52.4	1838	9	AK022349	Homo sapi
15	1771.2	50.5	3159	10	BC025800	Mus muscu
16	1726.8	49.3	3046	10	MMENASEMB	X85991 M.musculus
17	1605.8	45.8	164168	9	AL135927	Human DNA
18	1605.8	45.8	164179	9	AC007227	Homo sapi
19	698.2	19.9	775	6	AX866805	Sequence
20	698.2	19.9	775	6	BD146867	Primer fo
21	651	18.6	1223	6	AX704742	Sequence
22	499.6	14.3	567	6	AX872305	Sequence
23	499.6	14.3	567	6	BD152367	Primer fo
24	486.6	13.9	184850	2	AC102388	Mus muscu
25	486.6	13.9	249206	2	AC145168	Mus muscu
26	470	13.4	988	6	AX430331	Sequence
27	436.4	12.5	230635	2	AC128319	Rattus no
28	436.4	12.5	246036	2	AC097816	Rattus no
29	436.4	12.5	289877	2	AC119762	Rattus no
30	327	9.3	2405	6	AX879101	Sequence
31	327	9.3	2405	6	BD157650	Primer fo
32	327	9.3	2405	9	AK022416	Homo sapi
33	278.8	8.0	106784	2	AC136250	Rattus no
34	262.6	7.5	3766	6	BD171175	Novel gen
35	262.6	7.5	3766	6	BD183514	Novel gen
36	262.6	7.5	3781	6	AB051532	Homo sapi
37	262.6	7.5	3781	6	AX376386	Sequence
38	262.6	7.5	3781	6	AX697184	Sequence
39	262.6	7.5	3781	9	AY358392	Homo sapi
40	262.6	7.5	3807	9	AY445887	Homo sapi
41	250.6	7.1	3528	9	AK026108	Homo sapi
42	245	7.0	2390	6	AX418422	Sequence
43	237.8	6.8	3293	6	AX174731	Sequence
44	236.6	6.8	2153	6	AX060303	Sequence
45	236.6	6.8	2156	6	AX060313	Sequence

ALIGNMENTS

RESULT 1
BC020974
LOCUS
DEFINITION Homo sapiens hypothetical protein FLJ12287 similar to semaphorins,
mRNA (cdna clone MGC:9542 IMAGE:3847802), complete cds.
ACCESSION BC020974
VERSION BC020974.1 GI:18088092
KEYWORDS MGC.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3257)
Srausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
PRI 03-OCT-2003

Db 721 AAAGCCCTTTGACCCCTTCAAGCATACGGGTGCTTGGTGAATGGGATGCTCTATT 780
QY CTGTTACTATGAACAACCTTCTGGGAGTGAAGCCATCTTATGATGCGACACTGGGATCCC 846
Db 781 CTGGTACTATGAACAACCTTCTGGGAGTGAAGCCATCTTATGATGCGACACTGGGATCCC 840
QY 847 AGCCTGTCTCAAGACGACAACTTCTCCGCTGGCTGCATCATGACGCTCTCTTTGG 906
Db 841 AGCCTGTCTCAAGACGACAACTTCTCCGCTGGCTGCATCATGACGCTCTCTTTGG 900
QY 907 CAGCCATCCCTTCGACCCAGGTGCTACTTCTTCTTCGAGGAGACAGCCAGGATTTG 966
Db 901 CAGCCATCCCTTCGACCCAGGTGCTACTTCTTCTTCGAGGAGACAGCCAGGATTTG 960
QY 967 ACTTCTTTGAGGGCTCACACATCGCGGTGGCTAGAGTCTGCAAGATGACGTGGCG 1026
Db 961 ACTTCTTTGAGGGCTCACACATCGCGGTGGCTAGAGTCTGCAAGATGACGTGGCG 1020
QY 1027 GCGAAAGCTGTGCGAAGAGTGGACACCTTCTTGAAGGCCAGCTGTCTGCAACC 1086
Db 1021 GCGAAAGCTGTGCGAAGAGTGGACACCTTCTTGAAGGCCAGCTGTCTGCAACC 1080
QY 1087 AGCCGGGAGTGCCTTTCAAGCTATCCGACAGCGGTCTGTCTCCCGCCGATTTCTC 1146
Db 1081 AGCCGGGAGTGCCTTTCAAGCTATCCGACAGCGGTCTGTCTCCCGCCGATTTCTC 1140
QY 1147 CCACAGCTCCCACATCTACGAGCTTTCACTCCAGTGGCAGGTGGCGGACACGGA 1206
Db 1141 CCACAGCTCCCACATCTACGAGCTTTCACTCCAGTGGCAGGTGGCGGACACGGA 1200
QY 1207 GCTCTGCGGTTGTGCTCTCTCTTTGGACATTTGAACGTGTCTTTAAGGGGAAATACA 1266
Db 1201 GCTCTGCGGTTGTGCTCTCTCTTTGGACATTTGAACGTGTCTTTAAGGGGAAATACA 1260
QY 1267 AAGAGTTGAACAAAGAACTTCAAGCTGACTTATAGGGGCTTGAAGCAACACCCC 1326
Db 1261 AAGAGTTGAACAAAGAACTTCAAGCTGACTTATAGGGGCTTGAAGCAACACCCC 1320
QY 1327 GGCAGGAGTGTGCTCAGTGGGCTCTCTCTGATAGGGCTTGAAGCAACACAGGAC 1386
Db 1321 GGCAGGAGTGTGCTCAGTGGGCTCTCTCTGATAGGGCTTGAAGCAACAGGAC 1380
QY 1387 ATTTCTGTATGATGAGCAAGTGTGGGAGCGCCCTCTGCTGTGTAATCTGGCTGGAGT 1446
Db 1381 ATTTCTGTATGATGAGCAAGTGTGGGAGCGCCCTCTGCTGTGTAATCTGGCTGGAGT 1440
QY 1447 ATACAGGCTTGCAGTGGAGACAGCCAGGGCTTGTATGGGACAGCCATCTTGTCTATGT 1506
Db 1441 ATACAGGCTTGCAGTGGAGACAGCCAGGGCTTGTATGGGACAGCCATCTTGTCTATGT 1500
QY 1507 ACTCGGAACCAACAGGCTCGTCCACAGGCTGTGGTAAGTGGGACAGCAAGTGTCTC 1566
Db 1501 ACTCGGAACCAACAGGCTCGTCCACAGGCTGTGGTAAGTGGGACAGCAAGTGTCTC 1560
QY 1567 ATCTGTGGAAGAGATTGAGCTGTTCCTTCAAGCTGTTCGCAACCTGACAGCTGG 1626
Db 1561 ATCTGTGGAAGAGATTGAGCTGTTCCTTCAAGCTGTTCGCAACCTGACAGCTGG 1620
QY 1627 CCCCACCCAGGCTGAGGTTGTAGGCTTCTCAGAGGTTGTCTGAGAGGTGTGCCCCGAG 1686
Db 1621 CCCCACCCAGGCTGAGGTTGTAGGCTTCTCAGAGGTTGTCTGAGAGGTGTGCCCCGAG 1680
QY 1687 CCAACTGTATGTATGAGAGCTGTGTGAGCTGTCTTGGCCGAGACCCCACTGTG 1746
Db 1681 CCAACTGTATGTATGAGAGCTGTGTGAGCTGTCTTGGCCGAGACCCCACTGTG 1740
QY 1747 CTGGGACCTTGAATCCCGAACTGTGTCTCTGTCTGCCCCCACTGAACTCTTGGGA 1806
Db 1741 CTGGGACCTTGAATCCCGAACTGTGTCTCTGTCTGCCCCCACTGAACTCTTGGGA 1800
QY 1807 AGCAGACATGAGCGGGGACCCAGAGTGGGATGTGCGAGTGGCCCTTGTGACGAGA 1866

Db 1801 AGCAGACATGAGCGGGGAAACCAGAGTGGGATGTGCCAGTGGCCCCCATGAGCAGA 1860
QY 1867 GCCTTCGGCTCAGAGCGCCCGCAAAATCATTAAGAAAGTCTGTGCTGTCCCTAACTCCA 1926
Db 1861 GCCTTCGGCTCAGAGCGCCCGCAAAATCATTAAGAAAGTCTGTGCTGTCCCTAACTCCA 1920
QY 1927 TCCCTGAGCTCCCTGCGCCCACTGTGAGCCTTGGCTCTTATTTATTTGAGTCAATGGCC 1986
Db 1921 TCCCTGAGCTCCCTGCGCCCACTGTGAGCCTTGGCTCTTATTTATTTGAGTCAATGGCC 1980
QY 1987 CAGCAGCTCCCAAGAGCTCTTCCACTGTCTA CAATGGCTCCCTTGTGTGA TAGTGC 2046
Db 1981 CAGCAGCTCCCAAGAGCTCTTCCACTGTCTA CAATGGCTCCCTTGTGTGA TAGTGC 2040
QY 2047 AGATCGAGTGGGGTCTCTACAGTGTGGGAACTGAGAAATGGCTTTTCAATACCTCG 2106
Db 2041 AGATCGAGTGGGGTCTCTACAGTGTGGGAACTGAGAAATGGCTTTTCAATACCTCG 2100
QY 2107 TGAATCTCTACTGCTGGGTGAGCAGCAGGACCCAGACCTTGGCCCTTGAATCTCTGAATGGCAG 2166
Db 2101 TGAATCTCTACTGCTGGGTGAGCAGCAGGACCCAGACCTTGGCCCTTGAATCTCTGAATGGCAG 2160
QY 2167 GCATCCCGGGGAGCATGTGAAGTCCCTTGCAGAGGTGAGTGGGGCGCCCTCG 2226
Db 2161 GCATCCCGGGGAGCATGTGAAGTCCCTTGCAGAGGTGAGTGGGGCGCCCTCG 2220
QY 2227 CTGCCCAGCAGTCTACTGCGCCCACTTTTGTCACTGTCTCACTGTCTCTTTTGTCTTAGTGC 2286
Db 2221 CTGCCCAGCAGTCTACTGCGCCCACTTTTGTCACTGTCTCACTGTCTCTTTTGTCTTAGTGC 2280
QY 2287 TTTTCAGAGCTCATCATCTCTGTGGCTTCCCATTTGAGAGCACTCCGGGCTCGGGCA 2346
Db 2281 TTTTCAGAGCTCATCATCTCTGTGGCTTCCCATTTGAGAGCACTCCGGGCTCGGGCA 2340
QY 2347 AGTTTCAGGCTGTGAGACCTTGCCTGGGAGAAAGCCCTGTTAAGCAGAGAGCAAC 2406
Db 2341 AGTTTCAGGCTGTGAGACCTTGCCTGGGAGAAAGCCCTGTTAAGCAGAGAGCAAC 2400
QY 2407 ACTTCAGTCTCCCAAGAAATGACAGACCTCTGCGCAGTGTGAGAGCTGACCAACT 2466
Db 2401 ACTTCAGTCTCCCAAGAAATGACAGACCTCTGCGCAGTGTGAGAGCTGACCAACT 2460
QY 2467 GCCTTCAGCTAGAGTGTAACTTCTAGGACAGCCGGGCTCGGTGCGAGCACCT 2526
Db 2461 GCCTTCAGCTAGAGTGTAACTTCTAGGACAGCCGGGCTCGGTGCGAGCACCT 2520
QY 2527 GGCATGCTGTGGCGGCCCAAGCAGACCTCTGATAGGATGACAGCAGCAAAAAGA 2586
Db 2521 GGCATGCTGTGGCGGCCCAAGCAGACCTCTGATAGGATGACAGCAGCAAAAAGA 2580
QY 2587 CCACTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCTACTGATGACCTCAGCAGG 2646
Db 2581 CCACTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCTACTGATGACCTCAGCAGG 2640
QY 2647 GTGATGCACAGCAGTCTGCTCCCTTATGGGACTCCCTTCTACCAAGCACTGAGCTCTC 2706
Db 2641 GTGATGCACAGCAGTCTGCTCCCTTATGGGACTCCCTTCTACCAAGCACTGAGCTCTC 2700
QY 2707 TAAAGGGTGGGGCTTACCCCGAGCTGCTCTACCTGATGATGAGAACTGAGAG 2766
Db 2701 TAAAGGGTGGGGCTTACCCCGAGCTGCTCTACCTGATGATGAGAACTGAGAG 2760
QY 2767 GATCCTTCACTGCTGGCCATTTCCAGGAGCCCTCCAGAAACACAGTGTTCAGAGACCT 2826
Db 2761 GATCCTTCACTGCTGGCCATTTCCAGGAGCCCTCCAGAAACACAGTGTTCAGAGACCT 2820
QY 2827 AAAAACTGCTTCCAGGACCTTATGGTAAATGAACCAAACTCTTAAACATCAT 2886
Db 2821 AAAAACTGCTTCCAGGACCTTATGGTAAATGAACCAAACTCTTAAACATCAT 2880
QY 2887 TGCTTAACTGCCACTCTGGAACCTCACTCTGAAAGCTGCGCTTTGGACACCAACTC 2946
Db 2881 TGCTTAACTGCCACTCTGGAACCTCACTCTGAAAGCTGCGCTTTGGACACCAACTC 2940

Db 1454 GGACAGCAAGTGTCTATCTGTGGAGAGATTTCAGCTGTTCCTGACCCCTGAACTGTTTCG 1513
Qy 1613 CAACCTGACAGCTGGGCCCCCACCAGGCTGCAGTGTTCCTGAGGAGTGTCTG 1672
Db 1514 CAACCTGACAGCTGGGCCCCCACCAGGCTGCAGTGTTCCTGAGGAGTGTCTG 1573
Qy 1673 GAGGCTGCCCCAGGCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTTCGCGG 1732
Db 1574 GAGGCTGCCCCAGGCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTTCGCGG 1633
Qy 1733 GAGCCCCCACTGTGCTGGGACCTTGAGTCCCGAACTGTTCCTGCTGTGCCCCCAA 1792
Db 1634 GAGCCCCCACTGTGCTGGGACCTTGAGTCCCGAACTGTTCCTGCTGTGCCCCCAA 1693
Qy 1793 CTGAACTCTCTGGAAGCAGGA CATGAGAGGGGGGAAACCCAGAGTGGGCAATGTCAGTGG 1852
Db 1694 CTGAACTCTCTGGAAGCAGGA CATGAGAGGGGGGAAACCCAGAGTGGGCAATGTCAGTGG 1753
Qy 1853 CCCATGAGCAGGAGCTTCGGCTCAGAGCGCGCGCAAACTTAAGAAAGTCTCTGGC 1912
Db 1754 CCCATGAGCAGGAGCTTCGGCTCAGAGCGCGCGCAAACTTAAGAAAGTCTCTGGC 1813
Qy 1913 TGTCCCTAACTCACTCTGAGACTCCCTGCCCCCACTGTGAGCTTCCTGCTTTGCTTTA 1972
Db 1814 TGTCCCTAACTCACTCTGAGCTCCCTGCCCCCACTGTGAGCTTCCTGCTTTA 1873
Qy 1973 TTGGAGTCATGCCAGCAGCAGTCCCAAGAGCTTCCTCACTGTCTCAATGCTCCCT 2032
Db 1874 TTGGAGTCATGCCAGCAGCAGTCCCAAGAGCTTCCTCACTGTCTCAATGCTCCCT 1933
Qy 2033 CTGTCTGATGAGCAGGATGGAGTGGGGTCTCTACCACTGTGGGCAACTGGAATGG 2092
Db 1934 CTGTCTGATGAGCAGGATGGAGTGGGGTCTCTACCACTGTGGGCAACTGGAATGG 1993
Qy 2093 CTGTTCATACCTGTGATCTCTACTGAGTGGAGCAGCAGCAGCAGCTGGGCTGGA 2152
Db 1994 CTGTTCATACCTGTGATCTCTACTGAGTGGAGCAGCAGCAGCAGCTGGGCTGGA 2053
Qy 2153 TCTGAACTGGCAGGATCCCCCGGAGCATGTGAAGTCCCGTTGACCACTGAGAGCACT 2212
Db 2054 TCTGAACTGGCAGGATCCCCCGGAGCATGTGAAGTCCCGTTGACCACTGAGAGCACT 2113
Qy 2213 TGGGGCGGCTGGTGGCCAGCAGTCTACTTGGGCGCCACTTGTGCTGCTGCTGCT 2272
Db 2114 TGGGGCGGCTGGTGGCCAGCAGTCTACTTGGGCGCCACTTGTGCTGCTGCTGCT 2173
Qy 2273 CTGTGCTTGTGCTTTAGGAGCCTCATCATCTGCTGGCTCCCACTGAGAGCACT 2332
Db 2174 CTGTGCTTGTGCTTTAGGAGCCTCATCATCTGCTGGCTCCCACTGAGAGCACT 2233
Qy 2333 CCGGCTCGGGCAAGTTTCAAGCTGTGAGACCTCGCGCCCTGGGGAAGGCCCGCTT 2392
Db 2234 CCGGCTCGGGCAAGTTTCAAGCTGTGAGACCTCGCGCCCTGGGGAAGGCCCGCTT 2293
Qy 2393 AAGCAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTTGCAGTGTGGA 2452
Db 2294 AAGCAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTTGCAGTGTGGA 2353
Qy 2453 CGCTGCAACAACTGCTAGGCACTAGGAGTCTTAACTTTCAGCAGCAGGCCGGGCTG 2512
Db 2354 CGCTGCAACAACTGCTAGGCACTAGGAGTCTTAACTTTCAGCAGCAGGCCGGGCTG 2413
Qy 2513 CGGTGAGGCACTGGCCATGCTGGCTGGCGCGCCCAAGCAGCAGCCCTGACTAGGATGAC 2572
Db 2414 CGGTGAGGCACTGGCCATGCTGGCTGGCGCGCCCAAGCAGCAGCCCTGACTAGGATGAC 2473
Qy 2573 AGCAGCAAAAAGACCACTTTTCCCTCTGAGAGGAGCTTCTGCTACTCTGCACTGA 2632
Db 2474 AGCAGCAAAAAGACCACTTTTCCCTCTGAGAGGAGCTTCTGCTACTCTGCACTGA 2533
Qy 2633 TGCACCTGACAGGCTGATGCACAGAGTCTGCTCCCTCCCTATGGAGCTCCCTTACCAA 2692

Db 2534 TGACATCTAGCAGGGTGATGCACAGCAGTGTGCTCTCCCTATGGGACTCCCTTCTACCAA 2593
Qy 2693 GCACATGAGCTCTTAACAGGGTGGGGGTACCCCCAGACCTGCTCTCACTGATATTG 2752
Db 2594 GCACATGAGCTCTTAACAGGGTGGGGGTACCCCCAGACCTGCTCTCACTGATATTG 2653
Qy 2753 AAGAACTGAGAGGATCTTTCAGTTCGCTCCATTCAGGAGCCCTCCAGAAACACAGTG 2812
Db 2654 AAGAACTGAGAGGATCTTTCAGTTCGCTCCATTCAGGAGCCCTCCAGAAACACAGTG 2713
Qy 2813 TTTCAAGAGACCCCTAAAAAACCCTGCTGCCACGAGACCTTATGTAATGAACCAACAA 2872
Db 2714 TTTCAAGAGACCCCTAAAAAACCCTGCTGCCACGAGACCTTATGTAATGAACCAACAA 2773
Qy 2873 TCTAAACAATCATATGTAACATGCCACTCTCTGGAACCTCACTCTGAAGCTGCCCTTT 2932
Db 2774 TCTAAACAATCATATGTAACATGCCACTCTCTGGAACCTCACTCTGAAGCTGCCCTTT 2833
Qy 2933 GGCACCAACACTCCCTTCTCCAGGAGTATGTCAGGAGTCTGCTCCCTCTGCTTCCCTT 2992
Db 2834 GGCACCAACACTCCCTTCTCCAGGAGTATGTCAGGAGTCTGCTCCCTCTGCTTCCCTT 2893
Qy 2993 ACCAGTGTGCACCGCTGACTCCAGAGAGTCTTCCCTGAGTCTGACCACTTCTTCT 3052
Db 2894 ACCAGTGTGCACCGCTGACTCCAGAGAGTCTTCTTCTGAGTCTGACCACTTCTTCT 2953
Qy 3053 TGCTTCAAGTGGGGCAGACTCTGATCCCTCTGCTGCGAGAAATGGAGGGGTAATCTG 3112
Db 2954 TGCTTCAAGTGGGGCAGACTCTGATCCCTCTGCTGCGAGAAATGGAGGGGTAATCTG 3013
Qy 3113 AGCTTCTTCACTCTTACCTTAGCTGAGCCCTTCACTCTCCCTGCTTCTTCTTCTT 3172
Db 3014 AGCTTCTTCACTCTTACCTTAGCTGAGCCCTTCACTCTCCCTGCTTCTTCTTCTT 3073
Qy 3173 GTTTGGGATTCAGAAAACCTGCTTGTGAGAGCTGTTTATTTTATTAATAATAAAGG 3232
Db 3074 GTTTGGGATTCAGAAAACCTGCTTGTGAGAGCTGTTTATTTTATTAATAATAAAGG 3133
Qy 3233 CTTA 3236
Db 3134 CTTA 3137

RESULT 3
AY358531
LOCUS
DEFINITION Homo sapiens clone DNA71166 semaphorin 3 (UNQ783) mRNA, complete cds.
ACCESSION AY358531
VERSION AY358531.1 GI:37182184
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3143)
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vanden, R., Watanabe, C., Weiland, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I., and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL
PUBMED 12975309
REFERENCE 2 (bases 1 to 3143)
AUTHORS Clark, H.F.
TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

source 1..3143

source

```

1. 3143
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA71166"
1. 3143
gene
105. 2390
/locus_tag="UNQ783"
105. 2390
/locus_tag="UNQ783"
/notes="PRO1317"
/codon_start=1
/product="semaphorin B"
/protein_id="AA088895.1"

```

gene

```

1. 1013
/locus_tag="UNQ783"
105.2390
/locus_tag="UNQ783"

```

```

/mode= FKO1317
/codon start=1

```

```

"/product"=>"semaphorin B",
"/protein_id"=>"Q888895.1",
"/db_xref="GI:37182185",
"/translation="MALPALGLDPLD
YAGERRALSFHHQKGLDQFDLTL
WPASDRKSKCAFKKSNETQCFFN
LLPISEDKMEGKQSFDPFAHKH
KTNDFRLWLHSDASVAAIESTVQ
KLQKQWTFLLKQKLTQCPQGLP
SSAYCAFSLLDIIRVFCKGYKELN
KDFLMDQVQVGFPLLVKSGEYVL
DSSAHLVYVQLQDPDEPVNQLL
ARDPHCAMDPESTRICLLSAPNLN
EVLAVPNSILLPECPHSALASYYI
WATENGSPYPIVSYWDSQDTQLA
HFVTVTLLFALVLSGALLILVASP
ECRTSSADVDADNNICAGTEVA"

```

ORIGIN

```
Query Match      87.3%; Score 3060.8; DB 9; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

173	Qy	AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCACGCTTGGGCTCTGGACCC	238
74	Db	AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCACGCTTGGGCTCTGGACCC	133
233	Qy	CTGGAGCTCCTCGGCGCTTTTCCCTCTTCCAACTGCTTCCAGCTGCTGCTGCGACGACGAC	292
134	Db	CTGGAGCTCCTCGGCGCTTTTCCCTCTTCCAACTGCTTCCAGCTGCTGCTGCGACGACGAC	193
293	Qy	CGCGGGGGAGGGCGGGGACGGGGCCATGGCCGAGGTCAGATACTATGACGGGGATGAACG	353
194	Db	CGCGGGGGAGGGCGGGGACGGGGCCCATGCCAGGGTCAGATACTATGACGGGGATGAACG	253
353	Qy	TAGGGCACTTAGCTTCTTCCACACAGAGGGGCTCCAGGATTTTGACACTCTGTCTCTTGAG	412
254	Db	TAGGGCACTTAGCTTCTTCTCCACAGAGGGGCTCCAGGATTTTGACACTCTGTCTCTTGAG	313
413	Qy	TGGTGATGGAAATACTCTTACTGTGGGGGCTCGAGAGCCATTTCTGGCTTTGGATATCCA	472
314	Db	TGGTGATGGAAATACTCTTACTGTGGGGGCTCGAGAGCCATTTCTGGCTTTGGATATCCA	373
473	Qy	GGATCCAGGGGTCCCAGGCTTAAAGAACATCATACCGTGGCGACGACAGTGACAGAAAAA	532
374	Db	GGATCCAGGGGTCCCAGGCTTAAAGAACATCATACCGTGGCGACGACAGTGACAGAAAAA	433
533	Qy	GAGTGAATGTGCCCTTTAAGAAAGAAAGCAATGAGACACAGTGGTTTCAACTTCCTCGTGT	592
434	Db	GAGTGAATGTGCCCTTTAAGAAAGAAAGCAATGAGACACAGTGGTTTCAACTTCCTCGTGT	493
593	Qy	CCTGGTTTCTTATCAATGTCAACCATCTCTACACCTGGGGCACCTTTCGCTTCAGCCCTGC	652
494	Db	CCTGGTTTCTTATCAATGTCAACCATCTCTACACCTGGGGCACCTTTCGCTTCAGCCCTGC	553
653	Qy	TTGTACCTTCAATTGAACTTCAAGATTTCTACTGTGGCCCATCTCTCGAGAGCAAGGTCAT	712
554	Db	TTGTACCTTCAATTGAACTTCAAGATTTCTACTGTGGCCCATCTCTCGAGAGCAAGGTCAT	613

QY	713	GGAGGGAAAGGCGCAAAAGCCGCTTTGACCCGCTCACAAGCATACGGCTGCTTGGTGGGA	772
DB	614	GGAGGGAAAGGCGCAAAAGCCGCTTTGACCCGCTCACAAGCATACGGCTGCTTGGTGGGA	673
QY	773	TGGGATGCTCTATTCTTGATATGAAACAATCTTCTGGGAGTGAGCCCATCTCTGATGCG	832
DB	674	TGGGATGCTCTATTCTTGATATGAAACAATCTTCTGGGAGTGAGCCCATCTCTGATGCG	733
QY	833	CACACTGGGATCCGAGCCTGCTTCAAGACGGACAACTTCTCCTCGCTGGCTGCATCATGA	892
DB	734	CACACTGGGATCCGAGCCTGCTTCAAGACGGACAACTTCTCCTCGCTGGCTGCATCATGA	793
QY	893	CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTCGAGGAGAC	952
DB	794	CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTCGAGGAGAC	853
QY	953	AGCAGCGAGTTTGACTTCTTTCGAGAGGCTCCACACATCGGGGTGGCTAGAGTCTGCAA	1012
DB	854	AGCAGCGAGTTTGACTTCTTTCGAGAGGCTCCACACATCGGGGTGGCTAGAGTCTGCAA	913
QY	1013	GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAAGATGGAACCACTTCTTGAAGGGCCA	1072
DB	914	GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAAGATGGAACCACTTCTTGAAGGGCCA	973
QY	1073	GCTGCTGTGCACCCAGCGGGGAGCTGCCCTTCAACGTCAATCCGACACGGCGTCTCTGCT	1133
DB	974	GCTGCTGTGCACCCAGCGGGGAGCTGCCCTTCAACGTCAATCCGACACGGCGTCTCTGCT	1033
QY	1133	CCCCCGGATTTCTCCACAGCTCCCCCAATCTACGCAAGTCTTCACTCCCTCCAGTGGCAGGT	1193
DB	1034	CCCCCGGATTTCTCCACAGCTCCCCCAATCTACGCAAGTCTTCACTCCCTCCAGTGGCAGGT	1093
QY	1193	TGGCGGGACCAGGAGCTTCGGGTTTGTGCTTCTCTCTGTGACATTTGAACGTGTCTT	1253
DB	1094	TGGCGGGACCAGGAGCTTCGGGTTTGTGCTTCTCTCTGTGACATTTGAACGTGTCTT	1153
QY	1253	TAAGGGAAATACAAAGAGTTGAACAAAGAACTTCAACGTGAGCTACTTTATAGGGGCC	1312
DB	1154	TAAGGGAAATACAAAGAGTTGAACAAAGAACTTCAACGTGAGCTACTTTATAGGGGCC	1213
QY	1313	TGACACCAACCCCGGCGAGCAGTGTCTCAGTGGGCCCCCTCTGATAGAGCCCTTGAC	1372
DB	1214	TGACACCAACCCCGGCGAGCAGTGTCTCAGTGGGCCCCCTCTGATAGAGCCCTTGAC	1273
QY	1373	CTTCATGAAGGAACATTTCTGATGAGATGAGCAAGTGGTGGGAGCGCCCCCTGCTGTGTGAA	1432
DB	1274	CTTCATGAAGGAACATTTCTGATGAGATGAGCAAGTGGTGGGAGCGCCCCCTGCTGTGTGAA	1333
QY	1433	ATCTGGCGTGGAGTATACACGGCTTGACAGTGGAGACACCCAGGGCCCTTGATGGGCACAG	1492
DB	1334	ATCTGGCGTGGAGTATACACGGCTTGACAGTGGAGACACCCAGGGCCCTTGATGGGCACAG	1393
QY	1493	CCATCTTTGATGTAACCTGGGAAACCAACAGGGTTCGTCCACAAGGCTGTGGTAAAGTGG	1552
DB	1394	CCATCTTTGATGTAACCTGGGAAACCAACAGGGTTCGTCCACAAGGCTGTGGTAAAGTGG	1453
QY	1553	GGACAGCAGTGTCTCATCTGGTGGGAAGAGATTACAGCTGTCCCTGACCCCTGAACTGTTCG	1612
DB	1454	GGACAGCAGTGTCTCATCTGGTGGGAAGAGATTACAGCTGTCCCTGACCCCTGAACTGTTCG	1513
QY	1613	CAACCTGGAGCTGGCCCCCGACCCAGGCTGCAAGTGTGTGTAGGCTTCTCAGGAGGTGTCTG	1672
DB	1514	CAACCTGGAGCTGGCCCCCGACCCAGGCTGCAAGTGTGTGTAGGCTTCTCAGGAGGTGTCTG	1573
QY	1673	GAGGGTGCCCGAGCCAACTGTAGTGTCTATAGAGAGTGTGTGAGCTGTGTCTTGTGCCCG	1732
DB	1574	GAGGGTGCCCGAGCCAACTGTAGTGTCTATAGAGAGTGTGTGAGCTGTGTCTTGTGCCCG	1633
QY	1733	GGACCCCAACTGTGGACCTGTAGTCCCGAACCTGTGTGCTCCTGCTGTGCCCCCAA	1792
DB	1634	GGACCCCAACTGTGCTCTGGACCTGTAGTCCCGAACCTGTGTGCTCCTGCTGTGCCCCCAA	1693
QY	1793	CCTGAACTCTCTGGGAAGCAGGACATGAGACGGGGGAAACCCAGAGTGGGCATGTGCCAGTGG	1853

1694 CTTGAATCTCTGGAAGCAGGACATGAGCGGGGAACCCAGAGTGGCATGTGCGAGTGG 1753
1853 CCCATGACGAGGAGCTTGGGCTTCAGAGCGCGCGGCAATCATTAAGAAGTCTCGGC 1912
1754 CCCATGACGAGGAGCTTGGGCTTCAGAGCGCGCGGCAATCATTAAGAAGTCTCGGC 1813
1913 TGTCCCTAACTCCATCTCTGAGAGTCCCTTGGCCCTCCACCTGTGAGCGCTTGGCCCTCTATTATTA 1972
1814 TGTCCCCCACTCCATCTCTGAGAGTCCCTTGGCCCTCCACCTGTGAGCGCTTGGCCCTCTATTATTA 1873
1973 TTGAGTCAATGGCCAGAGCAGTCCAGAGGCTTTCACATGTCTACATATGGTCTCCCT 2032
1874 TTGAGTCAATGGCCAGAGCAGTCCAGAGGCTTTCACATGTCTACATATGGTCTCCCT 1933
2033 CTTGTCTGATGTCAGGATGGAGTGGGGTCTCTACACAGTGTCTGGGCACTGAGAAATGG 2092
1934 CTTGTCTGATGTCAGGATGGAGTGGGGTCTCTACACAGTGTCTGGGCACTGAGAAATGG 1993
2093 CTTTTCATACCTGTGATCTCTACTGTGGTGGAGCAGCCAGCCAGCCCTGGCCCTGGGA 2152
1994 CTTTTCATACCTGTGATCTCTACTGTGGTGGAGCAGCCAGCCAGCCCTGGCCCTGGGA 2053
2153 TCCGTGAATGGCAGGATCCCGGCGAGCATGTGAAGTCCGTTGACACAGGTCAGTGG 2212
2054 TCCGTGAATGGCAGGATCCCGGCGAGCATGTGAAGTCCGTTGACACAGGTCAGTGG 2113
2213 TGGGGCGGCTGGTGGCCAGCAGTCTCTACGCCCCCACTTTGTGTCACATGTCTCT 2272
2114 TGGGGCGGCTGGTGGCCAGCAGTCTCTACTGGCCCCCACTTTGTGTCACATGTCTCT 2173
2273 CTTTTCATACCTGTGATCTCTACTGTGGTGGAGCAGCCAGCCAGCCCTGGCCCTGGGA 2332
2174 CTTTTCATACCTGTGATCTCTACTGTGGTGGAGCAGCCAGCCAGCCCTGGCCCTGGGA 2233
2333 CCGGGCTGGGGCAAGTTCAGGGCTGTGAGACCTCTGCGCCCTGGGGCAAGGCCCGCTT 2392
2234 CCGGGCTGGGGCAAGTTCAGGGCTGTGAGACCTCTGCGCCCTGGGGCAAGGCCCGCTT 2293
2393 AAGCAGAGCAGACACTCTCAGTCTCCAGGAGTCCAGGACCTGCGCAGTGTATGTGA 2452
2294 AAGCAGAGCAGACACTCTCAGTCTCCAGGAGTCCAGGACCTGCGCAGTGTATGTGA 2353
2453 CGTGTACAACTGCTTAGGACCTGAGGTAGTCTAACTTAGGACAGCGCGGGGCTG 2512
2354 CGTGTACAACTGCTTAGGACCTGAGGTAGTCTAACTTAGGACAGCGCGGGGCTG 2413
2513 CGTGTAGGACCTGAGGTAGTCTGAGTGGCGGCGCCAGCAGCAGCCCTGACTAGGATGAC 2572
2414 CGTGTAGGACCTGAGGTAGTCTGAGTGGCGGCGCCAGCAGCAGCCCTGACTAGGATGAC 2473
2573 AGCAGCAAAAGACCACTTTCTCCCTCAGAGGAGCTTCTGCTACTCTGCACTCACTGA 2632
2474 AGCAGCAAAAGACCACTTTCTCCCTCAGAGGAGCTTCTGCTACTCTGCACTCACTGA 2533
2633 TGACACTCAGAGGATGATGACAGAGTGTGCTGCTCCCTATGGAGTCTCTCTACCAA 2692
2534 TGACACTCAGAGGATGATGACAGAGTGTGCTGCTCCCTATGGAGTCTCTCTACCAA 2593
2693 GCACATGAGTCTCTAAAGGTTGGGGCTTACCCCAAGACCTGCTCTACATGATATG 2752
2594 GCACATGAGTCTCTAAAGGTTGGGGCTTACCCCAAGACCTGCTCTACATGATATG 2653
2753 AAGAACTGGAGAGGATCTCTAGTCTTGGCCATTCAGGAGACCTTCCAGAAACACAGTG 2812
2654 AAGAACTGGAGAGGATCTCTAGTCTTGGCCATTCAGGAGACCTTCCAGAAACACAGTG 2713
2813 TTTTCAAGAGCCCTTAAAGACCTTCTGCTGCTCCAGGACCTTATGTAATGAACACCAACA 2872
2714 TTTTCAAGAGCCCTTAAAGACCTTCTGCTGCTCCAGGACCTTATGTAATGAACACCAACA 2773
2873 TCTAAACAATCATATGCTAAACATGCCACTCTCGTGAACCTCACTCTGAAAGTCCCGCTT 2932

2774 TCTAAACAATCATATGCTAACTCCACTCTCTGAAAACCTCCACTCTGAAGTCCCGCTT 2833
2933 GGACACCAACACTCCCTTCTCCAGGATCATGAGGATCTGCTCCCTCTGCTTCCCTT 2992
2834 GGACACCAACACTCCCTTCTCCAGGATCATGAGGATCTGCTCCCTCTGCTTCCCTT 2893
2993 ACCAGTCTGACCGCTGACTCCAGAGTCTTCTGAGTCTGAGTCTGACACCTTCTTCT 3052
2894 ACCAGTCTGACCGCTGACTCCAGAGTCTTCTGAGTCTGAGTCTGACACCTTCTTCT 2953
3053 TGCTTCAGTTGGGCGACACTCTGATCCCTTCTGCTGCGAGAAATGGCAGGGTAAATCTG 3112
2954 TGCTTCAGTTGGGCGACACTCTGATCCCTTCTGCTGCGAGAAATGGCAGGGTAAATCTG 3013
3113 AGCCTTCTTCACTCTTTCACCTGAGTCCCTTCACTCTCCCTCTGCTTCTTCTTCT 3172
3014 AGCCTTCTTCACTCTTTCACCTGAGTCCCTTCACTCTCCCTCTGCTTCTTCTTCT 3073
3173 GTTTCAGTTGGGCGACACTCTGATCCCTTCTGCTGCGAGAAATGGTAAATATAAAGG 3232
3074 GTTTCAGTTGGGCGACACTCTGATCCCTTCTGCTGCGAGAAATGGTAAATATAAAGG 3133
3233 CTTA 3236
3134 CTTA 3137

RESULT 4
AB029394 3252 bp mRNA linear PRI 06-JAN-2001
LOCUS Homo sapiens mRNA for SEMB, complete cds.
DEFINITION
ACCESSION AB029394
VERSION AB029394.1 GI:12248381
KEYWORDS SEMB.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3252)
AUTHORS Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
Miyajima,N. and Saito,T.
TITLE Human semaphorin B
JOURNAL Published Only in DataBase (2001)
REFERENCE
2 (bases 1 to 3252)
AUTHORS Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
Miyajima,N. and Saito,T.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Toshiyuki Saito, National Institute of
Radiological Sciences, Genome Research Group, Inage-ku Anagawa
4-9-1, Chiba, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp,
Tel:81-43-201-3135, Fax:81-43-251-9818)

FEATURES
source

1. 3252
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..3252
/gene="SEMB"
209..2497
/codon_start=1
/product="SEMB"
/protein_id="BAB20087.1"
/db_xref="GI:12248382"

gene

CDS

/translation="MALPALGLDPLWLLGLFLFOLLQLLLPTTAGGGGGPMRVRV
YAGDERALSEFFHQKQDEFDTLLSGDNTLVYVAREAILAQIDQFGRKKNMIP
WPASDRKSECFKAKKSNETQCFNFIYLVSYNTHLYTCTGFAPCFACFIEQDSY
LLPTSEKVMKGGQSPFPAHKHTAVLVDMGLYSGTMNPLGSEPTLMETLGSQPV
KTNFLWLHDAFVAAPSTQVYFFFEETASEFDFERLHTRVARVCKNDVGG
KLLQKWTFLKALQLSAPSGSCPTSSATRSPPILPOLPTSTOSSPPSGVGGT
RSSAVCAFLDIERVFKPKFKELKETSRTTYRGPTNRPQSCSVGSSDKALTF
MDHFLMDEQVLLDIERVFKPKFKELKETSRTTYRGPTNRPQSCSVGSSDKALTF
GDSSAHLVEIEQLFDPDPVNLQLAPTQGAFLVFGSGGVRVRFRANCSTYESCVDCV

LARDPHANDPBRSTCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPOSRII
KEVLAVPNSILEPCHLSALASYWHSHPAAVPEASSTVYNGSLIIVQDGGGLYQ
CWATENGFSVPVLSYVDSQDPTLADPELAGI PREHVKVPLTRVSGGAALAAQOSYV
PHFVTVLFLVLSGALIILVASPLRLARNGKVGCCETLRPEKAPLSREHQLQSP
KECRTSASDVDDADNCLGTEVA"

ORIGIN

Query Match 86.8%; Score 3043.8; DB 9; Length 3252;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3077; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

QY	151	GTGGCTGTTCAAGGGTATGTGAGAGCTCCCTCGTGACAGTCTGTGGCTGAGCATGGCC	210
DB	156	GTGCCGGGTGCCTGTTCCCGAGACCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCC	215
QY	211	TCCAGCCCTGGGCTGGACCCCTGAGACCTCTCTGGGCTTTTCTCTTCCAACTGCTTC	270
DB	216	TCCAGCCCTGGGCTGGACCCCTGAGACCTCTCTGGGCTTTTCTCTTCCAACTGCTTC	275
QY	271	AGCTGCTGCTCCGAGACACCGCGGGGAGGCGGAGGCGGCCCATGCCCAGGGTCA	330
DB	276	AGCTGCTGCTCCGAGACACCGCGGGGAGGCGGAGGCGGCCCATGCCCAGGGTCA	335
QY	331	GATACTATGAGGGGATGAACGTAGGCACTTAGCTTCTTCCACAGAGGGCTCCAGG	390
DB	336	GATACTATGAGGGGATGAACGTAGGCACTTAGCTTCTTCCACAGAGGGCTCCAGG	395
QY	391	ATTTTGACACTCTGCTCCTGAGTGGTGTAGTGAATACTCTACGTGGGGCTCGAGAG	450
DB	396	ATTTTGACACTCTGCTCCTGAGTGGTGTAGTGAATACTCTACGTGGGGCTCGAGAG	455
QY	451	CCATTCTGGCTTGGATATCCAGGATCCAGGGTCCCGAGGCTAAAGAAATGATACCGT	510
DB	456	CCATTCTGGCTTGGATATCCAGGATCCAGGGTCCCGAGGCTAAAGAAATGATACCGT	515
QY	511	GGCAGCAGTGCAGAGAAAGTGAATGCTGCTTAAGAGAGAGCATGAGACAC	570
DB	516	GGCAGCAGTGCAGAGAAAGTGAATGCTGCTTAAGAGAGAGCATGAGACAC	575
QY	571	AGTGTTCACACTTCACTCCGTGCTGCTTCTTACAAATGTCAACCTCTCTACACCTGG	630
DB	576	AGTGTTCACACTTCACTCCGTGCTGCTTCTTACAAATGTCAACCTCTCTACACCTGG	635
QY	631	GCACCTTGGCTTCCAGCCCTGCTGTACCTTCAATGAATCTTGAAGTCTTACCTGTTCG	690
DB	636	GCACCTTGGCTTCCAGCCCTGCTGTACCTTCAATGAATCTTGAAGTCTTACCTGTTCG	695
QY	691	CCATCTCGAGGACAAGGTCACTGGAGGAAAGGCCAAAGCCCTTTGACCCCGCTCACA	750
DB	696	CCATCTCGAGGACAAGGTCACTGGAGGAAAGGCCAAAGCCCTTTGACCCCGCTCACA	755
QY	751	AGCATAGGCTGTCTTGGTGGATGGATGCTCTATTCTGTACTATGAACAATCTCTGG	810
DB	756	AGCATAGGCTGTCTTGGTGGATGGATGCTCTATTCTGTACTATGAACAATCTCTGG	815
QY	811	GCAGTAGGCCCATCTCTGATGCGACACTGGGATCCCGAGCTGTCTTCAAGACCGCAACT	870
DB	816	GCAGTAGGCCCATCTCTGATGCGACACTGGGATCCCGAGCTGTCTTCAAGACCGCAACT	875
QY	871	TCCTCCGCTGGCTGATCATGAGCTCTCTTGTGGAGGCCATCCCTTGAACCGAGGTGG	930
DB	876	TCCTCCGCTGGCTGATCATGAGCTCTCTTGTGGAGGCCATCCCTTGAACCGAGGTGG	935
QY	931	TCTACTTCTTCTTCGAGGACACGACGAGTTCCTTCTTGTGAGAGGCTCCACACAT	990
DB	936	TCTACTTCTTCTTCGAGGACACGACGAGTTCCTTCTTGTGAGAGGCTCCACACAT	995
QY	991	CGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGGGCGCGGAAAGCTGCTGCAAGAAAT	1050
DB	996	CGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGGGCGCGGAAAGCTGCTGCAAGAAAT	1055
QY	1051	GGACCACTTCTGAGGCGCCAGCTG--CTCTGACCCAGCGGCGAGCTGCCCTTCAA	1108

DB	1056	GGACCACTTCTGTAAGGCCACAGCTCTCTCTGCAACCCAGCCGCGGGCAGCTGCCCTTCAA	1115
QY	1109	CGTCATCCGCGCACGCGCTCTGCTCCCGCGCGGATTTCCACACAGCTCCCGACATCTACGC	1168
DB	1116	CGTCATCCGCGCACGCGCTCTGCTCCCGCGCGGATTTCCACACAGCTCCCGACATCTACGC	1175
QY	1169	AGTCTTCACTCCAGT--GGCAGGTTGGCGGACAGGAGCTCTCGGGTTTGGCTTCT	1227
DB	1176	AGTCTTCACTCCAGTGGGCGAGGTTGGCGGACCCAGGAGCTCTCGGGTTTGGCTTCT	1235
QY	1228	CTCTCTTGGACATTTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTTGAACAAAGAACTT	1287
DB	1236	CTCTCTTGGACATTTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTTGAACAAAGAACTT	1295
QY	1288	CACCTGGAATCTTATAGGGGCTCGAGACCAACCCCGCGGACAGGAGTTGCTCAGTGG	1347
DB	1296	CACCTGGAATCTTATAGGGGCTCGAGACCAACCCCGCGGACAGGAGTTGCTCAGTGG	1355
QY	1348	GCCCTCTCTGATAAGGCCCTGACCTTCATGAAGGACCAATTTCTGATGATGAGCAAG	1407
DB	1356	GCCCTCTCTGATAAGGCCCTGACCTTCATGAAGGACCAATTTCTGATGATGAGCAAG	1415
QY	1408	TGTTGGGGAACGCGCTCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAGTGAGA	1467
DB	1416	TGTTGGGGAACGCGCTCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAGTGAGA	1475
QY	1468	CAGCCCAAGGGCTTGTATGGGCACAGCCATCTTGTCTATGTACCTGGGAAACCAACACAGGGT	1527
DB	1476	CAGCCCAAGGGCTTGTATGGGCACAGCCATCTTGTCTATGTACCTGGGAAACCAACACAGGGT	1535
QY	1528	CGCTCCAAGGGCTTGTATGGGCACAGCCATCTTGTCTATGTACCTGGGAAACCAACACAGGGT	1587
DB	1536	CGCTCCAAGGGCTTGTATGGGCACAGCCATCTTGTCTATGTACCTGGGAAACCAACACAGGGT	1595
QY	1588	TGTTCCCTGACCCCTGTTTCGCAACCTGTCAGCTGGGCCCCCACCACCGAGTGCAGTGT	1647
DB	1596	TGTTCCCTGACCCCTGTTTCGCAACCTGTCAGCTGGGCCCCCACCACCGAGTGCAGTGT	1655
QY	1648	TGTTAGGCTTCTCAGGAGGTGTCTGGAGGTGCCCGAGCAACCTGTAGTGTCTATGAGA	1707
DB	1656	TGTTAGGCTTCTCAGGAGGTGTCTGGAGGTGCCCGAGCAACCTGTAGTGTCTATGAGA	1715
QY	1708	GCTGTGTGACTGTCTTCCCGGACCCCACTGTGTGCTGGGACCTCTGAGTGCAGTGCAGAA	1767
DB	1716	GCTGTGTGACTGTCTTCCCGGACCCCACTGTGTGCTGGGACCTCTGAGTGCAGTGCAGAA	1775
QY	1768	CCTGTGTCTCTCTGTGCCCCCAACTGAACTCTGGAAGCAGGACATGAGCGGGGA	1827
DB	1776	CCTGTGTCTCTCTGTGCCCCCAACTGAACTCTGGAAGCAGGACATGAGCGGGGA	1835
QY	1828	ACCCAGAGTGGGACATGTGCCAGTGGCCCCCATGAGCAGGAGCTTCCGCTCAGAGCGCC	1887
DB	1836	ACCCAGAGTGGGACATGTGCCAGTGGCCCCCATGAGCAGGAGCTTCCGCTCAGAGCGCC	1895
QY	1888	CGCAAAATCATTAAGAAAGTCTGTGCTCTCCCTAACTCCATCTCTGGAGCTCCCTGCCCCC	1947
DB	1896	CGCAAAATCATTAAGAAAGTCTGTGCTCTCCCACTCCATCTCTGGAGCTCCCTGCCCCC	1955
QY	1948	ACCTGTGAGCTTGGCTCTTATTTTGGAGTCTATGGCCGAGCAGCAGCTCCGAGAGCT	2007
DB	1956	ACCTGTGAGCTTGGCTCTTATTTTGGAGTCTATGGCCGAGCAGCAGCTCCGAGAGCT	2015
QY	2008	CTTCCACTGTCTACAATGGCTCTCTTGTGTGATGTGAGGAGTGGAGTGGGGGTCTCT	2067
DB	2016	CTTCCACTGTCTACAATGGCTCTCTTGTGTGATGTGAGGAGTGGAGTGGGGGTCTCT	2075
QY	2068	ACAGTGTCTGGGAACTGAGAAATGGCTTTTCTATACCTCTGTGATCTCTACTTGGTGACA	2127
DB	2076	ACAGTGTCTGGGAACTGAGAAATGGCTTTTCTATACCTCTGTGATCTCTACTTGGTGACA	2135
QY	2128	GCCAGGACACAGCTGCGCTGATCTGAACTTGGCAGGACATCCCCCGGGAGCATGTGA	2187
DB	2136	GCCAGGACACAGCTGCGCTGATCTGAACTTGGCAGGACATCCCCCGGGAGCATGTGA	2195

2188	QY	AGTCCCGTTGA	CCAGGGTCAGTGGTGGGGCCGCGCCCTGGCTGCCCAAGCACTCTACTGGC	2247
2196	DB	AGGTCCCGTTGAC	CCAGGGTCAGTGGTGGGGCCGCGCCCTGGCTGCCCAAGCACTCTACTGGC	2255
2248	QY	CCCACTTTGTCACT	GTGCACATGTCCTCTTTTGGCTTTAGTGCTTTTTCAGGAGCCCTCATCATCC	2307
2256	DB	CCCACTTTGTCACT	GTGCACATGTCCTCTTTTGGCTTTAGTGCTTTTTCAGGAGCCCTCATCATCC	2315
2308	QY	TCGTGGCCCTCCC	CAATTGAGAGCACTCCGGGCTCGGGCAAGGTTTCAAGGCTGTGAGACCC	2367
2316	DB	TCGTGGCCCTCCC	CAATTGAGAGCACTCCGGGCTCGGGCAAGGTTTCAAGGCTGTGAGACCC	2375
2368	QY	TGCGCCCTCGGG	AGAGGCCCGGTTTAAGCAGAGAGCAACACCTTCCAGTCTCCCAAGGAAT	2427
2376	DB	TGCGCCCTCGGG	AGAGGCCCGGTTTAAGCAGAGAGCAACACCTTCCAGTCTCCCAAGGAAT	2435
2428	QY	GCAGGACCTCTGC	CAGTGATGTGGACGCTGACAACTCCCTAGGCACTGAGGTAGCTT	2487
2436	DB	GCAGGACCTCTGC	CAGTGATGTGGACGCTGACAACTCCCTAGGCACTGAGGTAGCTT	2495
2488	QY	AAACTCTAGGCA	CAGGCCGGGGCTGGTCGAGGCACTCGGCCCATGCTGGCTGGGGCGCC	2547
2496	DB	AAACTCTAGGCA	CAGGCCGGGGCTGGTCGAGGCACTCGGCCCATGCTGGCTGGGGCGCC	2555
2548	QY	CAAGCAGAGCCCT	GACTAGGATGACAGCAGCAAAAAGACCACTTTCTCTCCCTGAGAGG	2607
2556	DB	CAAGCAGAGCCCT	GACTAGGATGACAGCAGCAAAAAGACCACTTTCTCTCCCTGAGAGG	2615
2608	QY	AGCTTCTGCTACT	CTGTGCATCACTGATGACACTCAGCAGGGTGATGACACGACTTGCCT	2667
2616	DB	AGCTTCTGCTACT	CTGTGCATCACTGATGACACTCAGCAGGGTGATGACACGACTTGCCT	2675
2668	QY	CCCCATGGGACT	CCCCCTTACCAAGACATGAGCTCTTAAACAGGGTGGGGGCTACCCC	2727
2676	DB	CCCCATGGGACT	CCCCCTTACCBAGACATGAGCTCTTAAACAGGGTGGGGGCTACCCC	2735
2728	QY	CAGACCTGTCTTA	CACTGATATTGAAGAACCTGGAGAGGATTCCTTCAGTTCTTGGCCATT	2787
2736	DB	CAGACCTGTCTTA	CACTGATATTGAAGAACCTGGAGAGGATTCCTTCAGTTCTTGGCCATT	2795
2788	QY	CCAGGGACCTCTC	AGAAACAACAGTGTTTCAAGAGACCTTAAAAAACCCTGCTGTCCGAGG	2847
2796	DB	CCAGGGACCTCTC	AGAAACAACAGTGTTTCAAGAGACCTTAAAAAACCCTGCTGTCCGAGG	2855
2848	QY	ACCTATGGTAAT	GAAACCAAAACATCTAAACAATCATATGCTAAACATGCACTCTCGGA	2907
2856	DB	ACCTATGGTAAT	GAAACCAAAACATCTAAACAATCATATGCTAAACATGCACTCTCGGA	2915
2908	QY	AACTCCACTCTGA	AGCTGCGGCTTTTGACACCAACACTCCCTTCTCCAGGGTCAAGCAG	2967
2916	DB	AACTCCACTCTGA	AGCTGCGGCTTTTGACACCAACACTCCCTTCTCCAGGGTCAAGCAG	2975
2968	QY	GGATCTGCTCCCT	CTCTTCCCTTACCAGTGTGCAACCGCTGACTCCCAAGGAAGTCTTC	3027
2976	DB	GGATCTGCTCCCT	CTCTTCCCTTACCAGTGTGCAACCGCTGACTCCCAAGGAAGTCTTC	3035
3028	QY	CCCTGAAGTCTGA	CCACTTCTTCTTCTTTCAGTTGGGGCAGACTCTGATCCCTCTGTC	3087
3036	DB	CCCTGAAGTCTGA	CCACTTCTTCTTCTTTCAGTTGGGGCAGACTCTGATCCCTCTGTC	3095
3088	QY	CTGCGAAGATGGC	AGGGGTAATCTGAGCCCTTCTTCACTCTCTTTACCTAGCTGACCCCTT	3147
3096	DB	CTGCGAAGATGGC	AGGGGTAATCTGAGCCCTTCTTCACTCTCTTTACCTAGCTGACCCCTT	3155
3148	QY	CACCTCTCCCGCT	CCCCCTTTTCTTGTGGGATTCAGAAACTGCTTCTCAGAGACTG	3207
3156	DB	CACCTCTCCCGCT	CCCCCTTTTCTTGTGGGATTCAGAAACTGCTTCTCAGAGACTG	3215
3208	QY	TTTATTTTTTATTA	AAAAAATAAAGGCTTATGTATGAT	3244
3216	DB	TTTATTTTTTATTA	AAAAAATAAAGGCTTATGTATGAT	3252

Db 258 GCTCCAGGATTTTGACATCTCTCTCTGAGTGGTATGAAATATCTCTACGTGGGG 317
Qy 442 CTCGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGTCCCGAGCTAAAGAAACA 501
Db 318 CTCGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGTCCCGAGCTAAAGAAACA 377
Qy 502 TGAATCCGTGGCCAGCCAGTGCAGAAAGAGTGAATGTGCTTTAAGAAAGAGAGCA 561
Db 378 TGATACCGTGGCCAGCCAGTGCAGAAAGAGTGAATGTGCTTTAAGAAAGAGAGCA 437
Qy 562 ATGAGACACAGTGTTCATCTTCATCCGTGTCTCTGTTTCTTACAAATGTCACCCATCTCT 621
Db 438 ATGAGACACAGTGTTCATCTTCATCCGTGTCTCTGTTTCTTACAAATGTCACCCATCTCT 497
Qy 622 ACACCTGGCCAGCTTCGCTTCAGCCCTGCTTGTACCTTCATTTGAACTTCAGATTCCT 681
Db 498 ACACCTGGCCAGCTTCGCTTCAGCCCTGCTTGTACCTTCATTTGAACTTCAGATTCCT 557
Qy 682 ACCTGTTGCCCATCTCGAGGACAAAGTTCATGGAGGAAAGGCCAAAGCCCTTTGACC 741
Db 558 ACCTGTTGCCCATCTCGAGGACAAAGTTCATGGAGGAAAGGCCAAAGCCCTTTGACC 617
Qy 742 CCCTCACAGCATACGGCTCTCTTGTGTGATGGATGCTTATTTCTGTAATATGAACA 801
Db 618 CCGCTCACAGCATACGGCTCTCTTGTGTGATGGATGCTTATTTCTGTAATATGAACA 677
Qy 802 ACTTCTCGGCGAGTGAAGCCCATCTGATGGGCACACTGGGATCCAGCCTGTCTCAAGA 861
Db 678 ACTTCTCGGCGAGTGAAGCCCATCTGATGGGCACACTGGGATCCAGCCTGTCTCAAGA 737
Qy 862 CCGACAACTTCTCGGCGAGTGAAGCCCATCTGATGGGCACACTGGGATCCAGCCTGTCTCA 921
Db 738 CCGACAACTTCTCGGCGAGTGAAGCCCATCTGATGGGCACACTGGGATCCAGCCTGTCTCA 797
Qy 922 CCGAGGTGCTACTCTTCTCGAGGACAGCCAGGATTTGACTTCTTTGAGAGGC 981
Db 798 CCGAGGTGCTACTCTTCTCGAGGACAGCCAGGATTTGACTTCTTTGAGAGGC 857
Qy 982 TCACACATCCGGGTGGCTAGAGTCTGGAAGATGACGTGGCGCGGAAAGCTCTGCG 1041
Db 858 TCACACATCCGGGTGGCTAGAGTCTGGAAGATGACGTGGCGCGGAAAGCTCTGCG 917
Qy 1042 AGAAGAGTGAAGCCATCTCTGAGGCCAGCTGTCTGACCCAGCCGGGCGAGCTGC 1101
Db 918 AGAAGAGTGAAGCCATCTCTGAGGCCAGCTGTCTGACCCAGCCGGGCGAGCTGC 977
Qy 1102 CTTTCAACGTATCCGCCACCGCGTCTGCTCCCGCGGATTCCTCCACAGCTCCCAACA 1161
Db 978 CTTTCAACGTATCCGCCACCGCGTCTGCTCCCGCGGATTCCTCCACAGCTCCCAACA 1037
Qy 1162 TCTACGAGTCTTACCTCCAGTGGCAGGTGGCGGACAGAGCTCTGCGGTTTGTG 1221
Db 1038 TCTACGAGTCTTACCTCCAGTGGCAGGTGGCGGACAGAGCTCTGCGGTTTGTG 1097
Qy 1222 CTTTCTCTCTTTGGAATTAAGCTGTCTTTAAGGGAAATACAAAGAGTTGAACAAAG 1281
Db 1098 CTTTCTCTCTTTGGAATTAAGCTGTCTTTAAGGGAAATACAAAGAGTTGAACAAAG 1157
Qy 1282 AATCTTCAAGTGAATTAAGGGCCCTGAGACCCAGCCCGGCGAGGAGTGTCT 1341
Db 1158 AATCTTCAAGTGAATTAAGGGCCCTGAGACCCAGCCCGGCGAGGAGTGTCT 1217
Qy 1342 CAGTGGGCCCCCTCTCTGATAAGSCCTGACCTTTCATGAAGGACCAATTCCTGATGATG 1401
Db 1218 YARTGGGCCCCCTCTCTGATAAGSCCTGACCTTTCATGAAGGACCAATTCCTGATGATG 1277
Qy 1402 AGCAAGTGGGGAAGCCCTCTGATGAATCTGCGTGGAGTATACAGGCTTGAG 1461
Db 1278 AGCAAGTGGGGAAGCCCTCTGATGAATCTGCGTGGAGTATACAGGCTTGAG 1337
Qy 1462 TGGAGACAGCCAGGCGCTTGATGGGACAGCCATCTTGTCTATGTACCTGGGAAACCA 1521

Db 1338 TGGAGACAGCCAGGCGCTTGATGGGACACAGCCATCTTGTCTATGTACCTGGGAACCA 1397
Qy 1522 CAGGGTCTCTCCACAGAGCTGTGTAGTGGGACAGAGTGTCTCATCTGTGTGAAGAGA 1581
Db 1398 CAGGGTCTCTCCACAGAGCTGTGTAGTGGGACAGAGTGTCTCATCTGTGTGAAGAGA 1457
Qy 1582 TTCAAGCTGTTTCCCTGACCTCTGAACCTGTTCCGAACCTGCACTGTGCTGGGACCCCA 1641
Db 1458 TTCAAGCTGTTTCCCTGACCTCTGAACCTGTTCCGAACCTGCACTGTGCTGGGACCCCA 1517
Qy 1642 CAGTGTGTTAGGCTTCTCAGAGAGTGTCTGAGAGGTGCTCCGAGCCCACTGTAGTGTCT 1701
Db 1518 CAGTGTGTTAGGCTTCTCAGAGAGTGTCTGAGAGGTGCTCCGAGCCCACTGTAGTGTCT 1577
Qy 1702 ATGAGAGCTGTGTGAGTGTCTGCTTCCCGGAGACCCCACTGTGCTGGGACCCCTGAGT 1761
Db 1578 ATGAGAGCTGTGTGAGTGTCTGCTTCCCGGAGACCCCACTGTGCTGGGACCCCTGAGT 1637
Qy 1762 CCGGAACTGTTGCTCTCTGCTGCTCCCGGAGACCCCACTGTGCTGGGACCCCTGAGT 1821
Db 1638 CCGGAACTGTTGCTCTCTGCTGCTCCCGGAGACCCCACTGTGCTGGGACCCCTGAGT 1697
Qy 1822 GGGGGAACCCAGAGTGGGACATGTGCCAGTGGGCCCATGAGCAGGAGCTTTCGGCTCAGA 1881
Db 1698 GGGGGAACCCAGAGTGGGACATGTGCCAGTGGGCCCATGAGCAGGAGCTTTCGGCTCAGA 1757
Qy 1882 GCCGCCCGGAAATCATTAAAGAGTCTGTGCTGTCTCTTAACTCTGCTGGAGCTCCCT 1941
Db 1758 GCCGCCCGGAAATCATTAAAGAGTCTGTGCTGTCTCTTAACTCTGCTGGAGCTCCCT 1817
Qy 1942 GCCGCCCGGAAATCATTAAAGAGTCTGTGCTGTCTCTTAACTCTGCTGGAGCTCCCT 2001
Db 1818 GCCGCCCGGAAATCATTAAAGAGTCTGTGCTGTCTCTTAACTCTGCTGGAGCTCCCT 1877
Qy 2002 AAGCTCTTTCACATGTCTACAAATGGCTCCCTTGTGCTGATGTGAGTGGAGTGGG 2061
Db 1878 AAGCTCTTTCACATGTCTACAAATGGCTCCCTTGTGCTGATGTGAGTGGAGTGGG 1937
Qy 2062 GTCTCTACAGTGTGGGACACTGAGAAATGGCTTTTCTATCCCTGTGATCTCTTACTGGG 2121
Db 1938 GTCTCTACAGTGTGGGACACTGAGAAATGGCTTTTCTATCCCTGTGATCTCTTACTGGG 1997
Qy 2122 TGGACAGCAGGACAGACCCCTGGATCTCTGAACTCTGAACTGGCAGGAGCTCCCGGAGC 2181
Db 1998 TGGACAGCAGGACAGACCCCTGGATCTCTGAACTCTGAACTGGCAGGAGCTCCCGGAGC 2057
Qy 2182 ATGTGAAGTTCCTGTTGACAGGCTCAGTGTGGGGCGGCTGGCTGGCTGGCTGGCTGGCT 2241
Db 2058 ATGTGAAGTTCCTGTTGACAGGCTCAGTGTGGGGCGGCTGGCTGGCTGGCTGGCTGGCT 2117
Qy 2242 ACTGGCCCCACTTGTCTCACTGTCTCTTGTGCTTTAGTGTCTTTTCAAGGAGCCCTCA 2301
Db 2118 ACTGGCCCCACTTGTCTCACTGTCTCTTGTGCTTTAGTGTCTTTTCAAGGAGCCCTCA 2177
Qy 2302 TCATCTCTGTGCTCTCCCATTTAGAGACACTCGGGCTCGGGGACAGGTTTCAGGCTGTG 2361
Db 2178 TCATCTCTGTGCTCTCCCATTTAGAGACACTCGGGCTCGGGGACAGGTTTCAGGCTGTG 2237
Qy 2362 AGACCTCGGCTCTGGGAGAGCCCGCTTAAAGCAGAGAGCAACACTTCCAGTCTCCCA 2421
Db 2238 AGACCTCGGCTCTGGGAGAGCCCGCTTAAAGCAGAGAGCAACACTTCCAGTCTCCCA 2297
Qy 2422 AGGAATGAGAGACCTCTGCGAGTGTGAGAGCTGAGCACTGCTGCTAGGAGCTGAGG 2481
Db 2298 AGGAATGAGAGACCTCTGCGAGTGTGAGAGCTGAGCACTGCTGCTAGGAGCTGAGG 2357
Qy 2482 TAGCTTAACTCTTAGGACAGGCGGGCTGCGGTGAGGCACTGCTGCTAGGCTGG 2541
Db 2358 TAGCTTAACTCTTAGGACAGGCGGGCTGCGGTGAGGCACTGCTGCTAGGCTGG 2417
Qy 2542 GCGGCCCAAGCAGACCTGTAGATGACAGCAGCAGCAAAAGACCACTTCTTCCCT 2601
Db 2418 GCGGCCCAAGCAGACCTGTAGATGACAGCAGCAGCAAAAGACCACTTCTTCCCT 2477

```
QY 2602 GAGAGGAGCTTCTGCTACTCTGCTACATGATGACATCAGAGGATGATGACAGCAGT 2661
Db 2478 GAGAGGAGCTTCTGCTACTCTGCTACTCTGATGACATCAGAGGATGATGACAGCAGT 2537
QY 2662 CTGCTCTCCCTATGAGGACTCCCTTCTACCAAGCAGCATGAGCTCTCTAACAGGGTGGGGGC 2721
Db 2538 CTGCTCTCCCTATGAGGACTCCCTTCTACCAAGCAGCATGAGCTCTCTAACAGGGTGGGGGC 2597
QY 2722 TACCCCCAGAGCTGCTCTCTACATGATATGAGAGACCTGAGAGGATCCTTCACTGCTG 2781
Db 2598 TACCCCCAGAGCTGCTCTCTACATGATATGAGAGACCTGAGAGGATCCTTCACTGCTG 2657
QY 2782 GCCATTCCAGGAGACCTCCAGAAACACAGTGTCTTCAAGAGACCTTAAAAAACCCTGCTGT 2841
Db 2658 GCCATTCCAGGAGACCTCCAGAAACACAGTGTCTTCAAGAGACCTTAAAAAACCCTGCTGT 2717
QY 2842 CCAGAGACCTATGATGATGAAACACAAACATCTTAAACATATGATGATGATGATGATGAT 2901
Db 2718 CCAGAGACCTATGATGATGAAACACAAACATCTTAAACATATGATGATGATGATGATGAT 2777
QY 2902 CTGGAACCTCCACTCTGAGCTGCGCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2961
Db 2778 CTGGAACCTCCACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2837
QY 2962 ATGAGGAGATGCTGCTCTCTGCTCTGCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3021
Db 2838 ATGAGGAGATGCTGCTCTCTGCTCTGCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2897
QY 3022 GTCTTCTCCCTGAGTCTGAGTCTGCTCTCTGCTCTGCTTCTGAGTGTGAGTGTGAGTGT 3081
Db 2898 GTCTTCTCCCTGAGTCTGAGTCTGCTCTCTGCTCTGCTTCTGAGTGTGAGTGTGAGTGT 2957
QY 3082 TCTGCTCTGAGTCTGAGTCTGCTCTCTGCTCTGCTTCTGAGTGTGAGTGTGAGTGTGAGT 3141
Db 2958 TCTGCTCTGAGTCTGAGTCTGCTCTCTGCTCTGCTTCTGAGTGTGAGTGTGAGTGTGAGT 3017
QY 3142 CCCCTTCACTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCT 3201
Db 3018 CCCCTTCACTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCT 3077
QY 3202 AGACTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3236
Db 3078 AGACTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3112

RESULT 6
HSM807023
LOCUS
DEFINITION Homo sapiens mRNA; cDNA DKFZp686D04248 (from clone DKFZp686D04248);
complete cds.
ACCESSION BX640891
VERSION BX640891.1 GI:34365195
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3151)
Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.,
The German Human cDNA Consortium
Direct Submission
Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp686D04248) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
```

```
at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
1..3151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="1q22"
/clone="DKFZp686D04248"
/issue_type="human salivary gland"
/clone_lib="686 (synonym: hccc3). Vector pSport1_sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
1..3151
/gene="DKFZp686D04248"
217..2388
/gene="DKFZp686D04248"
/note="Semaphorin B, differentially spliced"
/codon_start=1
/product="hypothetical protein"
/protein_id="CA45942.1"
/db_xref="GI:34365196"
/translation="MPRVRYAGDERRALSFFHQKGLQDFDTLLSGDGNLTLYVGARE
AILALDIQDPGVRLKNMIPASDRKKSECAFKKSNETQCFNFRVLVSYNVTHLY
TGTFAPFACFTFELQDSYLLPISEDKVMKGQSPDPAPKHTAVLVDGMLYSQTM
NPLSEPIIMTLGSPQVILKNDVGGKLLQKWTTLKRAQLCTQPGQLPFPNIRHVALLPADS
FRLHTSRVARKTKNDVGGKLLQKWTTLKRAQLCTQPGQLPFPNIRHVALLPADS
PTAHTYAVFTSQWGTGTRSAVCAFLSDIERVFKGKYLKELNKTSTRTYRGDET
NRPFGSCVSPSSKALTFMKDFLMDQVGTPLLVKSGVETBLATVTAQGLDGH
HLVMTGTPGSLHRAVSGDSSAHLVERIQLPDPPEPVRLQLAPTQCAVFGSGG
WVRPRANGSVYECVCLARDPHCAVMDPESTCCLLSAPNLKQDMQMERGNPEWA
CAGPMRSRLRQSSPQIIEVLAVPNSIIELEPCPHLSALASVYMSHSGPAAYPEASST
VNGSLLLVLDQVGGGLQCAWTENGFSYFVSYVSDQDTLADLPDLGAGIPIREHVK
VPLTRVSGAALAAQSSYMFHFVTITVLPALVLSGALILVILASPLRALRARKVQGCC
TLRPGEKAPLSREQLHQSPEKRTSASVDVADNDCNLGTEVA"
polyA_signal 3117..3122
polyA_site /gene="DKFZp686D04248"
3134
/gene="DKFZp686D04248"
ORIGIN
Query Match 85.8%; Score 3008.8; DB 9; Length 3151;
Best Local Similarity 96.6%; Pred. NO. 0;
Matches 3127; Conservative 0; Mismatches 2; Indels 107; Gaps 1;
QY 1 GGCTTTGGCATGATGGGCACCTGGAGGGCGGCACCTCCCTTCCAGCCAGGCTGAGCCTTC 60
Db 7 GGCTTTGGCATGATGGGCACCTGGAGGGCGGCACCTCCCTTCCAGCCAGGCTGAGCCTTC 66
QY 61 TGTCCTCTGCTCTGGGGCTTGGGAACCCCTCTTCTTTCTCTGAATGGACCCCTG 120
Db 67 TGTCCTCTGCTCTGGGGCTTGGGAACCCCTCTTCTTTCTCTGAATGGACCCCTG 126
QY 121 CCTAGAAATCCAGACACCGAGTTCCCACTGGCTGCTTCAAGGCTATGTGAGACTCC 180
Db 127 CCTAGAAATCCAGACACCGAGTTTCCCACTGGCTGCTTCAAGGCTATGTGAGACTCC 186
QY 181 CTGCTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTTGGAGCC 240
Db 187 CTGCTGACAGTCTGTGGCTGAGCAT----- 211
QY 241 TCCTGGGCTTTTCTCTTCCAACTGCTTCCAGCTGCTGCTGGCGACGACGACGCGGGGG 300
Db 212 ----- 211
QY 301 GAGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCGAGGGATGAACCTAGGGCAC 360
Db 212 -----GCCCCATGCCCAGGGTCAGATACTATGCGAGGGATGAACCTAGGGCAC 259
QY 361 TTAGCTTTCTTCCACAGAGGGCTCCAGGATTTTGACACTCTGCTCTGAGTGTGATG 420
Db 260 TTAGCTTTCTTCCACAGAGGGCTCCAGGATTTTGACACTCTGCTCTGAGTGTGATG 319
QY 421 GAAATACTCTCTACGTGGGGGCTCGAGGAAGCCATTCTGCGCTTGGATATCCAGGATCCAG 480
```

Db 320 GAAATATCTCTACGTGGGGGCTCGAGAGCCATTTCTGGCCCTTGGATATCCAGGATCCAG 379
Qy 481 GGGTCCCGACGCTAAAGAAATGATACCGTGGCCAGCCAGTGAACAGAAAGAGAGTGAAT 540
Db 380 GGGTCCCGACGCTAAAGAAATGATACCGTGGCCAGCCAGTGAACAGAAAGAGAGTGAAT 439
Qy 541 GTGCTTTTAAAGAAAGAGCAATGAGACACAGTGTTCATTCCTGTCCTGTTT 600
Db 440 GTGCTTTTAAAGAAAGAGCAATGAGACACAGTGTTCATTCCTGTCCTGTTT 499
Qy 601 CTTACAAATGTCACCAATCTCTACACCTCGGGCACTTCGCTTCAGCCCTGCTGTGACCT 660
Db 500 CTTACAAATGTCACCAATCTCTACACCTCGGGCACTTCGCTTCAGCCCTGCTGTGACCT 559
Qy 661 TCAATGAACTTCAAGATTCCTACCTGTTGCCATCTCGAGGACAAAGGTCATGGAGGGAA 720
Db 560 TCAATGAACTTCAAGATTCCTACCTGTTGCCATCTCGAGGACAAAGGTCATGGAGGGAA 619
Qy 721 AAGGCCAAAGCCCTTTGACCCCGCTCACAGCATACGGCTGCTTGGTGGATGGGATGC 780
Db 520 AAGGCCAAAGCCCTTTGACCCCGCTCACAGCATACGGCTGCTTGGTGGATGGGATGC 679
Qy 781 TCTATTCTGTACTATGAACAACTTCTGGGCAGTGAAGCCATTCCTGATGCGCACACTGG 840
Db 680 TCTATTCTGTACTATGAACAACTTCTGGGCAGTGAAGCCATTCCTGATGCGCACACTGG 739
Qy 841 GATCCCAAGCTGTCCCTCAAGACGACAACTTCTCCGCTGGCTGATCATGACGCTCCT 900
Db 740 GATCCCAAGCTGTCCCTCAAGACGACAACTTCTCCGCTGGCTGATCATGACGCTCCT 799
Qy 901 TTGTGGCAGCATCCCTTGACCCAGTCTGTACTTCTTCTGAGGAGACAGCCAGCG 960
Db 800 TTGTGGCAGCATCCCTTGACCCAGTCTGTACTTCTTCTGAGGAGACAGCCAGCG 859
Qy 961 AGTTTGAATCTTTGAGAGCTCCACATCGCGGGTGGCTAGTCTCGAAGATGACG 1020
Db 860 AGTTTGAATCTTTGAGAGCTCCACATCGCGGGTGGCTAGTCTCGAAGATGACG 919
Qy 1021 TGGCGCGGAAAAGCTGCTGAGAGAAAGTGACACCTTCTCTGAAGGCCAGCTGCTCT 1080
Db 920 TGGCGCGGAAAAGCTGCTGAGAGAAAGTGACACCTTCTCTGAAGGCCAGCTGCTCT 979
Qy 1081 GCACCCAGCGGGGACGTGCTTCAAGTCTATCGCCACGCGGTCTGTCTCCCGCGCG 1140
Db 980 GCACCCAGCGGGGACGTGCTTCAAGTCTATCGCCACGCGGTCTGTCTCCCGCGCG 1039
Qy 1141 ATTCTCCACAGCTCCCCACATCTACGAGTCTTCACTTCCAGTGGCAGGTTGGCGGGA 1200
Db 1040 ATTCTCCACAGCTCCCCACATCTACGAGTCTTCACTTCCAGTGGCAGGTTGGCGGGA 1099
Qy 1201 CCAGGAGCTCTGGGGTTGGCTTCTCTCTTGGACATGTAACGTGTCTTAAAGGGGA 1260
Db 1100 CCAGGAGCTCTGGGGTTGGCTTCTCTCTTGGACATGTAACGTGTCTTAAAGGGGA 1159
Qy 1261 AATACAAAGAGTTGAAACAAAGAACTTCAAGTGGGACTTATAGGGGCCCTGAGACCA 1320
Db 1160 AATACAAAGAGTTGAAACAAAGAACTTCAAGTGGGACTTATAGGGGCCCTGAGACCA 1219
Qy 1321 ACCCGCGGACGAGTTGCTAGTGGGCCCTTCTCTGATGAAGGCCCTGACCTTCATGA 1380
Db 1220 ACCCGCGGACGAGTTGCTAGTGGGCCCTTCTCTGATGAAGGCCCTGACCTTCATGA 1279
Qy 1381 AGGACCAATTCCTGATGGATGAGCAAGTGTGGGGACGCGCCCTGTGGTGAATCTGGCG 1440
Db 1280 AGGACCAATTCCTGATGGATGAGCAAGTGTGGGGACGCGCCCTGTGGTGAATCTGGCG 1339
Qy 1441 TGGAGTATACCGGCTTGCATGTGAGACAGCCAGGCCCTTGTAGTGGGACAGCCATCTTG 1500
Db 1340 TGGAGTATACCGGCTTGCATGTGAGACAGCCAGGCCCTTGTAGTGGGACAGCCATCTTG 1399
Qy 1501 TCATGTACCTGGGAAACACACAGGCTCGCTCCACAGGCTGTGGTAAAGTGGGGACAGCA 1560

Db 1400 TCATGTACCTGGGAAACACCCCGGTCGCTCCACAAGGCTGTGGTAAAGTGGGACAGCA 1459
Qy 1561 GTGCTCATCTGCTGGAAGAGATTTCAGCTGTTCCTCTGACCCCTGAAACCTGTTTCGCAACCTGC 1620
Db 1460 GTGCTCATCTGCTGGAAGAGATTTCAGCTGTTCCTCTGACCCCTGAACTGTTTCGCAACCTGC 1519
Qy 1621 AGCTGGCCCCCACCACAGGGTGCAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGAGGGGTGC 1680
Db 1520 AGCTGGCCCCCACCACAGGGTGCAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGAGGGGTGC 1579
Qy 1681 CCCGAGGCCAACTGTAGTGTGTATGAGAGCTGTGTGAGACTGTGTCTTGCCTGGGAGACCCCC 1740
Db 1580 CCCGAGGCCAACTGTAGTGTGTATGAGAGCTGTGTGAGACTGTGTCTTGCCTGGGAGACCCCC 1639
Qy 1741 ACTGTGCTGGGACCCCTGAGTTCCTGAAACCTGTGTGCTCTCTGTGTGCCCCCAACCTGAACT 1800
Db 1640 ACTGTGCTGGGACCCCTGAGTTCCTGAAACCTGTGTGCTCTCTGTGTGCCCCCAACCTGAACT 1699
Qy 1801 CCTGGAAGCAGACATGAGCGGGGAAACCCAGAGTGGGATGTGCGAGTGGCCCCCATGA 1860
Db 1700 CCTGGAAGCAGACATGAGCGGGGAAACCCAGAGTGGGATGTGCGAGTGGCCCCCATGA 1759
Qy 1861 GCAGGAGCTTTCGGCCTCAGAGCGCCCGCCAAATCATTAAGAAAGTCTCTGGCTGTCTCCTA 1920
Db 1760 GCAGGAGCTTTCGGCCTCAGAGCGCCCGCCAAATCATTAAGAAAGTCTCTGGCTGTCTCCTA 1819
Qy 1921 ACTCATCTCGAGCTCCCTGCCCCCAGCTGTGAGCTTGGCTCTTATTATTGAGATC 1980
Db 1820 ACTCATCTCGAGCTCCCTGCCCCCAGCTGTGAGCTTGGCTCTTATTATTGAGATC 1879
Qy 1981 ATGCCCCAGCAGAGTCCCAAGAGCTCTTCCACTGTCTACAATGGCTCCCTCTTGTCTGA 2040
Db 1880 ATGCCCCAGCAGAGTCCCAAGAGCTCTTCCACTGTCTACAATGGCTCCCTCTTGTCTGA 1939
Qy 2041 TAGTGCAAGATGGAAGTTGGGGTCTCTACAGTGTCTGGGCACTGAGAAATGGCTTTTCAT 2100
Db 1940 TAGTGCAAGATGGAAGTTGGGGTCTCTACAGTGTCTGGGCACTGAGAAATGGCTTTTCAT 1999
Qy 2101 ACCCTGTGATCTCTACTGTGGTGGACAGCAGGACCAAGCCCTGGCCCTGATCTCTGAAC 2160
Db 2000 ACCCTGTGATCTCTACTGTGGTGGACAGCAGGACCAAGCCCTGGCCCTGATCTCTGAAC 2059
Qy 2161 TGGCAGGACATCCCGGGGAGCATGTGAAGTCCGCTTGAACAGGTCAGTGGTGGGGCG 2220
Db 2060 TGGCAGGACATCCCGGGGAGCATGTGAAGTCCGCTTGAACAGGTCAGTGGTGGGGCG 2119
Qy 2221 CCCTGGCTGCCAGCAGTCTCTACTGGCCCCCACTTTGTCTACTGTCTCTCTTTCCT 2280
Db 2120 CCCTGGCTGCCAGCAGTCTCTACTGGCCCCCACTTTGTCTACTGTCTCTCTTTCCT 2179
Qy 2281 TAGTGCTTTAGGAGCCCTCATCTCTGTGGCTCCCTCATTTGAGAGCACTCCGGCTC 2340
Db 2180 TAGTGCTTTAGGAGCCCTCATCTCTGTGGCTCCCTCATTTGAGAGCACTCCGGCTC 2239
Qy 2341 GGGGCAAGTTTCAGGGCTGTGAGACCCCTGGGCCCTGGGGAGAGGCCCTTAAAGCAGAG 2400
Db 2240 GGGGCAAGTTTCAGGGCTGTGAGACCCCTGGGCCCTGGGGAGAGGCCCTTAAAGCAGAG 2299
Qy 2401 AGCAACACCTCAGTCTCCAGGAATGACAGACCTCTGCGAGTGTGTGAGCGCTGACA 2460
Db 2300 AGCAACACCTCAGTCTCCAGGAATGACAGACCTCTGCGAGTGTGTGAGCGCTGACA 2359
Qy 2461 ACACTGCTAGGCACTGAGGTAGCTTAAACTCTAGGACAGGCCCGGGGCTGGCGTGCAG 2520
Db 2360 ACACTGCTAGGCACTGAGGTAGCTTAAACTCTAGGACAGGCCCGGGGCTGGCGTGCAG 2419
Qy 2521 GCACTGGCGCATGTGGTGGCGGCCAAGCAAGCCCTGACTAGGATGACAGCAGCAC 2580
Db 2420 GCACTGGCGCATGTGGTGGCGGCCAAGCAAGCCCTGACTAGGATGACAGCAGCAC 2479
Qy 2581 AAAAGACCACTCTCTCCCTGAGAGGAGCTCTGTCTACTCTGATCACTGATGACACTC 2640
Db 2480 AAAAGACCACTCTCTCCCTGAGAGGAGCTCTGTCTACTCTGATCACTGATGACACTC 2539

QY 2641 AGCAGGGTATGTCACAGCAGTCTGCTCCCTATGCGGACTCCCTTCTTACCAAGCACATGA 2700
Db 2540 AGCAGGGTATGTCACAGCAGTCTGCTCCCTATGCGGACTCCCTTCTTACCAAGCACATGA 2599
QY 2701 GCTCTCTAACAGGGTGGGGGCTACCCAGAGCCTCTCTCTACACTGATATTCAAGAACT 2760
Db 2600 GCTCTCTAACAGGGTGGGGGCTACCCAGAGCCTCTCTCTACACTGATATTGAAGAACT 2659
QY 2761 GGAGAGGATCCTTTCAGTCTTGCGCATTCAGGAGACCTCCAGAAACACAGTGTTCAGA 2820
Db 2660 GGAGAGGATCCTTTCAGTCTTGCGCATTCAGGAGACCTCCAGAAACACAGTGTTCAGA 2719
QY 2821 GACCCCTAAAAACCTGCTCTGCTCCAGGACCTCTGCTGATGAACCAACCAACATCTAACA 2880
Db 2720 GACCCCTAAAAACCTGCTCTGCTCCAGGACCTCTGCTGATGAACCAACCAACATCTAACA 2779
QY 2881 ATCATATGCTAACATGCTCCTCTGGAACCTCTGAGCTCCCGCTTTGGACCA 2940
Db 2780 ATCATATGCTAACATGCTCCTGGAACCTCTGAGCTCCCGCTTTGGACCA 2839
QY 2941 ACACTCCCTTCTCCAGGGTCTATGAGGATCTGCTCCCTCTGCTTCCCTTACCAGTCG 3000
Db 2840 ACACTCCCTTCTCCAGGGTCTATGAGGATCTGCTCCCTCTGCTTCCCTTACCAGTCG 2899
QY 3001 TGCACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTTCTTCTTCAG 3060
Db 2900 TGCACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGACCACTTCTTCTTCTTCAG 2959
QY 3061 TTGGGGCAGACTCTGATCCCTTCTCCCTGCGGAGATGCGAGGGTAACTCTGAGCTTCT 3120
Db 2960 TTGGGGCAGACTCTGATCCCTTCTCCCTGCGGAGATGCGAGGGTAACTCTGAGCTTCT 3019
QY 3121 TCACTCTTTACCTAGCTAGCCCTTCACTCTCCCTCTCCCTTCTCTTTTGGG 3180
Db 3020 TCACTCTTTACCTAGCTAGCCCTTCACTCTCCCTCTCCCTTCTCTTTTGGG 3079
QY 3181 ATTCAGAAACCTGCTGTCAGAGCTGTTTATTTTATTAATAATATAGCTTA 3236
Db 3080 ATTCAGAAACCTGCTGTCAGAGCTGTTTATTTTATTAATAATATAGCTTA 3135

RESULT 7
AX746794 2981 bp mRNA linear PAT 20-JUN-2003
LOCUS AX746794
DEFINITION Sequence 319 from Patent EP1308459.
ACCESSION AX746794
VERSION AX746794.1 GI:321311182
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
Full-length cDNA sequences
Patent: EP 1308459-A 319 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
Location/Qualifiers
source 1..2981
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

TITLE
JOURNAL
FEATURES
source 1..2981
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 76.5%; Score 2682.2; DB 6; Length 2981;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 99; Gaps 1;

341 AGGGGATGACGCTAGGGCACTTAGCTTCTTCCACAGAGGGGCTCCAGATTTTGACAC 400
186 AGGGGATGACGCTAGGGCACTTAGCTTCTTCCACAGAGGGGCTCCAGATTTTGACAC 245
401 TCTGCTCTTCTAGTGGTGAATGGAATTAATCTCTACAGTGGGGGCTCGAGAACCCATTCTGGC 460
246 TCTGCTCTTCTAGTGGTGAATGGAATTAATCTCTACAGTGGGGGCTCGAGAACCCATTCTGGC 305
461 CTGAGGATATCCAGGATCCAGGGTCCAGAGCTTAAAGAAACATGATACCGTGGGCCAGCCAG 520
306 CTGAGGATATCCAGGATCCAGGGTCCAGAGCTTAAAGAAACATGATACCGTGGGCCAGCCAG 365
521 TGACAGAAAAAGAGTGAATGTGCTTTTAAAGAAAGAGCAATGAGACAGTGTTCAA 580
366 TGACAGAAAAAGAGTGAATGTGCTTTTAAAGAAAGAGCAATGAG- 411
581 CTTTCATCCGCTGCTCTGCTTCTTACAAATGTACCCATCTCTACACCTGCGGCACCTTCGC 640
412 ----- 411
641 CTTTCAGCCCTGCTTGTACCTTCAATTGAACCTTCAAGATTTCTACCTGTTGCCATCTCGGA 700
412 -----GAACTTCAAGATTTCTACCTGTTGCCATCTCGGA 446
701 GGAAGGTCATCGAGGGAAGGCCAAAGCCCTTTGACCCCGCTCAAGCATACGGC 760
447 GGAAGGTCATCGAGGGAAGGCCAAAGCCCTTTGACCCCGCTCAAGCATACGGC 506
761 TGTCTTGTGGTGGATGCTCTATTTCTGATATATGAACAACTTCTCTGGGAGTGGAGCC 820
507 TGTCTTGTGGTGGATGCTCTATTTCTGATATATGAACAACTTCTCTGGGAGTGGAGCC 566
821 CATCTGATCGGACACTTGGGATCCAGCTTCTTCAAGACCGACAACTTCTCTCGCTG 880
567 CATCTGATCGGACACTTGGGATCCAGCTTCTTCAAGACCGACAACTTCTCTCGCTG 626
881 GCTGATCATGAGCCCTTCTTGTGGCAGCCATCTTCTGACCCAGTCTCTTCTTCTTCTT 940
627 GCTGATCATGAGCCCTTCTTGTGGCAGCCATCTTCTGACCCAGTCTCTTCTTCTTCTT 686
941 CTTTCGAGGACAGCCAGGAGTGTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGC 1000
687 CTTTCGAGGACAGCCAGGAGTGTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGC 746
1001 TAGAGTCTGCAAGATGACGTGGGCGGCGAAAAGCTGCTGCAAGAAAGTGGACCACTT 1060
747 TAGAGTCTGCAAGATGACGTGGGCGGCGAAAAGCTGCTGCAAGAAAGTGGACCACTT 806
1061 CTTGAAAGGCCAGCTGCTCTGCAACCCAGCGGGGAGCTGCTTCAACGCTCATCCGCCA 1120
807 CTTGAAAGGCCAGCTGCTCTGCAACCCAGCGGGGAGCTGCTTCAACGCTCATCCGCCA 866
1121 CGGGTCTCTCCCGCGGATTTCTCCACAGCTCCCACTCTAGCAGTCTTCACTTC 1180
867 CGGGTCTCTCTCCCGCGGATTTCTCCACAGCTCCCACTCTAGCAGTCTTCACTTC 926
1181 CCAGTGGCAGGTTGGCGGGACCAAGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACAT 1240
927 CCAGTGGCAGGTTGGCGGGACCAAGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACAT 986
1241 TGAACGTTCTTTAAGGGGAATACAAAGAGTTGAACAAAGAACTTCAAGCTGGACTAC 1300
987 TGAACGTTCTTTAAGGGGAATACAAAGAGTTGAACAAAGAACTTCAAGCTGGACTAC 1046
1301 TTATAGGGGCCCTGAGACCAACCCCGCGGAGGAGTGTCTAGTGGGCCCTCTCTTGA 1360
1047 TTATAGGGGCCCTGAGACCAACCCCGCGGAGGAGTGTCTAGTGGGCCCTCTCTTGA 1106
1361 TAAGGCCCTGACCTTCAATGAGGACCAATTTCTGATGATGAGCAAGTGTGGGGAGCC 1420
1107 TAAGGCCCTGACCTTCAATGAGGACCAATTTCTGATGATGAGCAAGTGTGGGGAGCC 1166
1421 CTTCTGCTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACACCCCGGCGCT 1480

Db	2247	AGCCGGGGCTGCGGTGCAGGCACTGGGCAATGCTGGCTGGGGGGGCCCAAGCACAGCCCT	2300
Qy	2561	GACTAGGATGACAGCAGCAAAAGACCACTTTCTCCCTCTGAGAGGAGCTTCTGCTACT	2620
Db	2307	GACTAGGATGACAGCAGCAAAAGACCACTTTCTCCCTCTGAGAGGAGCTTCTGCTACT	2366
Qy	2621	CTGCATCACTGATGACACTCAGCAGGGTGATGCAAGCAGTCTGCGCTCCCTATGGAGCT	2680
Db	2367	CTGCATCACTGATGACACTCAGCAGGGTGATGCAAGCAGTCTGCGCTCCCTATGGAGCT	2426
Qy	2681	CCCTTTCTACCAAGCACATGAGCTCTCTAAACAGGGTGGGGGCTACCCCCAGACCTGCTCTCT	2740
Db	2427	CCCTTTCTACCAAGCACATGAGCTCTCTAAACAGGGTGGGGGCTACCCCCAGACCTGCTCTCT	2486
Qy	2741	ACACTGATATTGAAGAACTGGAGAGGATCTTTCAGTCTTGCGCATTCAGGAGACCTCTC	2800
Db	2487	ACACTGATATTGAAGAACTGGAGAGGATCTTTCAGTCTTGCGCATTCAGGAGACCTCTC	2546
Qy	2801	AGAAACACAGCTGTTTCAAGAGACCTTAAAAAACCTCCCTGTGCCAGGACCTATGGAAT	2860
Db	2547	AGAAACACAGCTGTTTCAAGAGACCTTAAAAAACCTCCCTGTGCCAGGACCTATGGAAT	2606
Qy	2861	GAACACAAACTCTTAAACAATCATATGCTTAACATGCCACTCTCTGGAACTCCACCTCTGA	2920
Db	2607	GAACACAAACTCTTAAACAATCATATGCTTAACATGCCACTCTCTGGAACTCCACCTCTGA	2666
Qy	2921	AGCTGCGCTTTTGGACACCAACTCCCTCTCCAGGGTCAAGCAGGATCTGCTCCCT	2980
Db	2667	AGCTGCGCTTTTGGACACCAACTCCCTCTCCAGGGTCAAGCAGGATCTGCTCCCT	2726
Qy	2981	CCTGCTTCCCTTACCAGTCTGTGACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGAC	3040
Db	2727	CCTGCTTCCCTTACCAGTCTGTGACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGAC	2786
Qy	3041	CACCTTCTCTTGTCTCAGTTGGGGCAGACTCTGATCCCTTCTGCGCTGGCAGAAATGCC	3100
Db	2787	CACCTTCTCTTGTCTCAGTTGGGGCAGACTCTGATCCCTTCTGCGCTGGCAGAAATGCC	2846
Qy	3101	AGGGGTAATCTGAGCCTTCTTCACTCCTTTACCTTACCTTACCTTACCTTCCCTCCCT	3160
Db	2847	AGGGGTAATCTGAGCCTTCTTCACTCCTTTACCTTACCTTACCTTACCTTCCCTCCCT	2906
Qy	3161	CCCTTTTCCCTTGTGTTGGGATTCAGAAAACCTGCTTGTTCAGAGACTGTTATTTTATT	3220
Db	2907	CCCTTTTCCCTTGTGTTGGGATTCAGAAAACCTGCTTGTTCAGAGACTGTTATTTTATT	2966
Qy	3221	AAAAATATAAGCTT 3235	
Db	2967	AAAAATATAAGCTT 2981	
RESULT 8			
AK091127			
LOCUS			
DEFINITION	AK091127	2981 bp	linear
	Homo sapiens	cdNA FLJ33808	fis, clone CTONG2001749, highly similar to SEMAPHORIN 4A PRECURSOR.
ACCESSION	AK091127		
VERSION	AK091127.1	GI:21749423	
KEYWORDS			oligo capping; fis (full insert sequence).
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS			1
			Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuno,Y., Negai,K. and Isegai,T.
TITLE			NEDO human cDNA sequencing project
JOURNAL			Unpublished

REFERENCE 2 (bases 1 to 2981)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
Location/Qualifiers
1..2981
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CTONG2001749"
/tissue type="tongue, tumor tissue"
/clone_lib="CTONG2"
/note="cloning vector: pME18SFL3"
ORIGIN
Query Match 76.5%; Score 2682.2; DB 9; Length 2981;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 99; Gaps 1;
QY 341 AGGGATGAACCTAGGACCTTAGCTTCTCCACAGAGGCGCTCCAGGATTTTGACAC 400
DB 186 AGGGATGAACCTAGGACCTTAGCTTCTCCACAGAGGCGCTCCAGGATTTTGACAC 245
QY 401 TCTGCTCTGATGGTATGGAATACTCTCTACGTGGGGCTCGAAGCCATCTGGC 460
DB 246 TCTGCTCTGATGGTATGGAATACTCTCTACGTGGGGCTCGAAGCCATCTGGC 305
QY 461 CTTGGATATCCAGGATCCAGGGGTCCAGGGTAAAGAACATGATACCGTGGCCAGCAG 520
DB 306 CTTGGATATCCAGGATCCAGGGGTCCAGGGTAAAGAACATGATACCGTGGCCAGCAG 365
QY 521 TGACGAAAAAGAGTAAATGTCCTTTAAGAAAGAGCAATGACACAGTGTTCAA 580
DB 366 TGACGAAAAAGAGTAAATGTCCTTTAAGAAAGAGCAATGATGAG----- 411
QY 581 CTTATCCCGTCTCTGTTCTTACAAATGTACCCATCTCTACACCTGGGACCTTCGC 640
DB 412 ----- 411
QY 641 CTTACGCCCTGCTGTGACCTTCAATGAACTTCAAGATTCCTACCTGTGGCCATCTCGGA 700
DB 412 -----GAACTTCAAGATTCCTACCTGTGGCCATCTCGGA 446
QY 701 GGACAGGTATGAGGGAAGGCGCAAGCCCTTTGACCCCGCTCAAGCATACCGC 760
DB 447 GGACAGGTATGAGGGAAGGCGCAAGCCCTTTGACCCCGCTCAAGCATACCGC 506
QY 761 TGTCTTGGTGGATGCTCTATTCTGTGTACTATGAACAACTTCTGGGCACTGAGCC 820
DB 507 TGTCTTGGTGGATGCTCTATTCTGTGTACTATGAACAACTTCTGGGCACTGAGCC 566
QY 821 CATCTGTATGGGACACTGGATCCAGCTCTCTCAAGACCGCAACTTCTCCGCTG 880
DB 567 CATCTGTATGGGACACTGGATCCAGCTCTCTCAAGACCGCAACTTCTCCGCTG 626
QY 881 GCTGCATCATGAGCCCTCTTTGTGGACCCATCTCTCGACCCAGTCTCTACTTCTT 940
DB 627 GCTGCATCATGAGCCCTCTTTGTGGACCCATCTCTCGACCCAGTCTCTACTTCTT 686
QY 941 CTTGAGGAGACAGCCAGGAGTTTGAATCTTTTGGAGGCTTCCACATCCGGGTGGC 1000
DB 687 CTTGAGGAGACAGCCAGGAGTTTGAATCTTTTGGAGGCTTCCACATCCGGGTGGC 746

QY 1001 TAGAGTCTGCAAGATGACGTGGGGCGGAAAGCTGTGTGAGAGAAAGTGACACACCTT 1060
DB 747 TAGAGTCTGCAAGATGACGTGGGGCGGAAAGCTGTGTGAGAGAAAGTGACACACCTT 806
QY 1061 CTTGAAGGCGCAGCTCTCTGTGACACCGCGGGGAGCTGCCCTTCAAGCTCATCGGCA 1120
DB 807 CTTGAAGGCGCAGCTCTCTGTGACACCGCGGGGAGCTGCCCTTCAAGCTCATCGGCA 866
QY 1121 CGGGGTCTGTCTCCCGCGGATTTCTCCACAGCTCCCAATCTACGAGTCTTCACTTC 1180
DB 867 CGGGGTCTGTCTCCCGCGGATTTCTCCACAGCTCCCAATCTACGAGTCTTCACTTC 926
QY 1181 CAGTGGCAGGTTGGGGGACAGAGCTCTGGGTTTGTGCTTCTCTCTTGGACAT 1240
DB 927 CCAGTGGCAGGTTGGGGGACAGAGCTCTGGGTTTGTGCTTCTCTCTTGGACAT 986
QY 1241 TGAACCTGTCTTTAAGGGGAATACAAAGAGTTGAACAAAGAACTTCACTGTGAGTAC 1300
DB 987 TGAACCTGTCTTTAAGGGGAATACAAAGAGTTGAACAAAGAACTTCACTGTGAGTAC 1046
QY 1301 TTATAGGGCCCTGAGACCAACCCCGGCGAGGAGTTGCTCAGTGGGGCCCTCTCTGA 1360
DB 1047 TTATAGGGCCCTGAGACCAACCCCGGCGAGGAGTTGCTCAGTGGGGCCCTCTCTGA 1106
QY 1361 TAAGGCCCTGACCTTCATGAAGGACCATTTCTGTATGATGAGCAAGTGGTGGGACGCC 1420
DB 1107 TAAGGCCCTGACCTTCATGAAGGACCATTTCTGTATGATGAGCAAGTGGTGGGACGCC 1166
QY 1421 CTTGCTGCTGAAATCTGGCTGGAGTATACCGCTTTCAGTGGAGACAGCCAGGGCT 1480
DB 1167 CTTGCTGCTGAAATCTGGCTGGAGTATACCGCTTTCAGTGGAGACAGCCAGGGCT 1226
QY 1481 TGAATGGCAGACCATCTTGTCTATGTACCTGGGAACCAACACAGGGTCCCTCCAAAGGC 1540
DB 1227 TGAATGGCAGACCATCTTGTCTATGTACCTGGGAACCAACACAGGGTCCCTCCAAAGGC 1286
QY 1541 TGTGTTAAGTGGGGACAGCAGTGTCTCATCTGTGTGGAAGAGATTCAGCTGTCCCTGACC 1600
DB 1287 TGTGTTAAGTGGGGACAGCAGTGTCTCATCTGTGTGGAAGAGATTCAGCTGTCCCTGACC 1346
QY 1601 TGAACCTGTTCGCAACTGTGACGTGCCCCCAGGCTGCAGTGTGTGTAGGCTTCTC 1660
DB 1347 TGAACCTGTTCGCAACTGTGACGTGCCCCCAGGCTGCAGTGTGTGTAGGCTTCTC 1406
QY 1661 AGGAGTGTCTGAGAGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGTGTGTGAGCTG 1720
DB 1407 AGGAGTGTCTGAGAGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGTGTGTGAGCTG 1466
QY 1721 TGTCTTGGCCGGGACCCCACTGTGCTGGGACCTGTAGTCCCGAACCTGTGTGCTCCT 1780
DB 1467 TGTCTTGGCCGGGACCCCACTGTGCTGGGACCTGTAGTCCCGAACCTGTGTGCTCCT 1526
QY 1781 GTCTGCCCCCAACTGTGAACCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGGC 1840
DB 1527 GTCTGCCCCCAACTGTGAACCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGGC 1586
QY 1841 ATGTGCGAGTGGCCCCATGAGCAGAGGAGCTTGGCCCTCAGAGCGCCCGCAATCATTTAA 1900
DB 1587 ATGTGCGAGTGGCCCCATGAGCAGAGGAGCTTGGCCCTCAGAGCGCCCGCAATCATTTAA 1646
QY 1901 AGAAGTCTCGGCTGTCCCTAACTCTCTGAGTCCCTGCGCCCACTGTGAGCTT 1960
DB 1647 AGAAGTCTCGGCTGTCCCTAACTCTCTGAGTCCCTGCGCCCACTGTGAGCTT 1706
QY 1961 GGCTCTTTATTTGAGTCAATGGCCAGCAGCAGTCCAGAAAGCTCTTTCACCTGTCTA 2020
DB 1707 GGCTCTTTATTTGAGTCAATGGCCAGCAGCAGTCCAGAAAGCTCTTTCACCTGTCTA 1766
QY 2021 CAATGGCTCCCTCTTCTGATAGTGCAGGATGAGTTGGGGTCTCTACAGTGTGGGC 2080
DB 1767 CAATGGCTCCCTCTTCTGATAGTGCAGGATGAGTTGGGGTCTCTACAGTGTGGGC 1826
QY 2081 AACTGAGATGGCTTTTTCATACCCCTGTGATCTCTCTACTGAGTGGACAGCAGCAGAC 2140

Db 1827 AACAGAAATGGGCTTTTATACACCTGTGATCTCTCTGCTGGGAGGACGACGAC 1886
Qy 2141 CTTGGCCCTCGATCTCTGAACTGGCAGGATCCCGCGGAGCATGTGAAGGTCCCGTTGAC 2200
Db 1887 CTTGGCCCTCGATCTCTGAACTGGCAGGATCCCGCGGAGCATGTGAAGGTCCCGTTGAC 1946
Qy 2201 CAGGTCAGTGTGGGCGCCCTTGGTGCACAGCATGCTACTGCGCCGACATTTGTGAC 2260
Db 1947 CAGGTCAGTGTGGGCGCCCTTGGTGCACAGCATGCTACTGCGCCGACATTTGTGAC 2006
Qy 2261 TGTCACTGTCTCTTTTGGCTTAGTGTCTTTCAGAGAGCCCTCATCATCTCTGTGAGCTCCCG 2320
Db 2007 TGTCACTGTCTCTTTTGGCTTAGTGTCTTTCAGAGAGCCCTCATCATCTCTGTGAGCTCCCG 2066
Qy 2321 ATTGAGAGCATCTGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCTCGGCGCTGGGA 2380
Db 2067 ATTGAGAGCATCTGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCTCGGCGCTGGGA 2126
Qy 2381 GAAGGCCCTTAAAGCAGAGCAACACCTCCAGTCTCCCAAGGAATCAGAGACCTCTGC 2440
Db 2127 GAAGGCCCTTAAAGCAGAGCAACACCTCCAGTCTCCCAAGGAATCAGAGACCTCTGC 2186
Qy 2441 CAGTGTGTGGAGCGCTGACAACTGCTTAGGCACTGAGGTAGCTTAACTCTAGGCA 2500
Db 2187 CAGTGTGTGGAGCGCTGACAACTGCTTAGGCACTGAGGTAGCTTAACTCTAGGCA 2246
Qy 2501 AGGCGGGGCTGGGCTGAGCAGCACCCTGGCCATGCTGGTGGGGGCGCCAGCAGCCCT 2560
Db 2247 AGGCGGGGCTGGGCTGAGCAGCACCCTGGCCATGCTGGTGGGGGCGCCAGCAGCCCT 2306
Qy 2561 GACTAGGATGACAGCAGCAGCAAAAGACCACTTTCTCCCTGTAGAGGAGCTTCTGTACT 2620
Db 2307 GACTAGGATGACAGCAGCAGCAAAAGACCACTTTCTCCCTGTAGAGGAGCTTCTGTACT 2366
Qy 2621 CTGCATCAGTATGACACTCAGCAGAGGTGATGACAGCAGTCTGCTCCCTATGGACT 2680
Db 2367 CTGCATCAGTATGACACTCAGCAGAGGTGATGACAGCAGTCTGCTCCCTATGGACT 2426
Qy 2681 CCCTTTACCAAGCAGATGAGCTCTCTAACAGGGTGGGGGCTACCCCGCAGACCTGTCT 2740
Db 2427 CCCTTTACCAAGCAGATGAGCTCTCTAACAGGGTGGGGGCTACCCCGCAGACCTGTCT 2486
Qy 2741 ACATGTATATGAGAACCTGGAGGATCTTTCAGTCTTCGGCATTCAGAGGACCTCC 2800
Db 2487 ACATGTATATGAGAACCTGGAGGATCTTTCAGTCTTCGGCATTCAGAGGACCTCC 2546
Qy 2801 AGAACACAGTGTTCAGAGACCTTAAAGAACCTGCTGTCCAGGACCTCTATGGTAAT 2860
Db 2547 AGAACACAGTGTTCAGAGACCTTAAAGAACCTGCTGTCCAGGACCTCTATGGTAAT 2606
Qy 2861 GAACACCAACATCTAAACATATGCTAAATGCAATGCACTCTGGAATCTCACTTGA 2920
Db 2607 GAACACCAACATCTAAACATATGCTAAATGCAATGCACTCTGGAATCTCACTTGA 2666
Qy 2921 AGCTGCGGCTTTGACACCACTCCCTTTCTCCAGGGTCTATGAGGATCTGCTCCCT 2980
Db 2667 AGCTGCGGCTTTGACACCACTCCCTTTCTCCAGGGTCTATGAGGATCTGCTCCCT 2726
Qy 2981 CTTGCTTCCCTTACAGTGTGACCGCTGACTCCAGGAAGTCTTCCCTGAAGTCTGAC 3040
Db 2727 CTTGCTTCCCTTACAGTGTGACCGCTGACTCCAGGAAGTCTTTCCTGAAGTCTGAC 2786
Qy 3041 CACTTTTCTTCTGCTTTCAGTGGGGCAGACTCTGATCCCTTCTGCGCTGGCAGATGGC 3100
Db 2787 CACTTTTCTTCTGCTTTCAGTGGGGCAGACTTTCATCTTCTGCGCTGGCAGATGGC 2846
Qy 3101 AGGGTAACTGAGCCCTTCTTCACTCTTAACTAGCTGACCCCTTCACTCTCCCTCT 3160
Db 2847 AGGGTAACTGAGCCCTTCTTCACTCTTAACTAGCTGACCCCTTCACTCTCCCTCT 2906
Qy 3161 CCCTTTTCTTCTGCTTGGGATTCAGAAATCTGCTGTGAGACACTGTTTATTTTTATT 3220

Db 2907 CCCTTTTCTTCTGCTTGGGATTCAGAAATCTGCTGTGAGACACTGTTATTTTATT 2966
Qy 3221 AAAAATATAAGGCTT 3235
Db 2967 AAAAATATAAGGCTT 2981
RESULT 9
AX512887 2768 bp DNA linear PAT 03-OCT-2002
LOCUS
DEFINITION Sequence 35 from Patent WO02062841.
ACCESSION AX512887
VERSION AX512887.1 GI:23504046
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Tang, T. Y., Yue, H., Gandhi, A. R., Yao, M. G., Warren, B. A., Ding, L.,
Duggan, B. M., Xu, Y., Yang, J., Thangavelu, K., Lal, P. G.,
Honchell, C. D., Wallia, N. K., Lee, S., Lee, B. A., Richardson, T. W.,
Baughn, M. R. and Elliott, V. S.
TITLE Secreted proteins
JOURNAL Patent: WO 02062841-A 35 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
source
1. 2768
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 7487507CBI"
ORIGIN
Query Match 75.4%; Score 2642.8; DB 6; Length 2768;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2747; Conservative 0; Mismatches 2; Indels 93; Gaps 1;
Qy 5 TTGGCATGATGGGCACCTGAGAGGCGCCACTCCCGTTCCAGCCAGGCTGAGCCTTCTGTC 64
Db 1 TTGGCATGATGGGCACCTGAGAGGCGCCACTCCCGTTCCAGCCAGGCTGAGCCTTCTGTC 60
Qy 65 CCCTGCTCTGGGCGCTGGGAACCCCTTCTTCTTCTCTCTGTAATGGCAACCCCGCCCT 124
Db 61 CCCTGCTCTGGGCGCTGGGAACCCCTTCTTCTTCTCTGTAATGGCAACCCCGCCCT 120
Qy 125 AGAATCCAGACACCGAGTTTCCCACTGTGCTGTGTTCAAGGGTATGTGAGAGCTCCCTGG 184
Db 121 AGAATCCAGACACCGAGTTTCCCACTGTGCTGTGTTCAAGGGTATGTGAGAGCTCCCTGG 180
Qy 185 TGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGCCTCCT 244
Db 191 TGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGCCTCCT 240
Qy 245 GGGCCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCTCCAGACGACGACCCGGGGGAGG 304
Db 241 GGGCCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCTCCAGACGACGACCCGGGGGAGG 300
Qy 305 CGGCGAGGGGCCCATGCCAGGGTCACTACTATGACGGGGTGAACGTAAGGACACTTAG 364
Db 301 CGGCGAGGGGCCCATGCCAGGGTCACTACTATGACGGGGTGAACGTAAGGACACTTAG 360
Qy 365 CTCTCTCCACAGAGGGCCTCCAGGATTTTGAACACTCTGCTCTGAGTGGTGAATGAAA 424
Db 361 CTCTCTCCACAGAGGGCCTCCAGGATTTTGAACACTCTGCTCTGAGTGGTGAATGAAA 420
Qy 425 TACTCTCTACGTGGGGCTCGAGAGGCAATCTGGCCCTGGATATCCAGATCCAGGGT 484
Db 421 TACTCTCTACGTGGGGCTCGAGAGGCAATCTGGCCCTGGATATCCAGATCCAGGGT 480
Qy 485 CCCAGGCTTAAAGAACATGATACCGTGGCGCAGCCAGTGCAGAGAAAAAGAGTGAATGTC 544
Db 481 CCCAGGCTTAAAGAACATGATACCGTGGCGCAGCCAGTGCAGAGAAAAAGAGTGAATGTC 540

QY	545	CTTTAAGAAGAAGCAATGAGACACAGTGTCTTCAACTTCATCCGTGTCTGTGTTCTTTA	604
DB	541	CTTTAAGAAGAAGCAATGAGACACAGTGTCTTCAACTTCATCCGTGTCTGTGTTCTTTA	600
QY	605	CAATGTCAACCATCTCTACACCTCGGCACCTTCGCCCTCAGCCCTGCTGTACCTTCAT	664
DB	601	CAATGTCAACCATCTCTACACCTCGGCACCTTCGCCCTCAGCCCTGCTGTACCTTCAT	660
QY	665	TGAACCTTCAAGATTCTTCACTGTTGCCATCTCGGAGGACAAGGTCAATGAGGGAAGG	724
DB	661	TGAACCTTCAAGATTCTTCACTGTTGCCATCTCGGAGGACAAGGTCAATGAGGGAAGG	720
QY	725	CCAAAGCCCTTTGACCCCGCTCAACAGCATACGGCTGTCTTGGTGATGGGATGCTCTA	784
DB	721	CCAAAGCCCTTTGACCCCGCTCAACAGCATACGGCTGTCTTGGTGATGGGATGCTCTA	780
QY	785	TTCTGTACTATGAACAACCTTCTTGGGCAGTGAGCCCATCTGTATGGCACACTGGGATC	844
DB	781	TTCTGTACTATGAACAACCTTCTTGGGCAGTGAGCCCATCTGTATGGCACACTGGGATC	840
QY	845	CCAGCGTGTCTCAAGACCGACAACTTCCTCCGTGTGCTGCATCATGACGCTCTTTGT	904
DB	841	CCAGCGTGTCTCAAGACCGACAACTTCCTCCGTGTGCTGCATCATGACGCTCTTTGT	900
QY	905	GGCAGCCATCCCTTCGACCCACAGSTCGTCTACTTCTTCTCGAGGAGACAGCCACGAGTT	964
DB	901	GGCAGCCATCCCTTCGACCCACAGSTCGTCTACTTCTTCTCGAGGAGACAGCCACGAGTT	960
QY	965	TGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGG	1024
DB	961	TGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGG	1020
QY	1025	CGGCGAAAAGCTGTGTCAGAAAGAAGTGACACACCTTCTGAAGGCCCAGGTCTCTGCAC	1084
DB	1021	CGGCGAAAAGCTGTGTCAGAAAGAAGTGACACACCTTCTGAAGGCCCAGGTCTCTGCAC	1080
QY	1085	CCAGCGGGGAGCTGCCCTTCAAGTCAATCCGCCACGCGGTCTGTCTCCCGCCGATTC	1144
DB	1081	CCAGCGGGGAGCTGCCCTTCAAGTCAATCCGCCACGCGGTCTGTCTCCCGCCGATTC	1140
QY	1145	TCCACACAGCTCCCACACTACTACGAGTCTTCACTCCAGTGGCAGGTGTGGCGGACCA	1204
DB	1141	TCCACACAGCTCCCACACTACTACGAGTCTTCACTCCAGTGGCAGGTGTGGCGGACCA	1200
QY	1205	GAGCTCTCGGTTGTGCTTCTCTCTTTGGAATTTGAAGTGTCTTTAAGGGGAATA	1264
DB	1201	GAGCTCTCGGTTGTGCTTCTCTCTTTGGAATTTGAAGTGTCTTTAAGGGGAATA	1260
QY	1265	CAAGAGTTGAACAAGAAAATTCAACGCTGGACTACTTATAGGGGCCCTCGACACCAACC	1324
DB	1261	CAAGAGTTGAACAAGAAAATTCAACGCTGGACTACTTATAGGGGCCCTCGACACCAACC	1320
QY	1325	CCGGCCAGGATGTGCTCAGTGGGCCCTCTCTGTATAGGCCCTGACCTTCATGAAGGA	1384
DB	1321	CCGGCCAGGATGTGCTCAGTGGGCCCTCTCTGTATAGGCCCTGACCTTCATGAAGGA	1380
QY	1385	CCATTTCTGTATGATGAGCAGTGTGGGAGCCCTCGTGTGTAATCTGSCGTGGA	1444
DB	1381	CCATTTCTGTATGATGAGCAGTGTGGGAGCCCTCGTGTGTAATCTGSCGTGGA	1440
QY	1445	GTATACACGGCTTCAGTGGAGACAGCCAGGGCTTGTATGGGCACAGCCATCTGTTCAT	1504
DB	1441	GTATACACGGCTTCAGTGGAGACAGCCAGGGCTTGTATGGGCACAGCCATCTGTTCAT	1500
QY	1505	GTACTGGGAACCAACACAGAGTGTCTCCACAAGSGTGTGTAAAGTGGGACACAGTGC	1564
DB	1501	GTACTGGGAACCAACACAGAGTGTCTCCACAAGSGTGTGTAAAGTGGGACACAGTGC	1560
QY	1565	TCATCTGTGGAAGAGATTACGTGTTCCTTGACCCCTGGAACCTGTGTGCAACCTGACGT	1624
DB	1540	-----	1539

QY	1625	GGCCCCACCCAGGGTGCACTGTTTGTAGAGCTTCTCAGAGAGTGTCTGAGAGGTGTCTCCCG	1688
DB	1540	-----GGGTGCAGTGTATTGTAGGCTTCTCAGAGAGTGTCTGAGAGGTGTCTCCCG	1587
QY	1685	AGCCAACTGTAGTGTCTATCAGAGACTGTGTGGACTGTGTCTTGTCCCGGACCCGCCACTG	1744
DB	1588	AGCCAACTGTAGTGTCTATCAGAGACTGTGTGGACTGTGTCTTGTCCCGGACCCGCCACTG	1647
QY	1745	TGCTTGGGACCTTGAGTCCGAACTGTGTGCCTCTGTCTGTGCCCCCMAACTGAACTCCTG	1804
DB	1648	TGCTTGGGACCTTGAGTCCGAACTGTGTGCCTCTGTCTGTGCCCCCMAACTGAACTCCTG	1707
QY	1805	GAGCAGGACATGAGAGCGGGGGAACCCAGAGTGGGCAATGTGCCAGTGGGCCCCCATGAGCAG	1864
DB	1708	GAGCAGGACATGAGAGCGGGGGAACCCAGAGTGGGCAATGTGCCAGTGGGCCCCCATGAGCAG	1767
QY	1865	GAGCTTTGGCCTCAGAGCCGCCGCAAAATCATTAAGAAAGTCTGGCTGTCCCTAACTC	1924
DB	1768	GAGCTTTGGCCTCAGAGCCGCCGCAAAATCATTAAGAAAGTCTGGCTGTCCCTAACTC	1827
QY	1925	CATCTGGAGCTCCCTTGCCCCCACCTGTGAGCCTTGGCCCTTATTTATTTGGAGTCAATGG	1984
DB	1828	CATCTGGAGCTCCCTTGCCCCCACCTGTGAGCCTTGGCCCTTATTTATTTGGAGTCAATGG	1887
QY	1985	CCAGCAGCAGTCCCAAGAGCCTTTCCACTGTCTACAATGGTCCCTCTTGTGTATAGT	2044
DB	1988	CCAGCAGCAGTCCCAAGAGCCTTTCCACTGTCTACAATGGTCCCTCTTGTGTATAGT	1947
QY	2045	GCAGGATGGAGTTGGGGGTCTCTACAGTGTCTGGGCAACTGAGNAATGGCTTTTCATACCC	2104
DB	1948	GCAGGATGGAGTTGGGGGTCTCTACAGTGTCTGGGCAACTGAGNAATGGCTTTTCATACCC	2007
QY	2105	TGTGATCTCTACTTGGGTGGACAGCCAGGACCCAGACCTGGCCCTGTGATCTCTGAACTGGC	2164
DB	2008	TGTGATCTCTACTTGGGTGGACAGCCAGGACCCAGACCTGGCCCTGTGATCTCTGAACTGGC	2067
QY	2165	AGGCATCCCCCGGAGCAATGTGAAGTCCCGTTGACACAGGTCAGTGGTGGGGCGCCCT	2224
DB	2068	AGGCATCCCCCGGAGCAATGTGAAGTCCCGTTGACACAGGTCAGTGGTGGGGCGCCCT	2127
QY	2225	GGCTGCCAGCGTCTACTTGGCCCCACTTTGTCACTGTCACTGCTCTCTTTTGGCTTAGT	2284
DB	2128	GGCTGCCAGCGTCTACTTGGCCCCACTTTGTCACTGTCACTGCTCTCTTTTGGCTTAGT	2187
QY	2285	GCTTTACGAGCCCTCATCATCTCTGTGGCTTCCCATTTGAGAGCATCTCGGGTTCGGG	2344
DB	2188	GCTTTACGAGCCCTCATCATCTCTGTGGCTTCCCATTTGAGAGCATCTCGGGTTCGGG	2247
QY	2345	CAAGGTTACGGCTGTGAGACCTTGCCTCTGGGGAAGGCCCGTTAAGCAGAGACGA	2404
DB	2248	CAAGGTTACGGCTGTGAGACCTTGCCTCTGGGGAAGGCCCGTTAAGCAGAGACGA	2307
QY	2405	ACACTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGAATGGACGCTGCAACAA	2464
DB	2308	ACACTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGAATGGACGCTGCAACAA	2367
QY	2465	CTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGAGGAC	2524
DB	2368	CTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGAGGAC	2427
QY	2525	CTGGCCATGTGGCTGGGCGGCCCAAGCAGACCCCTCACTAGGATGACAGCAGCACAAA	2584
DB	2428	CTGGCCATGTGGCTGGGCGGCCCAAGCAGACCCCTCACTAGGATGACAGCAGCACAAA	2487
QY	2585	GACCACTTTCTCCCTTGAGAGGACTTGTGCTACTCTGTGATCACTGTGATGACATCTAGCA	2644
DB	2488	GACCACTTTCTCCCTTGAGAGGACTTGTGCTACTCTGTGATCACTGTGATGACATCTAGCA	2547
QY	2645	GGGTGATGCAAGAGTCTGCTCCCTATGGGACTCCCTTCTTACCAAGCAGCATGTAGCTC	2704
DB	2548	GGGTGATGCAAGAGTCTGCTCCCTATGGGACTCCCTTCTTACCAAGCAGCATGTAGCTC	2607
QY	2705	TCTAACAGGGTGGGGGTACCCCCAGACCTGCTCTCACTGTATTTTGAAGAACCTGGAG	2764

```
Db 2608 TCTAACAGGTGGGGGCTACCCGACACCTGCTCCCTACACTGATATGGAAGAACCTGGAG 2667
Qy 2765 AGGATCCTTCAGTCTGGCCATCCAGGAGCCCTCCAGAAACACAGTGTTCAGAGACC 2824
Db 2668 AGGATCCTTCAGTCTGGCCATCCAGGAGCCCTCCAGAAACACAGTGTTCAGAGACC 2727
Qy 2825 CTAAAAAACCTGCTGCCAG 2846
Db 2728 CTAAAAAACCTGCTGCCAG 2749

RESULT 10
AX528271/c 2281 bp DNA linear PAT 21-NOV-2002
LOCUS AX528271
DEFINITION Sequence 9 from Patent W00206339.
ACCESSION AX528271
VERSION AX528271.1 GI:25172573
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K.,
Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M.,
Sekerkes,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E.,
Shimkets,R.A. and Padigaru,M.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0206339-A 9 24-JAN-2002;
Curagen Corporation (US)
FEATURES
source
location/Qualifiers
1..2281
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 65.0%; Score 2279.4; DB 6; Length 2281;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 224 CCTGGACCCCTGGAGCCCTCTGGGCTTTTCCTCTTCCAACTGCTTCAGTGTCTGCTGCC 283
Db 2281 CCTGGACCCCTGGAGCCCTCTGGGCTTTTCCTCTTCCAACTGCTTCAGTGTCTGCTGCC 2222
Qy 284 GACGACGACCGGGGGGAGCGGGGAGGGGCCATGCCAGGTCAGATACATATGACAGG 343
Db 2221 GACGACGACCGGGGGGAGCGGGGAGGGGCCATGCCAGGTCAGATACATATGACAGG 2162
Qy 344 GGATGAACGTAGGCACTTAGCTTCTTCCACGAGAGGGGCTCCAGGATTTTGACACTCT 403
Db 2161 GGATGAACGTAGGCACTTAGCTTCTTCCACGAGAGGGGCTCCAGGATTTTGACACTCT 2102
Qy 404 GCTCCTGAGTGGTATGGAAATACTCTCTAGTGGGGGCTCGAAGAGCCATTCGCGCTT 463
Db 2101 GCTCCTGAGTGGTATGGAAATACTCTCTAGTGGGGGCTCGAAGAGCCATTCGCGCTT 2042
Qy 464 GGATATCCAGATCCAGGGTCCCGAGCTTAAAGAACATGATACCGTGGCCAGCAGTGA 523
Db 2041 GGATATCCAGATCCAGGGTCCCGAGCTTAAAGAACATGATACCGTGGCCAGCAGTGA 1982
Qy 524 CAGAAAAAGAGTGAATGTGCTTTTAAAGAAAGAGCAATGAGACACAGTGTTCAACTT 583
Db 1981 CAGAAAAAGAGTGAATGTGCTTTTAAAGAAAGAGCAATGAGACACAGTGTTCAACTT 1922
Qy 584 CATCCGTGCTCTGCTTTTCTACATGTACCCATCTCTACACCTGGGGACCTTCGCCCTT 643
Db 1921 CATCCGTGCTCTGCTTTTCTACATGTACCCATCTCTACACCTGGGGACCTTCGCCCTT 1862
Qy 644 CAGCCCTGCTGTACCTTCATTTGAACTTCAAGATTCCTACCTGTGCCCATCTCGAGGA 703
Db 1861 CAGCCCTGCTGTACCTTCATTTGAACTTCAAGATTCCTACCTGTGCCCATCTCGAGGA 1802
```

```
Qy 704 CAAGGTCAATGAGGGAAGAGCCAAAGCCCTTTTGACCCCGCTCACAAGCATACGGCTGT 763
Db 1801 CAAGGTCAATGAGGGAAGAGCCAAAGCCCTTTTGACCCCGCTCACAAGCATACGGCTGT 1742
Qy 764 CTTGGTGAATGGGATGTCTTATTCTGGTACTATGAACAACTTCTGGGAGTGAAGCCCAT 823
Db 1741 CTTGGTGAATGGGATGTCTTATTCTGGTACTATGAACAACTTCTGGGAGTGAAGCCCAT 1682
Qy 824 CTTGATGCGGACACATGGGATCCAGGCTGTCTCAGAACGACCACTTCTCCGCTGGCT 883
Db 1681 CTTGATGCGGACACATGGGATCCAGGCTGTCTCAGAACGACCACTTCTCCGCTGGCT 1622
Qy 884 GCATCATGACCCCTCTCTTTGTGGCAGCATCCCTTCGACCCAGGTCTCTACTTCTTCTT 943
Db 1621 GCATCATGACCCCTCTCTTTGTGGCAGCATCCCTTCGACCCAGGTCTCTACTTCTTCTT 1562
Qy 944 CGAGGAGACAGCCAGCGAGTTTGACTCTTTTGAGAGGCTCCACATCGCGGGTGGCTAG 1003
Db 1561 CGAGGAGACAGCCAGCGAGTTTGACTCTTTTGAGAGGCTCCACATCGCGGGTGGCTAG 1502
Qy 1004 AGTCTGCAAGAAATGACGTGGGCGGCGGAAAGCTCTCTCAGAAAGTGGACCACTTCTCT 1063
Db 1501 AGTCTGCAAGAAATGACGTGGGCGGCGGAAAGCTCTCTCAGAAAGTGGACCACTTCTCT 1442
Qy 1064 GAAGCCCGAGCTGTCTCTGCAACCCAGCGGGGAGCTGCTCCCTTCAACGTCTATCCGCCACGC 1123
Db 1441 GAAGCCCGAGCTGTCTCTGCAACCCAGCGGGGAGCTGCTCCCTTCAACGTCTATCCGCCACGC 1382
Qy 1124 GGTCTGCTCTCCCGCCGATTCCTCCACAGCTCCCCACATCTACGCACTTTCACCTCCCA 1183
Db 1381 GGTCTGCTCTCCCGCCGATTCCTCCACAGCTCCCCACATCTACGCACTTTCACCTCCCA 1322
Qy 1184 GTGGCAGGTTGGCGGACCAAGAGCTGTGGGTTTGTGCTCTCTCTTTGGACATGA 1243
Db 1321 GTGGCAGGTTGGCGGACCAAGAGCTGTGGGTTTGTGCTCTCTCTCTTTGGACATGA 1262
Qy 1244 ACCTGTCTTTAAGGGGAATACAAAGAGTTGAAACAAAGAACTTTCAGCTGGACTACTTA 1303
Db 1261 ACCTGTCTTTAAGGGGAATACAAAGAGTTGAAACAAAGAACTTTCAGCTGGACTACTTA 1202
Qy 1304 TAGGGGCCCTGAGACCAACCCCGGCGGAGGAGTGTCTCAGTGGGCGCTCTCTCTGTATAA 1363
Db 1201 TAGGGGCCCTGAGACCAACCCCGGCGGAGGAGTGTCTCAGTGGGCGCTCTCTCTGTATAA 1142
Qy 1364 GGCCCTGACCTTCATGAGGACCACTTCTCTGATGATGAGCAAGTGTGGGAGCGCCCT 1423
Db 1141 GGCCCTGACCTTCATGAGGACCACTTCTCTGATGATGAGCAAGTGTGGGAGCGCCCT 1082
Qy 1424 GCTGTGAAATCTGGCGTGGAGTATACACGCTTTCAGTGGAGACAGCCAGGCGCTTGA 1483
Db 1081 GCTGTGAAATCTGGCGTGGAGTATACACGCTTTCAGTGGAGACAGCCAGGCGCTTGA 1022
Qy 1484 TGGGACAGCCATCTTGTCTGATGATGAGTGGGAGCAACCAAGGCTGGCTCCACAGGCTGT 1543
Db 1021 TGGGACAGCCATCTTGTCTGATGATGAGTGGGAGCAACCAAGGCTGGCTCCACAGGCTGT 962
Qy 1544 GGTAAAGTGGGACAGCAGTGTCTCATCTGGTGGAAAGAGATTTCAGCTTTCCTTGAACCTTGA 1603
Db 961 GGTAAAGTGGGACAGCAGTGTCTCATCTGGTGGAAAGAGATTTCAGCTTTCCTTGAACCTTGA 902
Qy 1604 ACCTGTTTGGAACTTCAGCTGGGCGCCCAAGGCTGGGAGTGTGGTGTTCCTTGAACCTTGA 1663
Db 901 ACCTGTTTGGAACTTCAGCTGGGCGCCCAAGGCTGGGAGTGTGGTGTTCCTTGAACCTTGA 842
Qy 1664 AGGTGTCTGGAGGCTGGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGAGACTGTGT 1723
Db 841 AGGTGTCTGGAGGCTGGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGAGACTGTGT 782
Qy 1724 CTTTGGCCCGGACCCCACTGTGCTGGGACCTGAGTCCGAACTTGTGCTTCTCTCTGTC 1783
Db 781 CTTTGGCCCGGACCCCACTGTGCTGGGACCTGAGTCCGAACTTGTGCTTCTCTCTGTC 722
```



```
QY 1784 TGCCCCCAACCTGAACCTCTGTGAAGCAGACATGAGAGCGGGGAAACCCAGAGTGGCGATG 1843
Db 721 TGCCCCCAACCTGAACCTCTGTGAAGCAGACATGAGAGCGGGGAAACCCAGAGTGGCGATG 662
QY 1844 TGCCAGTGGCCCATGAGAGAGCGCTTGGGCTCAGAGCGCGCGGAAATCATTAAAGA 1903
Db 661 TGCCAGTGGCCCATGAGAGAGCGCTTGGGCTCAGAGCGCGCGGAAATCATTAAAGA 602
QY 1904 AGTCTGTGGTGTCCTAACTCCATCCTGTGAGCTCCCTGCCCCCAACCTGTGAGCTTGGC 1963
Db 601 AGTCTGTGGTGTCCTAACTCCATCCTGTGAGCTCCCTGCCCCCAACCTGTGAGCTTGGC 542
QY 1964 CTCCTATTATTGGAGTCATGAGAGAGCGCTTGGGCTCAGAGAGCGCTTCCACTGTCTACAA 2023
Db 541 CTCCTATTATTGGAGTCATGAGAGAGCGCTTGGGCTCAGAGAGCGCTTCCACTGTCTACAA 482
QY 2024 TGGCTCCCTCTTGTCTATAGTCAGAGATGGAGTGGGGGTCTTACCAAGTGTGGGCAAC 2083
Db 481 TGGCTCCCTCTTGTCTATAGTCAGAGATGGAGTGGGGGTCTTACCAAGTGTGGGCAAC 422
QY 2084 TGAGATGGCTTTTTCATACCTGTGATCTCTACTTGGGTGAGACAGCCAGGACCGCT 2143
Db 421 TGAGATGGCTTTTTCATACCTGTGATCTCTACTTGGGTGAGACAGCCAGGACCGCT 362
QY 2144 GGCCCTGGATCTGAACCTGGCAGGATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAAG 2203
Db 361 GGCCCTGGATCTGAACCTGGCAGGATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAAG 302
QY 2204 GGTAGTGTGGGGCGGCTGGCTGGCCAGCAGTCTCTACTTGGGCCCACTTTGTCACTGT 2263
Db 301 GGTAGTGTGGGGCGGCTGGCTGGCCAGCAGTCTCTACTTGGGCCCACTTTGTCACTGT 242
QY 2264 CACTGTCTCTTTGCTTAGTCTTTTCAAGGAGCCCTCATCTCTGCGGCTCCCACTT 2323
Db 241 CACTGTCTCTTTGCTTAGTCTTTTCAAGGAGCCCTCATCTCTGCGGCTCCCACTT 182
QY 2324 GAGACACTCCGGGTCTGGGGCAAGGTTCAAGGCTGTGAGACCTTGCCCTCGGGGAGAA 2383
Db 181 GAGACACTCCGGGTCTGGGGCAAGGTTCAAGGCTGTGAGACCTTGCCCTCGGGGAGAA 122
QY 2384 GSCCCCGTTAAGCAGAGACACCTCCAGTCTCCCAAGGAATGACAGACTCTGCCAG 2443
Db 121 GSCCCCGTTAAGCAGAGACACACCTCCAGTCTCCCAAGGAATGACAGACTCTGCCAG 62
QY 2444 TGATGTGACGTGACAACTGCTTAGGCACTGAGTGTGAGTAACTTAGGCACAGG 2503
Db 61 TGATGTGACGTGACAACTGCTTAGGCACTGAGTGTGAGTAACTTAGGCACAGG 2
QY 2504 C 2504
Db 1 C 1

RESULT 11
AX528269
LOCUS 2271 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 7 from Patent WO0206339.
ACCESSION AX528269
VERSION AX528269.1 GI:25172572
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Spaderna, S.K., Tchernev, V., Liu, X., Shenoy, S., Spytek, K.,
Zerhusen, B., Patturajan, M., Taupier, R.J., Rastelli, L., Grosse, W.M.,
Szekeres, E.S., Alsobrook, J.I., Lepley, D.M., Shen, L., Burgess, C.E.,
Shinkets, R.A. and Padigaru, M.
TITILE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0206339-A 7 24-JAN-2002;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
```

```
source 1. .2271
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 63.5%; Score 2226.8; DB 6; Length 2271;
Best Local Similarity 98.8%; Pred. NO. 0;
Matches 2259; Conservative 0; Mismatches 12; Indels 15; Gaps 1;

QY 204 ATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGCTCTCTGGGCTTTTCTCTTCCAA 263
Db 1 ATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGCTCTCTGGGCTTTTCTCTTCCAA 60
QY 264 CTCCTTCAGCTGTCTGCGAGCAGACCGCGGGGGAGCGGGCCATGCCCC 323
Db 61 CTCCTTCAGCTGTCTGCGAGCAGACCGCGGGGGAGCGGGCCATGCCCC 120
QY 324 AGGGTCAGATACATGACGGGGATGAACCTGAGGGCACTTAGCTTTCCACAGAGGGC 383
Db 121 AGGGTCAGATACATGACGGGGATGAACCTGAGGGCACTTAGCTTTCCACAGAGGGC 180
QY 384 CTCAGGATTTTGACACTCTGCTCTGAGTGTGATGGAATACTCTCTACGTGGGGCT 443
Db 181 CTCAGGATTTTGACACTCTGCTCTGAGTGTGATGGAATACTCTCTACGTGGGGCT 240
QY 444 CGAGAGCCATTCCTGGCTTGGATATCCAGGATCCAGGGTCCCGAGGCTTAAGAACATG 503
Db 241 CGAGAGCCATTCCTGGCTTGGATATCCAGGATCCAGGGTCCCGAGGCTTAAGAACATG 300
QY 504 ATACCGTGGCCAGCCAGTGAACAGAAAAAGAGTGAATGTGCCCTTTAAGAGAGAGCAAT 563
Db 301 ATACCGTGGCCAGCCAGTGAACAGAAAAAGAGTGAATGTGCCCTTTAAGAGAGAGCAAT 360
QY 564 GAGACAGTGTTCACACTTCCTGCTCCTGCTGCTTCTTCAATGCTCAACATCTCTAC 623
Db 361 GAGACAGTGTTCACACTTCCTGCTCCTGCTGCTTCTTCAATGCTCAACATCTCTAC 420
QY 624 ACCTGGGGCACTTCGCCCTTCAGCCCTGCTGTGACCTTCAATTGAACTTCAAGATTCCTAC 683
Db 421 ACCTGGGGCACTTCGCCCTTCAGCCCTGCTGTGACCTTCAATTGAACTTCAAGATTCCTAC 480
QY 684 CTGTTGCCATCTCGAGAGACAGTGCATGAGGGGAAAGCCAAAGCCCTTTGACCCC 743
Db 481 CTGTTGCCATCTCGAGAGACAGTGCATGAGGGGAAAGCCAAAGCCCTTTGACCCC 540
QY 744 GCTCACAAGCATACGGCTGTCTTGGTGGATGGATGCTCTATTCTGTGATATGAACAAC 803
Db 541 GCTCACAAGCATACGGCTGTCTTGGTGGATGGATGCTCTATTCTGTGATATGAACAAC 600
QY 804 TTCTTGGGCACTGAGCCCATCTGATGCGCACTGCGGATCCAGCTGTCTCTCAAGACC 863
Db 601 TTCTTGGGCACTGAGCCCATCTGATGCGCACTGCGGATCCAGCTGTCTCTCAAGACC 660
QY 864 GACAACTTCCTCGCTGGCTGCATCATGCGCTCCTTTGTGGCAGCCATCCCTTCGACC 923
Db 661 GACAACTTCCTCGCTGGCTGCATCATGCGCTCCTTTGTGGCAGCCATCCCTTCGACC 720
QY 924 CAGGTCTCTACTTCTTCTTCGAGGAGACAGCAGCGAGTTGACTTCTTTGAGAGGCTC 983
Db 721 CAGGTCTCTACTTCTTCTTCGAGGAGACAGCAGCGAGTTGACTTCTTTGAGAGGCTC 780
QY 984 CACACATCGGGGTGAGTGTCTGAGAGTGTGAGGGGCGGCGGCGGCGGCGGCGGCGGCGG 1043
Db 781 CACACATCGGGGTGAGTGTCTGAGAGTGTGAGGGGCGGCGGCGGCGGCGGCGGCGGCGG 840
QY 1044 AAGAAGTGGACCACTTCTCTGAGAGCCAGCTGCTCTGACCCAGCCGGGCGAGCTGCC 1103
Db 841 AAGAAGTGGACCACTTCTCTGAGAGCCAGCTGCTCTGACCCAGCCGGGCGAGCTGCC 900
QY 1104 TTCAACGTCTATCCGCCAGCGGCTCTGCTCCCGCGGATTTCTCCACAGCTCCCACTC 1163
Db 901 TTCAACGTCTATCCGCCAGCGGCTCTGCTCCCGCGGATTTCTCCACAGCTCCCACTC 960
```


1164 TAGCAGTCTTCACTCCAGTGGAGGTTGGGGACAGAGCTCTCGGTTGTGTC 1223
Dbb TAGCAGTCTTCACTCCAGTGGAGGTTGGGGACAGAGCTCTCGGTTGTGTC 1020
1224 TTCTCTCTTGGACATGAACCTGTCTTTAAGGGGAATACAAAGATTGAACAA 1283
Dbb TTCTCTCTTGGACATGAACCTGTCTTTAAGGGGAATACAAAGATTGAACAA 1080
1284 ACTTACGCTGGACTACTTATAGGGGCTGTAGAACCAACCCCGGCGAGCTGTGCTCA 1343
Dbb ACTTACGCTGGACTACTTATAGGGGCTGTAGAACCAACCCCGGCGAGCTGTGCTCA 1140
1344 GTGGGCGCTCTCTGATAGGCGCTGTGCTTATGAAGGACCATTTCTGTATGATGAG 1403
Dbb GTGGGCGCTCTCTGATAGGCGCTGTGCTTATGAAGGACCATTTCTGTATGATGAG 1200
1404 CAAGTGGTGGGAGCGGCTGTGCTGTGTAATCTGGGCTGGAGTATACAGGCTTGGAGTG 1463
Dbb CAAGTGGTGGGAGCGGCTGTGCTGTGTAATCTGGGCTGGAGTATACAGGCTTGGAGTG 1260
1464 GAGACAGCCAGGCGCTTGAATGGGACAGCATCTTGTCTATGTACCTGGGACCAACCA 1523
Dbb GAGACAGCCAGGCGCTTGAATGGGACAGCATCTTGTCTATGTATCTGGGACCAACCA 1320
1524 GGTCGCTTCAAGGCTGTGTAGTGGGACAGAGTGTCTATCTGTGTGAAGAGATT 1583
Dbb GGTCGCTTCAAGGCTGTGTAGTGGGACAGAGTGTCTATCTGTGTGAAGAGATT 1380
1584 CAGCTGTTCCTTCACTGAACTGTGCTGCACTGAGCTGCGCCCAACCCAGGCTGCA 1643
Dbb CAGCTGTTCCTTCACTGAACTGTGCTGCACTGAGCTGCGCCCAACCCAGGCTGCA 1440
1644 GTTTGTAGCTTCTCAGAGGTGTCTGGAGGTGCCCGGACCAACTGTATGTCTAT 1703
Dbb GTTTGTAGCTTCTCAGAGGTGTCTGGAGGTGCCCGGACCAACTGTATGTCTAT 1500
1704 GAGAGCTGTGTGACGTGTCTTGGCCCGGACCCCACTGTGCTGGAGCCCTGAGTCC 1763
Dbb GAGAGCTGTGTGACGTGTCTTGGCCCGGACCCCACTGTGCTGGAGCCCTGAGTCC 1560
1764 CGAACCTGTGTCTCTGTCTGCGCCCACTGTGCTGGAAGCAGGACATGAGCGG 1823
Dbb CGAACCTGTGTCTCTGTCTGCGCCCACTGTGCTGGAAGCAGGACATGAGCGG 1605
1824 GGGAAACCCAGAGTGGCATGTCCAGTGGCCCATGAGCAGGAGCTTGGGCTCAGAGC 1883
Dbb GGGAAACCCAGAGTGGCATGTCCAGTGGCCCATGAGCAGGAGCTTGGGCTCAGAGC 1665
1884 CGCCCGCAATCATTAAGAGTCTCTGCTGTCTTAACTCCATCTGAGCTCCCTGTC 1943
Dbb CGCCCGCAATCGTTAAAGAGTCTCTGCTGTCTTAACTCCATCTGAGCTCCCTGTC 1725
1944 CCCCAGCTGTGAGCTTGGCTCTTATTTAGTGTATGGGCTATGGCCAGGAGTCCAGAA 2003
Dbb CCCCAGCTGTGAGCTTGGCTCTTATTTAGTGTATGGGCTATGGCCAGGAGTCCAGAA 1785
2004 GCCTCTTCCAGTGTACAAATGGCTCCCTCTGTGTATGATGAGGAGTGGGGGT 2063
Dbb GCCTCTTCCAGTGTACAAATGGCTCCCTCTGTGTATGATGAGGAGTGGGGGT 1845
2064 CTCTACAGTGTGGGCACTAGAAATGGCTTTTATACCTGTGTATCTCTTCTGAGTG 2123
Dbb CTCTACAGTGTGGGCACTAGAAATGGCTTTTATACCTGTGTATCTCTTCTGAGTG 1905
2124 GACAGCAGGACAGACCTGGCCCTGTGATCTGAACTGGCAGGATATCCCGGAGCAT 2183
Dbb GACAGCAGGACAGACCTGGCCCTGTGATCTGAACTGGCAGGATATCCCGGAGCAT 1965
2184 GTGAAGTCCCGTTGACAGGTCAGTGGTGGGCGGCGCTGGCTGCGCCAGAGTCCTAC 2243
Dbb GTGAAGTCCCGTTGACAGGTCAGTGGTGGGCGGCGCTGGCTGCGCCAGAGTCCTAC 2025

2244 TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCTTGTAGTGTCTTTCAGAGAGCCCTCATC 2303
Dbb TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCTTGTAGTGTCTTTCAGAGAGCCCTCATC 2085
2304 ATCTCTGTGCTCCCTCCCATTTAGAGCACTCCGGCTCGGGGCAAGTTTCAAGGCTGTGAG 2363
Dbb ATCTCTGTGCTCCCTCCCATTTAGAGCACTCCGGCTCGGGGCAAGTTTCAAGGCTGTGAG 2145
2364 ACCCTGCGCCCTGGGGAAGAGCCCGTTAAGCAGAGAGCAACCTCTCAGTCTCCCAAG 2423
Dbb ACCCTGCGCCCTGGGGAAGAGCCCGTTAAGCAGAGAGCAACCTCTCAGTCTCCCAAG 2205
2424 GAATGCAAGACCTCTGCGAGTGTGAGCGCTGACAACTGCTAGGCACTGAGGTA 2483
Dbb GAATGCAAGACCTCTGCGAGTGTGAGCGCTGACAACTGCTAGGCACTGAGGTA 2265
2484 GCTTAA 2489
Dbb GCTTAA 2271

RESULT 12
AX879068
LOCUS AX879068 1838 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 13973 from Patent BP1074617.
ACCESSION AX879068
VERSION AX879068.1 GI:40033804
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: Ep 1074617-A 13973 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES
source Location/Qualifiers
1.1838
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
106..1092
/note="unnamed protein product"
/codon_start=1
/protein_id="CAE90357.1"
/db_xref="GI:40033805"
/translation="MYLGTGSLHKAIVVSGDSSAHLVBEIQLFPDPEVRNLQALPT
QGAVFVFGGVMRVPFRANCSVSCVDCLARDPHCAWDPSRTCCILSAPNLNSWK
QDMERNPWCASGPMRSLRPSRPIIKEVLAVPNSILELPCPHLSALASYYWSH
GPAAPVPSASTVYNGSLILIVODGVGLYQCWATENGFSYPIVSYWDSQDTLADP
ELAGIPREHVKPLTRVSGAALAAQCSYHPFHTVTVLFAVLGALLILVASPLRA
LRANGKVGQCELTURPGEKAPLSREHLQSPKCRTSASDVDDNNCLGTEVA"

ORIGIN
Query Match 52.4%; Score 1838; DB 6; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1398 GATGAGCAAGTGTGGGAGCGCCCTGCTGGTGAATCTGGCGTGGAGTATACAGGCTT 1457
Dbb 1 GATGAGCAAGTGTGGGAGCGCCCTGCTGGTGAATCTGGCGTGGAGTATACAGGCTT 60
Qy 1458 GCAGTGGAGACAGCCAGGCGCTTGTATGGGCAAGCCATCTTGTATGATCTGGGAACC 1517
Dbb 61 GCAGTGGAGACAGCCAGGCGCTTGTATGGGCAAGCCATCTTGTATGATCTGGGAACC 120
Qy 1518 ACCACAGGTCGCTCCACAGGCTGTGTAAGTGGGGAAGAGTGTCTCATCTGTGGAA 1577
Dbb 121 ACCACAGGTCGCTCCACAGGCTGTGTAAGTGGGGAAGAGTGTCTCATCTGTGGAA 180
Qy 1578 GAGATTGAGTGTCTCCCTGACCCCTGAACTGTGTCGCAACCTGAGCTGGCCCCCAG 1637


```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/mol_xref="taxon:9606"

ORIGIN
Query Match      52.4%; Score 1838; DB 6; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1398 GATGAGCAAGTGTGGGACGCCCTCTGTGTGTAATCTGGCGTGGAGATATACAGGCTT 1457
Db      1 GATGAGCAAGTGTGGGACGCCCTCTGTGTGTAATCTGGCGTGGAGATATACAGGCTT 60

Qy 1458 GCAGTGGAGACAGCCAGGGCTTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 1517
Db      61 GCAGTGGAGACAGCCAGGGCTTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 120

Qy 1518 ACCAAGGGTTCGTCACAAGGCTGTGTAAAGTGGGACAGCAGTGTCTCATCTGTGTGGAA 1577
Db      121 ACCAAGGGTTCGTCACAAGGCTGTGTAAAGTGGGACAGCAGTGTCTCATCTGTGTGGAA 180

Qy 1578 GAGATTGAGCTGTTCCCTGACCCCTGAACTGTTGCGAACCTGCGAGCTGGCCCCCACCACCG 1637
Db      181 GAGATTGAGCTGTTCCCTGACCCCTGAACTGTTGCGAACCTGCGAGCTGGCCCCCACCACCG 240

Qy 1638 GGTGCAGTGTGTTAGGCTTCTCAGGAGGTGTCCTGAGGGTGGCCCCGAGCCAACTGTAGT 1697
Db      241 GGTGCAGTGTGTTAGGCTTCTCAGGAGGTGTCCTGAGGGTGGCCCCGAGCCAACTGTAGT 300

Qy 1698 GTCTATGAGAGCTGTGTGAGTGTGTCCTGCGCCGGGACCCCACTGTGCTGTGGACCT 1757
Db      301 GTCTATGAGAGCTGTGTGAGTGTGTCCTGCGCCGGGACCCCACTGTGCTGTGGACCT 360

Qy 1758 GAGTCCCGAACCTGTTGCTCTCTGTGTCGCCCCAACCTGAACTCTCGAAGCAGGACATG 1817
Db      361 GAGTCCCGAACCTGTTGCTCTCTGTGTCGCCCCAACCTGAACTCTCGAAGCAGGACATG 420

Qy 1818 GAGCGGGGAACCCAGAGTGGCATGTGCGAGTGGCCCCCATGAGCAGGAGCTTCGGCCT 1877
Db      421 GAGCGGGGAACCCAGAGTGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCTTCGGCCT 480

Qy 1878 CAGAGCCCGCGCAAAATCATTTAAAGAACTCTGCGTGTCCCTAACTCCATCTCGAGATC 1937
Db      481 CAGAGCCCGCGCAAAATCATTTAAAGAACTCTGCGTGTCCCTAACTCCATCTCGAGATC 540

Qy 1938 CCCTGCCCCACCTGTGAGCCTTGGCCCTTTATTATTGGAGTCATGCCCCAGAGCAGATC 1997
Db      541 CCCTGCCCCACCTGTGAGCCTTGGCCCTTTATTATTGGAGTCATGCCCCAGAGCAGATC 600

Qy 1998 CCAGAAGCTCTTCCACATGTCTACAATGGCTCCCTCTTGCTGTAGTGCAGGATGAGATT 2057
Db      601 CCAGAAGCTCTTCCACATGTCTACAATGGCTCCCTCTTGCTGTAGTGCAGGATGAGATT 660

Qy 2058 GGGGGTCTCTACAGTGTGGCACTGAGAAATGGCTTTTCAATACCCTGTGATCTCTCTAC 2117
Db      661 GGGGGTCTCTACAGTGTGGCACTGAGAAATGGCTTTTCAATACCCTGTGATCTCTCTAC 720

Qy 2118 TGGGTGGACAGCCAGGACAGACCCCTGGCCCTTGAATCCTGAACTGGCAGGATCCCCCGG 2177
Db      721 TGGGTGGACAGCCAGGACAGACCCCTGGCCCTTGAATCCTGAACTGGCAGGATCCCCCGG 780

Qy 2178 GAGCATGTGAAGTCCCGTTGACAGAGGTTCAGTGTGGGGCGCCCTGGTGTCCGACGAG 2237
Db      781 GAGCATGTGAAGTCCCGTTGACAGAGGTTCAGTGTGGGGCGCCCTGGTGTCCGACGAG 840

Qy 2238 TCCTACTGSCCCACCTTTGTCTACTGTCTACTGTCTCTTTGCTTGTAGTCTTTTCAGGAGCC 2297
Db      841 TCCTACTGSCCCACCTTTGTCTACTGTCTACTGTCTCTTTTGCTTGTAGTCTTTTCAGGAGCC 900

Qy 2298 CTCATCATCTCTGTGGCTTCCCATGTGAGACATCCCGGGTTCGGGCAAGGTTTCAGGGC 2357
Db      901 CTCATCATCTCTGTGGCTTCCCATGTGAGACATCCCGGGTTCGGGCAAGGTTTCAGGGC 960

```

1 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiraori, A., Sudo, H., Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1838).
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@ri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- and 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
FEATURES
Location/Qualifiers
1..1838
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MAMMA1001771"
/tissue_type="Mammary gland"
/clone_lib="MAMMA1"
/note="Cloning vector: pME18SFL3"
106..1092
/note="unnamed protein product"
/codon_start=1
/db_xref="GI:10433728"
/translation="MYLGTTGSLHKAVVSGDSAHLEVIQLPPEPVRLNQLAFT QGAVFVGSGVNRVPXANSVYESCVDLARDPHCAWDPESRTECLLSAPNLNLSK QDMERGNPEWACASGPMRSILRQPSRQIIEVLAVPNSILELPCPHLSALASVYWSH ELPAAPRKSSTVYNGSLULLIQDVGGLYQCNATENGSPFVSIYVWDSQDQILADLP ELAGIPREKXVPLTRVYGGAAALAAQSQSYMPHFVTVLFPALVLSGALIILVASLPURA LRARKVQGGCTETLPBKEAPLSRQHPQLQSPKECRTSASDVEDADNCLGTEVA"
ORIGIN
Query Match 52.4%; Score 1838; DB 9; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1398 GATGAGCAAGTGTGGGGACGCCCTCTGCTGTAAGTCTGGCGTGGAGTATACAGGCTT 1457
Db 1 GATGAGCAAGTGTGGGGACGCCCTCTGCTGTAAGTCTGGCGTGGAGTATACAGGCTT 60
Qy 1458 GCAGTGGAGACAGCCACAGGGCTTGTGGGGACAGCCATCTTGTCATGTACTCTGGGAACC 1517
Db 61 GCAGTGGAGACAGCCACAGGGCTTGTGGGGACAGCCATCTTGTCATGTACTCTGGGAACC 120
Qy 1518 ACCACAGGGTCGCTCCACAGGCTGTGTAAGTGGGACAGCAGTGTCTCATCTGGTGAA 1577
Db 121 ACCACAGGGTCGCTCCACAGGCTGTGTAAGTGGGACAGCAGTGTCTCATCTGGTGAA 180
Qy 1578 GAGATTACAGCTTCCCTGACCCCTGACCTGCTTCGCACCTGCGAGCTGGCCCCCACCACG 1637
Db 181 GAGATTACAGCTTCCCTGACCCCTGACCTGTTTGCACACCTGCGAGCTGGCCCCCACCACG 240
Qy 1638 GGTGAGTGTGTGTAGGCTTCTCAGGAGGTTCTGTGGGGTGCCTCCGACCACTGTAGT 1697
Db 241 GGTGAGTGTGTGTAGGCTTCTCAGGAGGTTCTGTGGGGTGCCTCCGACCACTGTAGT 300
Qy 1698 GTCTATGAGACTGTGTGACATGTGTCTTCCCTCCCGGACCCCACTGTGCTGGGACCT 1757
Db 301 GTCTATGAGACTGTGTGACATGTGTCTTCCCTCCCGGACCCCACTGTGCTGGGACCT 360

```

Db      1441 CTGTCGCCGAGACCTATGGTAATGAACACCAAAACATCTTAACAAATCATATGCTAACATGC 1500
Qy      2998 CACTCTCGGAATCCACTGTAAGCTGCGCTTTGGACACCAACTCCCTTCTCCAG 2957
Db      1501 CACTCTCGGAATCCACTGTAAGCTGCGCTTTGGACACCAACTCCCTTCTCCAG 1560
Qy      2958 GGTTCATGACGAGTCTGCTCCCTCCCTGCTTCCCTTACCACTGCTGACCGCTGACTCCCA 3017
Db      1561 GGTTCATGACGAGTCTGCTCCCTCCCTGCTTCCCTTACCACTGCTGACCGCTGACTCCCA 1620
Qy      3018 GGAAGTCTTCCCTGAGTCTGACCACTCTTCTTCTTCTGCTTCACTTGGGACAGACTCTGAT 3077
Db      1621 GGAAGTCTTCCCTGAGTCTGACCACTCTTCTTCTTCTGCTTCACTTGGGACAGACTCTGAT 1680
Qy      3078 CCCTTCTGCTGCGCAATGGGAGGAGGATGATCTGAGCTTCTTCACTCTTACCTTACCTAG 3137
Db      1681 CCCTTCTGCTGCGCAATGGGAGGAGGATGATCTGAGCTTCTTCACTCTTACCTTACCTAG 1740
Qy      3138 CTGACCCCTTCACTCTTCCCTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 3197
Db      1741 CTGACCCCTTCACTCTTCCCTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 1800
Qy      3198 TCAGAGACTCTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 3235
Db      1801 TCAGAGACTCTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1838

RESULT 15
BC025800
LOCUS
DEFINITION
BC025800
3159 bp mRNA linear ROD 12-NOV-2003
Mus musculus sema domain, immunoglobulin domain (Ig), transmembrane
domain (TM) and short cytoplasmic domain, (semaphorin) 4A, mRNA
(CDNA clone MGC:35988 IMAGE:5102015), complete cds.
ACCESSION
BC025800
VERSION
BC025800.1 GI:19387926
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3159)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,A.M., Wang,J., Hsieh,P.,
Diatchenko,K., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Scaplehorn,M., Soares,M.B., Bonaldo,M.F., Udwin,T.B., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Sudd,J., Loguillano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gav,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalska,U., Smalhus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
PUBMED
12477932
REFERENCE
2 (bases 1 to 3159)
Strausberg,R.
Direct Submission
Submitted (11-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
REMARK

```

COMMENT

Contact: MGC help desk
Email: cgaps-rc@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Tsai, Nataaja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 57 Row: j Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7305468.

FEATURES

Location/Qualifiers

1..3159

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:35988 IMAGE:5102015"

/tissue_type="Liver, normal, 5 month old male mouse."

/clone_lib="NCI CGAP_Li9"

/lab_hosts="DH10B"

/note="vector: pCMV-SPORT6"

1..3159

/gene="Sema4a"

/note="synonym: SemaB"

/db_xref="LocustID:20351"

/db_xref="MGI:107560"

162..2444

/codon_start=1

/product="sema domain, immunoglobulin domain (Ig),

transmembrane domain (TM) and short cytoplasmic domain,

(semaphorin) 4A"

/protein_id="AAH25800.1"

/db_xref="GI:19387927"

/db_xref="LocustID:20351"

/translation="MALPSGQSWLLRVFPQLFLPSLPASGTGGGPMRVKY
HAGDHRALSFQKGLRDEFTLLSDGNTLVGAREAVLALNINPGIPRLKNMIP
WPASERKKTCAKSKNETQCFNFIKLVSNATHLYAGCTAFAPACTTFLQDLSL
LLPILIDKVMGKQSPFDFVHKHTAVLDGMLYSGTMNPLGSEFLMRTLGSPVL
KTDFIHLHADASFVAAPSTQVTFVFEETASEFDFEELYISRAVQCKDVGGE
KLQKQWTFKQALLCAOPQLPFNIIRHALLPADSPSVRIYAVFTSOMQVGTFR
SSAVCAPSLTDIERFVKGYKEINKETSRWTVYRGSEVSPRGSCMGSSDKALTFM
KDFPLDHEVGTPLAVKSGVETRLAVESAGLDGSSHWVYLTGTSGLHKAVPQ
DSSAYLVEELQLSPDSEPVNQLQAPQAVPAGFSGGIWRVPRANCVSYESVCVCL
ARDPHCAMDPELSCLLSGTSKPKQDMERGNFVWCTRGPMRFRQKSPPLQIKE
VLTPVNSILELPCPHLSALASYHSHGRAKISEASATVNGSLLLLPQDVGGLYQCV
ATENGSPYVYVDSQDFLADPELAGVPRVQVPLTRVGGGASMAAQRSPYKH
FLIVLVLALVLLGLVTLILASPLGALRGKVGCGCMLPPPRGKAPLSRDLQPSKD
HRTSASDVADANNHGLAEVA"

misc_feature

351..1595
/note="Sema; Region: Sema domain. The Sema domain occurs
in semaphorins, which are a large family of secreted and
transmembrane proteins, some of which function as
repellent signals during axon guidance. Sema domains also
occur in the hepatocyte growth factor receptor"

misc_feature

1647..1778
/note="PSI; Region: domain found in Plexins, Semaphorins
and Integrins"
/db_xref="CDD:pfam01403"

ORIGIN

Query March		50.5%;	Score 1771.2;	DB 10;	Length 3159;
Best Local Similarity		76.2%;	Pred. No 0;		
Matches 2404;		Conservative	0;	Mismatches 545;	Indels 104; Gaps 15;
QY	91	CCTTCTTTCTCTCTGAATGGACCCCCCGCCCTAGAAATCCAGACACCGAGTTTCCCACT	150		
DB	59	CCCCCTTCTTGGCTCGGATGGCA-CCCTGATTCAGGGTTTGAACACACAGCACTTCTCAGT	117		
QY	151	GTGGCTGGTTCAAGGGTATGTGAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGGCC	210		
DB	118	GTGGCTGGCTCAG-----GAACCATCTGGTGACCATCTCAGGCTGACCATGGGCC	168		
QY	211	TCCAGCCCTGGGCTGGACCCCTGGAGCCTCTCTGGGCCCTTTTCCTTTCCAACTGCTTC	270		
DB	169	TACCATCCCTGGGCCAGGACTCATGAGTCTCTCGCTGCTTTTTTTCTTCCAACTCTTCC	228		
QY	271	AGCTGTCTGCCGACGACGACCGCGGGGAGGCGGCGAGGGCCCATGCCCCAGGGTCA	330		
DB	229	TGCTGGCATCACTGCCACCTGCTTCTGGGACTGGTGTGAGGGCCCATGCCCCAGGTCA	288		
QY	331	GATATATGACGGGATGAACGTPAGGGCACTTAGCTTTTTCACCAAGAAAGGCCCTCCAGG	390		
DB	289	AATACCATGCTGGAGACGGGACAGGGCCCTCAGCTTCTTCCAAACAAAGGCCCTCCAG	348		
QY	391	ATTTTGACACTCTGCTCCTGAGTGGTGAATGGAATACTCTACCTGGGGGCTCGAGAG	450		
DB	349	ACTTTGACAGCTGCTCCTGAGTGAAGTGGCAACTCTCTATGTGGGGGCTCGAGAGG	408		
QY	451	CCATCTGGCCTTGGATATCCAGATCCAGGGTCCCGAGGCTAAAGAAATGATACCGT	510		
DB	409	CGTCTGGCTTGAATATCCAGAACCCAGGAATCCCAAGGCTAAAGAAATGATACCGT	468		
QY	511	GGCCAGCAGTGAAGAAAGAGTGAATGTGCTTTAAGAAAGAGCAATGAGACAC	570		
DB	469	GGCCAGCAGTGAAGAAAGAGTGAATGTGCTTTAAGAAAGAGCAATGAGACAC	528		
QY	571	AGTGTTCACACTTCCTCGTCTCTTACAAATGTCAACCATCTCTACACCTCGG	630		
DB	529	AGTGTTCACACTTCCTCGTCTCTTACAAATGTCAACCATCTCTACACCTCGG	588		
QY	631	GCACCTTGGCTTACGCTCTGTGATCCTTCAATGAACTTCAAGATTCCTACCTGTTCG	690		
DB	589	GGACCTTGTCTTACGCTCTGTGATCCTTCAATGAACTTCAAGATTCCTACCTGTTCG	648		
QY	691	CCATCTCGGAGGACAGGTCATGGAGGAAAGGCAAGCCCTTTGACCCCGCTCACA	750		
DB	649	CCATCTTGATAGACAGGTCATGGAGGAAAGGCAAGCCCTTTGACCCCGCTCACA	708		
QY	751	AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCTCG	810		
DB	709	AGCACACAGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCTCG	768		
QY	811	GCAGTGAGCCCATCTGTATGCGCACACTGGGATCCAGGCTGTCTTCAAGACCGACAAT	870		
DB	769	GCAGTGAGCCCATCTGTATGCGCACACTGGGATCCAGGCTGTCTTCAAGACCGACAAT	828		
QY	871	TCTCCGCTGGCTGATCATAGAGCTCTCTTTGTGGACCCATCCCTTCGACCCAGGTGCG	930		
DB	829	TCTTACGCTGGCTGACGCGGATGCTCTCTTGTGGACCCATCCCTTCGACCCAGGTGCG	888		
QY	931	TCTACTTCTTTCGAGGACAGCGAGGTTGACTTCTTGGAGGCTTCCACAT	990		
DB	889	TCTATTCTTCTTGGAGGACAGCGAGGTTGACTTCTTGGAGGCTTGTATAT	948		
QY	991	CGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGGGGCGGCAAGGCTGTGCAAGAAAGT	1050		
DB	949	CCAGGGTGGCTCAAGTCTGCAAGAACGACGTGGGGGTTGAAAGGCTGTGCAAGAAAGT	1008		
QY	1051	GGACCACTTCTTGAAGGCCAGCTGCTGTGACCCAGCGGGGAGCTGCCCTTCAAG	1110		
DB	1009	GGACCACTTCTTGAAGGCCAGCTGCTGTGACCCAGCGGGGAGCTGCCCTTCAAG	1068		
QY	1111	TCATCGGCCACGGGCTCTGCTCCCGCGGATTTCTCCACAGCTCCCACTATCAGCAG	1170		

DB	1069	TCATCCGCCACGGGCTCTGCTGCCCGCATTTCTCCCTCTGTTTCCCGCATCTACGCAG	1128		
QY	1171	TCCTTCACTCCGATGCGAGGTTGGCGGACACAGAGCTCTGCGGTTTGTGCTTCTCTC	1230		
DB	1129	TCCTTCACTCCGATGCGAGGTTGGCGGACACAGAGCTCTGCGGTTTGTGCTTCTCTC	1188		
QY	1231	TCCTTGGACATTTGAACGTTCTTTAAAGGGGAAATACAAAGAGTTGAAACAAAGAACTTCAC	1290		
DB	1189	TCACGACATTTGAGGAGTCTTTAAAGGGAAGTACAAAGAGCTGAACAAGAGACCTCCC	1248		
QY	1291	GCTGGACTACTTATPAGGGGCTTGAGACCAACCCCGCGCCAGGAGTTGCTCAGTGGGCC	1350		
DB	1249	GCTGGACCACTTACCGGGGCTCAGAGGTCAGCCCGAGGCGCAGGTTGCTTCCATGGGCC	1308		
QY	1351	CCTCCTCTGATTAAGGCCCTGACCTTCTATGAAGACCACTTCTCTGATGATGAGCAAGTGG	1410		
DB	1309	CCTCCTCTGACAAAGCCCTGACCTTCTATGAAGACCACTTCTCTGATGATGAGCAAGTGG	1368		
QY	1411	TGGGACCGCCCTGCTGCTGGAATCTGGCGTGAGATATACACGGCTTGGAGTGGAGACAG	1470		
DB	1369	TAGGAACACCCCTGCTGCTGGAAGTCTGCTGAGAGTACACACCGCTTGTCTGAGTCTCAG	1428		
QY	1471	CCAGGGCCTTGTATGGGACAGCCATCTTGTCTATGATCTGGGAAACCAACACAGGCTCGC	1530		
DB	1429	CTCGGGCCTTGTATGGGACAGCCATCTGCTATGATCTGAGTACCTTCCACGGGCTCCC	1488		
QY	1531	TCCACAAAGGCTGTGTTAAGTGGGACAGCAGTGTCTATCTGGTGGAAAGATTCAGCTGT	1590		
DB	1489	TGCAAAAGGCTGTGCTGCTCAGACAGCAGTGTCTATCTCTGCTGGAGAGATTCAGCTGA	1548		
QY	1591	TCCCTGACCTGACCTGTTGCGAACCTGCGAGCTGGCCCGCCACCCAGGCTGAGTGTGTTG	1650		
DB	1549	GCCCTGACTGTGAGCCTTGTGAAACCTGAGCTGGCCCGCCCGCCAGGCTGAGTGTGTTG	1608		
QY	1651	TAGGCTTCTCAGGAGGTTGTCTGGAGGTTGCCCGAGCAACTGTAGTGTCTATGAGAGCT	1710		
DB	1609	CAGGCTTCTCTGGAGGCTCTGGAGAGTTCACAGGCGCAATGTCAGTGTCTACGAGAGCT	1668		
QY	1711	GTGTGGAGTGTGCTTGTGCGGGACCCCGACTGTGCTGGACCTTGGACCTTCCGACCT	1770		
DB	1669	GTGTGGAGTGTGCTTGTGCGGGACCCCGACTGTGCTGGACCTTGGACCTTCCGACCT	1728		
QY	1771	GTTCCCTCTCTGCTGCCCCCAACCTGAACTCTTGGAGAGGACATGGAGCGGGGGAACC	1830		
DB	1729	GCAGCTTCTCTGCTGCTGCTTACC---AAGCCTTGGAGAGGAGACATGGAGCGGCAACC	1785		
QY	1831	CAGAGTGGGCAATGTGCGAGTGGCCCCATGAGCAGAGGCTTGGCCCTCAGAGCGGCCCGC	1890		
DB	1786	CGGAGTGGGTAATGCACCCGTGGCCCCATGGCCAGGAGCCCCCGCGCTCAGAGCCCCCTC	1845		
QY	1891	AAATCATTAAGAGAGTCTGCTGCTGCTTAACTCCATCTTGGAGCTCCCTGCCCCCACC	1950		
DB	1846	AACCTAATTAAGAGTCTCTGACAGTCCCGCACTCCATCTTGGAGCTGCTGCCCCCACC	1905		
QY	1951	TGTGAGCCTTGGCCTCTTATTTTGGAGTCAATGGCCCGACAGCAGTCCCAAGAGCTCTT	2010		
DB	1906	TGTGAGCAGTGGCCTCTTACCACTGGAGTCAATGGCCCGAGCCAAATCTCAGAGCTCTG	1965		
QY	2011	CCACTGTCTCAATAGGCTCCCTCTTGTGTATGTAGCAGGATGAGTGGGGGCTCTTACC	2070		
DB	1966	CTACCGTCTCAATAGGCTCCCTCTTGTGTGTGCGCAGGATGAGTGGGGGCTCTTACC	2025		
QY	2071	AGTCTCGGCAACTGAGAAATGGCTTTTTCATACCTGTGATCTCTCTACTGGTGGACAGCC	2130		
DB	2026	AGTGTGGCGACTGAGAACGGCTTACTATACCTGCTGCTCTCTATTGGGTGAGACAGCC	2085		
QY	2131	AGGACCAAGCCCTGGCCCTGATCTTGAACTGGCAGGCAATCCCCCGGAGCATGTGAAGG	2190		
DB	2086	AGGACCAAGCCCTGGCCCTGATCTGAACTGGCAGGCTTCCCCGTGAGCGTGTGAGG	2145		
QY	2191	TCCGCTTTCACAGGGGTGAGTGGTGGGCGCCCTTGGCTGGCCCGAGCTCTTACTTGGCCCC	2250		

Db 2146 TCCGCTGACAGGGTCGGAGGGAGGAGCTTCCATGGCTGCCAGCGGTCTACTGGCCCC 2205
Qy 2251 ACTTTGTCACTGTCACTGTCTCTTTGCTTAGTGTCTTTTCAGGAGCCCTCATCTCTCG 2310
Db 2206 ATTTTCTCATGTTACCGTCTCTCTGCGCATCGTGTCTCTGCGAGTGTCTCACTCTCTCC 2265
Qy 2311 TGGCTCCCATTTAGAGAGCACTCGGGCTCGGGCAAGTTTCAAGGCTGTGAGACCCCTGC 2370
Db 2266 TCGCTTCCCCACTGGGGCGCTCGGGCTCGGGTAAAGTTTCAAGGCTGTGGGATGCTGC 2325
Qy 2371 GCCCTGGGAGAGAGCCCGTTAAGCAGAGAGAGCAACCTTCCAGTCTCCCAAGGAATGCA 2430
Db 2326 CCCCACGGGAAAGGCTCCACTGAGCAGAGGACCCAGCACCTCCAGCCCTCCAGGACCA 2385
Qy 2431 GGACCTCTGCAGTGTGTGAGAGCTGAGAGCTGAGCAACAACTCCCTAGGCACTGAGGTAGCTTAA 2490
Db 2386 GGACCTCTGCAGTGTGTGAGAGCTGAGAGCTGAGCAACAACTCCCTAGGCACTGAGGTAGCTTAA 2445
Qy 2491 CTCTAGGCACAGGCGGGGCT--GCGGTGAGGACCTGGGCCATGCTGGCTGGGGCGGCC 2548
Db 2446 CAGGGACACAGATCCGAGCTGAGCAGAGCAAGCCACTGGCCCTGTTGCTATGC----- 2500
Qy 2549 AAGCAGAGCCCTGACTAGGATGACAGCAGCAGCAAAAGACCACTTCTCCCTGAGAGGA 2608
Db 2501 -----CAGGCACAGTGCCACTCTGACAGGGTAGGAGGC 2534
Qy 2609 GCTTCTGTACTCTGTGATGACACTGATGACACTCAGAGGGGTGATGACAGCAGTCTGCCTC 2668
Db 2535 TCTCTGCTAACGTGTGTACCTACAGCAACCAGTAGGT-----CCTC 2577
Qy 2669 CCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTTAACAGGGTGGGGGCTACCCCC 2728
Db 2578 CCCTGTGGGACTCTCTTCTGCAAGCACATTTGGGCTGTCT-----CC 2618
Qy 2729 AGACCTGCTCTACACTGATTAATGAAGAACCTGGAGAGGATCTTCACTTCTGGCCATTC 2788
Db 2619 ATACCTGTACTTGTGTGTGACAGGAAGAGCCAGAGAGGTTCTTTGATTTTGAATTGACC 2678
Qy 2789 CAGGACCCCTCCAGAAACACAGTGTGTTTCAAGAGACCTTAAACAACTGCTGCCAGGA 2848
Db 2679 CAAGAGCCCTCTGTAAACAACTGCTCCAGAGACCATGAAGAGTGTGGCTGTCTGGGA 2738
Qy 2849 CCCTATGTAATGAACACCAACATCTAAACATCATATGCTA-----ACATGCCACT 2901
Db 2739 TTCTGTGTGACAAAC--CTAAGCATCCAGCAAGCTGGGGCTATTCTGCAAACTCCATC 2797
Qy 2902 CCTGGAAACTCCACTCT----GAAGTGGCGCTTTGGACACCAACACTCCCTTC--TCCCA 2956
Db 2798 CTGAACGCTGTCACTCTAGAAGCAGCTGCTGCTTTGAACACCAAGCCACCCCTCTTCCCA 2857
Qy 2957 GGGTCATGCAGGATCTGCTCCCTCTGCTTCCCTTACAGTCTGTGCAACGCTGACTCCC 3016
Db 2858 AGAGTCTCTATGGAGTTGGCCCTTGTGTTTCCCTTACCACTCATGCCATACGTGTT--- 2914
Qy 3017 AGGAAGTCTTCCCTGAAGTCTGACCACTTTCTTCTTGTCTTCAAGTTGGGACAGCTCTGA 3076
Db 2915 GGGAAAGTCACTCTGAAGTCTTAACCACTTCTTCTTGTCTTCAAGTTGGGACAGATTGTTA 2974
Qy 3077 TCCCT---TCTGCCCTGGC--AGATGGCAGGGTAATCTGAGGCTTCTTCACTCCTTTAC 3132
Db 2975 TTATGTCTCTGCCCTGGCTAGAAATGGGGGCAATACTGAGCCTTGTTCCTTGTCCAG 3034
Qy 3133 CCTAGCTGACCCCTTCACTCTCCCTCCCTTTTCTTGTGTTTGGGATTCAGAAAACT 3192
Db 3035 TGTGGCTGACCCCTTGACCTCT--CCCTCTCTCCCTTGTGTTTGGGATTCAGAAAACT 3092
Qy 3193 GCTTGTGACAGACTGTTTATTTTATTTAAAA 3225
Db 3093 GCTTGTGACAGAAATTTATTTTATTTAAAA 3125

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 07:00:48 ; Search time 1451.53 Seconds
(without alignments)
16458.288 Million cell updates/sec

Title: US-10-051-835-12

Perfect score: 800

Sequence: 1 ctctctccagcagggtcag.....taaaagatgtctttttccc 800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum Match 100%

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:

2: em_esthum:

3: em_estin:

4: em_estmu:

5: em_estov:

6: em_estpl:

7: em_estro:

8: em_htc:

9: gb_est1:

10: gb_est2:

11: gb_htc:

12: gb_est3:

13: gb_est4:

14: gb_est5:

15: em_estfun:

16: em_estom:

17: em_ges_hum:

18: em_ges_inv:

19: em_ges_pln:

20: em_ges_vrt:

21: em_ges_fun:

22: em_ges_nam:

23: em_ges_mus:

24: em_ges_pro:

25: em_ges_rod:

26: em_ges_phg:

27: em_ges_vrl:

28: gb_ges1:

29: gb_ges2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792.6	99.1	861	13	BUI93627
2	777.4	97.2	978	13	BUI540102
3	775.4	96.9	821	13	BUI94796
4	719.6	90.0	816	12	B1770798

5	702.6	87.8	903	12	B1768969
6	663	82.9	705	14	CA419320
7	627.4	78.4	963	10	BE893633
8	623.8	78.0	890	12	BQ20473
9	613	76.6	653	12	B1460396
10	611.8	76.5	660	12	BM998183
11	611.2	76.4	642	12	BM761296
12	605.4	75.7	696	9	AV700754
13	599.6	75.0	832	13	BU940543
14	587.2	73.4	946	12	B1552760
15	576	72.0	614	14	CA419457
16	560.2	70.0	740	13	BU942323
17	529.6	66.2	578	12	BM984608
18	517.4	64.7	727	12	BQ527549
19	484.4	60.5	584	12	B1827304
20	455.8	57.0	745	12	B1549606
21	432	54.0	454	9	AA757285
22	414.8	51.8	418	9	AI355317
23	413.2	51.6	455	12	BM782882
24	412	51.5	954	13	BU595224
25	404.6	50.6	427	9	AA865734
26	396.4	49.5	433	9	AW102885
27	372	46.5	486	9	AI581344
28	343.2	42.9	583	12	BG718159
29	340.4	42.5	415	9	AV695928
30	243	30.4	289	10	BF751332
31	222.4	27.8	352	9	AV696887
32	208.2	26.0	867	12	BG680761
33	193.6	24.2	704	12	BM826625
34	190.4	23.8	709	14	CB438378
35	187.6	23.4	930	13	BX350756
36	186.2	23.3	2508	29	AV398883
37	178.4	22.3	696	12	BQ044923
38	173.6	21.7	881	13	BQ880096
39	166	20.8	605	14	CB162968
40	166	20.8	949	14	CD108543
41	163.2	20.4	3767	11	AK083942
42	162.8	20.4	508	12	B1712887
43	157.6	19.7	2508	29	AV398885
44	156.8	19.6	808	14	CB238339
45	154.6	19.3	643	14	CF362512

ALIGNMENTS

RESULT 1
BUI93627
LOCUS
DEFINITION AGENCOURT_7905281 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6160888
5', mRNA sequence.
ACCESSION BUI93627.1 GI:22707611
VERSION EST.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 861)
NTH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/PTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM13512 row: e column: 17
High quality sequence stop: 692.

FEATURES		Location/Qualifiers	
source			
1..861			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="IMAGE:616088"			
/tissue_type="melanotic melanoma"			
/lab_host="DH10B (phage-resistant)"			
/clone_lib="NIH MGC 72"			
/note="organ: skin; Vector: pcwv-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life Technologies."			
ORIGIN			
Query Match	99.1%;	Score 792.6;	DB 13; Length 861;
Best Local Similarity	99.4%;	Pred No. 1.5e-204;	
Matches	795;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	CTCTCTCCAGCAAGGT	CAGGACTTCAGGACTGTAACAATGACCGGATAAAACAGAGAAGG 60
Db	10	CTCTCTCCAGCAAGGT	CAGGACTTCAGGACTGTAACAATGACCGGATAAAACAGAGAAGG 69
Qy	61	TGGCTCTGATATCTGAAATCTGGTTTAAACGCTCCACGGGAATGTGACAGTCCTTCGTATC 120	
Db	70	TGGCTCTGATATCTGAAATCTGGTTTAAACGCTCCACGGGAATGTGACAGTCCTTCGTATC 129	
Qy	121	AGAAAAGGACAGGATGGCCCTGTGGCGACGAAACAAAGAGCGAGGACAGGCTTATTG 180	
Db	130	AGAAAAGGACAGGATGGCCCTGTGGCGACGAAACAAAGAGCGAGGACAGGCTTATTG 189	
Qy	181	CAGGCTCTGCCATGTCCTCAAGAAAAGAAAGCTTATGACAGGACATGCTATTCCACCCAGCC 240	
Db	190	CAGGCTCTGCCATGTCCTCAAGAAAAGAAAGCTTATGACAGGACATGCTATTCCACCCAGCC 249	
Qy	241	AATTGGATTCTCAGATTGATGATCTTCACTGGTTTCAGCAAGAGATAGGATGATCGAAGAC 300	
Db	250	AATTGGATTCTCAGATTGATGATCTTCACTGGTTTCAGCAAGAGATAGGATGATCGAAGAC 309	
Qy	301	CTGCTAGCAATGCACCTGTGGGAGGAAACGTTTACCAGCAGTTTCTCTGGAGATGACCTAG 360	
Db	310	CTGCTAGCAATGCACCTGTGGGAGGAAACGTTTACCAGCAGTTTCTCTGGAGATGACCTAG 369	
Qy	361	AATGCGAGAAACAGACCTCTCTCCAAAGCCACGAGAAATTAATGCTGATATAAAC 420	
Db	370	AATGCGAGAAACAGACCTCTCTCCAAAGCCACGAGAAATTAATGCTGATATAAAC 429	
Qy	421	GTAATTTAGTGAAGGAACTCCGATCGTGTGACAAATAATGAAATAATCTCGAATCG 480	
Db	430	GTAATTTAGTGAAGGAACTCCGATCGTGTGACAAATAATGAAATAATCTCGAATCG 489	
Qy	481	TTGAGGAGTGCAGAGACCTACTGCAGTCAGGACGGAATTTTGAATCCATCATCAAGG 540	
Db	490	TTGAGGAGTGCAGAGACCTACTGCAGTCAGGACGGAATTTTGAATCCATCATCAAGG 549	
Qy	541	AAGCAGCAAGATGTATGACAGCAGACTTTGTTTAAGCACCTTAAGAAGAAACTGAAACGTA 600	
Db	550	AAGCAGCAAGATGTATGACAGCAGACTTTGTTTAAGCACCTTAAGAAGAAACTGAAACGTA 609	
Qy	601	TGATTTGAGAAATCTTGTCCCTGGAGATATCACACCCCAATGCAATATCTCGTTAAT 660	
Db	610	TGATTTGAGAAATCTTGTCCCTGGAGATATCACACCCCAATGCAATATCTCGTTAAT 669	
Qy	661	GATTGAGGAGAGAAAAGGATCAGATTGCTGTTTTCTACAATGGAGCAGGATATTGCTGAA 720	
Db	670	GATTGAGGAGAGAAAAGGATCAGATTGCTGTTTTCTACAATGGAGCAGGATATTGCTGAA 729	
Qy	721	GTCCTCTGGCATATGTTACCGATCAATPAGCCTTCCAGAGGCTTAAGAAATTTCTGTAG 780	
Db	730	GTCCTCTGGCATATGTTACCGATCAATPAGCCTTCCAGAGGCTTAAGAAATTTCTGTAG 789	
Qy	781	TAAAGATGTTCTTTTTCCC 800	

QY	181	CAGGCTCTGCCATGTCTCCAAAGAAAAGAACCTTATGACAGGACATGCTTATTCACCCAGCC	240		
Db	207	CAGGCTCTGCCATGTCTCCAAAGAAAAGAACCTTATGACAGGACATGCTTATTCACCCAGCC	266		
QY	241	AATTGGATTCTCAGATTGATGACTTCACTGGTCTTTCAGCAAGATAGCATGTCAGAAAC	300		
Db	267	AATTGGATTCTCAGATTGATGACTTCACTGGTCTTTCAGCAAGATAGCATGTCAGAAAC	326		
QY	301	CTGGTAGCAATGACCTGTGGGAGGAAAGCTTACAGCAGATTCTCTGAGATGACCTTAG	360		
Db	327	CTGGTAGCAATGACCTGTGGGAGGAAAGCTTACAGCAGATTCTCTGAGATGACCTTAG	386		
QY	361	AATGCAGAGAAAACAGCCTCTCTCTCCCAAAAGCCAAACGAGAAATTAATGCTGATATAAAAC	420		
Db	387	AATGCAGAGAAAACAGCCTCTCTCTCCCAAAAGCCAAACGAGAAATTAATGCTGATATAAAAC	446		
QY	421	GTAAATTAGTGAAGAACTCCGATGCGTTTGGACAAAATATGAAAATCTTCGAAATGC	480		
Db	447	GTAAATTAGTGAAGAACTCCGATGCGTTTGGACAAAATATGAAAATCTTCGAAATGC	506		
QY	481	TTGAAGGAGTGCAGAGCACTTCTGTCAGTCAAGAACGATTTTTCGAAATCCATCAAGG	540		
Db	507	TTGAAGGAGTGCAGAGCACTTCTGTCAGTCAAGAACGATTTTTCGAAATCCATCAAGG	566		
QY	541	AAGCAGCAAGATGATGACAGCAGATTTTTCGAAATCCATCAAGG	600		
Db	567	AAGCAGCAAGATGATGACAGCAGATTTTTCGAAATCCATCAAGG	626		
QY	601	TGATTTGAGAACTACTTGTCTCCCTGGAGGATTTATCACACCCCAATGATTAATCTCGTTAAT	660		
Db	627	TGATTTGAGAACTACTTGTCTCCCTGGAGGATTTATCACACCCCAATGATTAATCTCGTTAAT	686		
QY	661	GATTGAGGAGAGAAAGGATCAGATTGCTTTTCTACATGGAGCAGATATTCGTGAA	720		
Db	687	GATTGAGGAGAGAAAGGATCAGATTGCTTTTCTACATGGAGCAGATATTCGTGAA	746		
QY	721	GTCTCTCGCATATGTTATCCGATCAATAG - CTTTCAGAGGCTAAGAAATTCGTGTTA	779		
Db	747	GTCTCTCGCATATGTTATCCGATCAATAG - CTTTCAGAGGCTAAGAAATTCGTGTTA	806		
QY	780	GTAAAGATGTTCTTTTTC	799		
Db	807	GTAAAGATGTTCTTTTTC	826		
RESULT 3					
LOCUS	BUI94796				
DEFINITION	AGENCOURT_7970656 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6163541	821 bp	linear EST 04-SEP-2000		
ACCESSION	BUI94796				
VERSION	BUI94796.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					

```

Db      790 ACTAAAGATGGTCTTTT 806

RESULT 4
BI770798
LOCUS   603061271F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210681 5',
DEFINITION mRNA sequence.
ACCESSION BI770798.1 GI:15762376
VERSION   BI770798
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   NIH-MGC http://mgs.nci.nih.gov/.
COMMENT   National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11528 row: m column: 18
          High quality sequence stop: 763.

FEATURES
source
1..816
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:5210681"
   /lab_host="DH10B"
   /clone_lib="NIH_MGC_122"
   /notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
   Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
   anonymous pool of 24 week female lung, 16 week female
   spleen, and 20-22 week male spleens. Library is oligo-dT
   primed, and directionally cloned (EcoRV site is destroyed
   upon cloning). Average insert size 1.4 kb, insert size
   range 1-3 kb. Library is normalized and enriched for
   full-length clones and was constructed by C. Gruber
   (Invitrogen). Research Genetics tracking code 026. Note:
   this is a NIH_MGC Library."

ORIGIN
Query Match      90.0%; Score 719.6; DB 12; Length 816;
Best Local Similarity 98.5%; Pred. No. 1e-184;
Matches 747; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY  44 CGATAAACAGAGAGTGGCTGTAGATCTCTGAACTGTGTTTAAACGTCCTCCAGGGAATG 103
Db  1  CGATAAACAGAGAGTGGCTGTAGATCTCTGAACTGTGTTTAAACGTCCTCCAGGGAATG 59
QY  104 TGACAGTCTTCTGATCAGAAAGGAGAGATGGCCCTGTGGCAAGGAAACAAGGAGC 163
Db  60 TGACAGTCTTCTGATCAGAAAGGAGAGATGGCCCTGTGGCAAGGAAACAAGGAGC 119
QY  164 AGGAGACAGCCTTATTGACGGCTCTGCCATGTCCAAAGAAAGAAAGACTTATGACAGGACA 223
Db  120 AGGAGACAGCCTTATTGACGGCTCTGCCATGTCCAAAGCAAGAAAGACTTATGACAGGACA 179
QY  224 TGCCTATCCACCCAGCAANTGATCTCAGATTGATGATTCACCTGGTTTCAGCAAGA 283
Db  180 TGCCTATCCACCCAGCAANTGATCTCAGATTGATGATTCACCTGGTTTCAGCAAGA 239
QY  284 TAGGATGATCAGAAACCTGGTAGCAATGCACTGTGGGAGGAAACGTTACCAGCAGTTT 343
Db  240 TAGGATGATCAGAAACCTGGTAGCAATGCACTGTGGGAGGAAACGTTACCAGCAGTTT 299

```

```

QY  344 CTCTGGAGATGACCTAGATGACAGAAAACAGCCTCTCTCCCAAGGCAACGAGAAAT 403
Db  300 CTCTGGAGATGACCTAGATGACAGAAAACAGCCTCTCTCCCAAGGCAACGAGAAAT 359
QY  404 TAATGCTGTATATAAAACGTAATTAAGTGAAGGAACCTCCGATGCGTTGGACAAAATATGA 463
Db  360 TAATGCTGTATATAAAACGTAATTAAGTGAAGGAACCTCCGATGCGTTGGACAAAATATGA 419
QY  464 AAAAATCTTCGAATGCTTGAAGGATGCAAGGACCTACTGCACTGAGGAGGATTTT 523
Db  420 AAAAATCTTCGAATGCTTGAAGGATGCAAGGACCTACTGCACTGAGGAGGATTTT 479
QY  524 TGAATCATCATCAAGGAAGCAGCAAGATGTATGACAGGAGCTTTGTTAAGCACCTTAA 583
Db  480 TGAATCATCATCAAGGAAGCAGCAAGATGTATGACAGGAGCTTTGTTAAGCACCTTAA 539
QY  584 GAGAAACTGAAACGATGATTTGAGAATACTTGTCCTGGAGGATATACACCCCA 643
Db  540 GAGAAACTGAAACGATGATTTGAGAATACTTGTCCTGGAGGATATACACCCCA 599
QY  644 TGCATATCTCGTTAATGATTGAGGAGAGAAAAGGATCAGATTGCTGTTTCTACATGG 703
Db  600 TGCATATCTCGTTAATGATTGAGGAGAGAAAAGGATCAGATTGCTGTTTCTACATGG 659
QY  704 AGCAGGATATGCTGAAGTCTCTGCGATATGTTACGGAATCAAATAGCTTCCAGAGC 763
Db  660 AGCAGGATATGCTGAAGTCTCTGCGATATGTTACGGAATCAAATAGCTTCCAGAGC 719
QY  764 TAGAAA-TTTCCTGTTAGTAAAGATGTTCTTTTCCC 800
Db  720 TAGAAA-TTTCCTGTTAGTAAAGATGTTCTTTTCCC 757

```

```

RESULT 5
BI768969
LOCUS   603058116F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207667 5',
DEFINITION mRNA sequence.
ACCESSION BI768969.1 GI:15760547
VERSION   BI768969
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT    Contact: Robert Strausberg, Ph.D.
          Email: cgabs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11520 row: p column: 04
          High quality sequence stop: 804.

```

```

FEATURES
source
1..903
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:5207667"
   /lab_host="DH10B"
   /clone_lib="NIH_MGC_122"
   /notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
   Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
   anonymous pool of 24 week female lung, 16 week female
   spleen, and 20-22 week male spleens. Library is oligo-dT

```

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 87.8%; Score 702.6; DB 12; Length 903;
 Best Local Similarity 97.9%; Pred. No. 4.5e-180;
 Matches 733; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 53 AGAAGAGTGGCTGTAGATCTGTAACCTGTTTAAACCTCCAGGGAATGTCAGATCC 112
 Db 1 AGAAGAGTGGCTGTAGATCTGTAACCTGTTTAAACCTCCAGGGAATGTCAGATCC 59
 QY 113 TTGCTATCAGAAAGCAGAGGATGCGCTGTTGGCAAGAAACAGAGCAGGAGACAG 172
 Db 60 TTGCTATCAGAAAGCAGAGGATGCGCTGTTGGCAAGAAACAGAGCAGGAGACAG 119
 QY 173 CTTTATGAGGCTTGCCATGTCCTCAAGAAAGAGCTTATGACAGGACATGCTATTCC 232
 Db 120 CTTTATGAGGCTTGCCATGTCCTCAAGAAAGAGCTTATGACAGGACATGCTATTCC 179
 QY 233 ACCAGCCCAATTGATTTCTCAGATTGATGACTTCACTGCTTTTTCAGCAAGATAGGATGAT 292
 Db 180 ACCAGCCCAATTGATTTCTCAGATTGATGACTTCACTGCTTTTTCAGCAAGATAGGATGAT 239
 QY 293 GCGAAACCTGTTAGCAATGCACTGTGGAGAAACGTTTACAGCAGTTTCTTGGAGA 352
 Db 240 GCGAAACCTGTTAGCAATGCACTGTGGAGAAACGTTTACAGCAGTTTCTTGGAGA 299
 QY 353 TGACCTTAGAATGACAGAAACAGCTCTCTCCAAAGCCCAAGAGAAATTAATGCTGA 412
 Db 300 TGACCTTAGAATGACAGAGGAATAGCTCTCTCCAAAGCCCAAGAGAAATTAATGCTGA 359
 QY 413 TATAAACCTGTAATAGTGAAGAACTCCGATGCGTTGGACAAAAATATGAAAAATCTT 472
 Db 360 TATAAACCTGTAATAGTGAAGAACTCCGATGCGTTGGACAAAAATATGAAAAATCTT 419
 QY 473 CGAAATGCTTGAAGAGTCAAGGACTTCACTGCTTTCAGAGAGCCTTTTGAATCCAT 532
 Db 420 CGAAATGCTTGAAGAGTCAAGGACTTCACTGCTTTCAGAGAGCCTTTTGAATCCAT 479
 QY 533 CATCAAGAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACCCTTAAGAAGAACT 592
 Db 480 CATCAAGAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACCCTTAAGAAGAACT 539
 QY 593 GAAACGTATGATTGGAATATCTTGTCCCTGAGGATTTATCACCCCAATGCTAATC 652
 Db 540 GAAACGTATGATTGGAATATCTTGTCCCTGAGGATTTATCACCCCAATGCTAATC 599
 QY 653 TCGTTAATGATTGAGAGAGAAAGATCAGATTGCTGTTTCTACAAATGGAGCAGGATA 712
 Db 600 TCGTTAATGATTGAGAGAGAAAGATCAGATTGCTGTTTCTACAAATGGAGCAGGATA 659
 QY 713 TTGCTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCCTTCAGAGGCTTAAGAAAT 772
 Db 660 TTGCTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCCTTCAGAGGCTTAAGAAAT 719
 QY 773 TCT-GTTAGTAAAGATGTTCTTTTCCC 800
 Db 720 TCTGTTAGTAAAGATGTTCTTTTCCC 748

RESULT 6

CA419320/c
 LOCUS
 DEFINITION UI-H-FHO-bch-o-11-0-UI-s1 NCI CGAP FHO Homo sapiens cDNA clone
 UI-H-FHO-bch-o-11-0-UI 3', mRNA sequence.
 CA419320
 ACCESSION
 VERSION CA419320.1 GI:24781975
 KEYWORDS EST.

SOURCE

Homo sapiens (human)
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (Bases 1 to 705)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-t@mail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD

POLYA-Yes

FEATURES

source

Location/Qualifiers

1..705
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FHO-bch-o-11-0-UI"
 /tissue_type="Human Chondrosarcoma Cell Line"
 /dev_stage="Adult"
 /lab_hosts="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FHO"
 /notes="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr James Martin from University of Iowa
 TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1 Chondrosarcoma
 TAG LIB=UI-H-FHO
 TAG_SEQ=AGAATCCGGC"

ORIGIN

Query Match 82.9%; Score 663; DB 14; Length 705;
 Best Local Similarity 97.8%; Pred. No. 2.5e-169;
 Matches 672; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 112 CTTGCTATCAGAAAGCAGAGGATGCGCTGTTGGCAAGAAACAGGAGCAGGAGACA 171
 Db 705 CTTGCTATCAGAAAGCAGAGGATGCGCTGTTGGCAAGAAACAGGAGCAGGAGACA 646
 QY 172 GCCTTATTGAGGCTCTGCCATGTCCAAAGAAAGAGCTTATGACAGGACATGCTATTCC 231
 Db 645 GCCTTATTGAGGCTCTGCCATGTCCAAAGAAAGAGCTTATGACAGGACATGCTATTCC 596
 QY 232 CACCCAGCCCAATTGGATTCTCAGATTGATGACTTCACTGTTTCAGCAAGATAGGATGA 291
 Db 585 CACCCAGCCCAATTGGATTCTCAGATTGATGACTTCACTGTTTCAGCAAGATAGGATGA 526
 QY 292 TGCAGAAACCTGCTAGCAATGCACTGTGGAGGAAACGTTTACCAGCAGTTTCTCTGGAG 351
 Db 525 TGCAGAAACCTGCTAGCAATGCACTGTGGAGGAAATGTTACCAGCAATTTCTCTGGAG 466
 QY 352 ATGACCTAGAAATGACAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTG 411
 Db 465 ATGACCTAGAAATGACAGAGGAAATAGCCTCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTG 406


```
QY 412 ATATAAACGTAATTAGTGAAGAACTCCGATCGCTTGACAAAATATGAAAAATCT 471
|
|
|
Db 405 ATATAAAATGTCAGTAGTGAAGAAATCCGATCGCTTGACGAAAATATGAAAAATCT 346
|
|
|
QY 472 TCGAAATGCTTGAAGGAGTGCAGGACCTACTGAGTCAGGAGAGCATTTTGTGATCCA 531
|
|
|
Db 345 TCGAAATGCTTGAAGGAGTGCAGGACCTACTGAGTCAGGAGAGCATTTTGTGATCCA 286
|
|
|
QY 532 TCATCAAGGAGCAGCAGGAGATGATGAGAGCAGGACTTTGTAAGCAGCTTAAAGAGAAAC 591
|
|
|
Db 285 TCATCAAGGAGCAGCAGGAGATGATGAGAGCAGGACTTTGTAAGCAGCTTAAAGAGAAAC 226
|
|
|
QY 592 TGAACCTGATGATTGAGGATGATGAGAGCAGGACTTTGTAAGCAGCTTAAAGAGAAAC 651
|
|
|
Db 225 TGAACCTGATGATTGAGGATGATGAGAGCAGGACTTTGTAAGCAGCTTAAAGAGAAAC 166
|
|
|
QY 652 CTCGTTAATGATTGAGGAGAGAAAGGATCAGATGCTGTTTCTACAATGGAGCAGGAT 711
|
|
|
Db 165 CTCGTTAATGATTGAGGAGAGAAAGGATCAGATGCTGTTTCTACAATGGAGCAGGAT 106
|
|
|
QY 712 ATTGCTGAAGTCTCTGCGATATGTTACCGAATCAATACCTTCCAGAGGCTTAAGAAAT 771
|
|
|
Db 105 ATTGCTGAAGTCTCTGCGATATGTTACCGAATCAATACCTTCCAGAGGCTTAAGAAAT 46
|
|
|
QY 772 TTCTGTTAGTAAAGATGTTCTTTTC 798
|
|
|
Db 45 TTCTGTTAGTAAAGATGTTCTTTTC 19
|
|
|

RESULT 7
BE893633
LOCUS
DEFINITION 60143643F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921607 5',
mRNA sequence.
ACCESSION BE893633
VERSION BE893633.1 GI:10355190
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 963)
NTH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9754 row: n column: 08
High quality sequence stop: 707.
FEATURES
Location/Qualifiers
1..963
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3921607"
/tissue_types="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 Kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 78.4%; Score 627.4; DB 10; Length 963;
```

```
Best Local Similarity 92.6%; Pred. No. 1.3e-159;
Matches 705; Conservative 0; Mismatches 46; Indels 10; Gaps 4;
QY 42 ACCGATATAACAGAGAGGTCGCTGTAGATCCTGAAATCTGTGTTTAAACGTCCTCCAGGAA 101
|
|
|
Db 1 ACCGATATAACAGAGAGGTCGCTGTAGATCCTGAAATCTGTGTTTAAACGTCCTCCAGGAA 60
|
|
|
QY 102 TGTGACAGTCCTTTCGTATCAGAAAGGAGGAGGATGCGCTTGTGGCAAGGAAACAGAGGA 161
|
|
|
Db 61 TGTGACAGTCCTTTCGTATCAGAAAGGAGGAGGATGCGCTTGTGGCAAGGAAACAGAGGA 120
|
|
|
QY 162 GCAGGAGACAGCCTTATTGACAGGCTCTGCCATGTCCTCAAGAAAGAAAGAGCTTATGACAGGA 221
|
|
|
Db 121 GCAGGAGACAGCCTTATTGACAGGCTCTGCCATGTCCTCAAGAAAGAAAGAGCTTATGACAGGA 180
|
|
|
QY 222 CATGCTATTCCACCCAGGCAATTCGATTCCTCAGATTGATGACTTCATGCTGTTTACAGAAA 281
|
|
|
Db 181 CATGCTATTCCACCCAGGCAATTCGATTCCTCAGATTGATGACTTCATGCTGTTTACAGAAA 240
|
|
|
QY 282 CATGAGGATGATGCAGAAACCTGCTGAGCAATGCACTGTGGAGGAGAAACGTTTACCAGCAGT 341
|
|
|
Db 241 GATGGGATGATGCAGAAACCTGCTGAGCAATGCACTGTGGAGGAGAAACGTTTACCAGCAAT 300
|
|
|
QY 342 TTCTCTGGAGATGACCTAGAAATGAGAGAGAAACAGCCTCTCTCCAAAAGCCAAACAGAGAA 401
|
|
|
Db 301 TTCTCTGGAGATGACCTAGAAATGAGAGAGAAACAGCCTCTCTCCAAAAGCCAAACAGAGAA 360
|
|
|
QY 402 ATTAATGCTGATATAAAACGTTAAATTAAGTGAAGGAACTCCGATCGCTTGGACAAAAATAT 461
|
|
|
Db 361 ATTAATGCTGATATAAAATGCTCAAGTAGTGAAGGAAATCCGATGCTTGGACGAAATAT 420
|
|
|
QY 462 GAAAAATCTTCGAAATGCTTTGAAAGGAGTGAAGGAGCTTACTGCGATCAGGAGAACGATTT 521
|
|
|
Db 421 GAAAAATCTTCGAAATGCTTTGAAAGGAGTGAAGGAGCTTACTGCGATCAGGAGAACGATTT 480
|
|
|
QY 522 TTTGAATCCATCATCAAGGAGCAGCAGAGATGATGAGACGAGACTTTGTTAAGCACCCTT 581
|
|
|
Db 481 TTTGAATCCATCATCAAGGAGCAGCAGAGATGATGAGACGAGACTTTGTTAAGCACCCTT 540
|
|
|
QY 582 AAGAGAAACCTGAAACCTGATGTTGAGATATCTGTCCTCGGAGGAGTATATCACACCCCA 641
|
|
|
Db 541 AAGAGAAACCTGAAACCTGATGTTGAGATATCTGTCCTCGGAGGAGTATATCACACCCCA 599
|
|
|
QY 642 AATGATATATCTGTTAATGATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 698
|
|
|
Db 600 AATGATATATCTGTTAATGATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
|
|
|
QY 699 AATG---GAGCAGGATATGCTGAAGTCTCTGCGATATGTTACCGAATCAAAATAGCCTT 755
|
|
|
Db 660 AATGGAGCAGCAGCATAATTTGCTGAAGTCTCTGCTGCTTATGTTACGAA---TCAATGGCTT 716
|
|
|
QY 756 CCAGAGGCTTAAAGAAATTTCTGTTAGTAAAGAGATGTTCTTTT 796
|
|
|
Db 717 CCAGAGGTTAAAGAAATTTCTGGGTGTAACAGAGGTCCTTTT 757
|
|
|

RESULT 8
BQ020473
LOCUS
DEFINITION BQ020473 690 bp mRNA linear EST 17-JUN-2002
IMAGE:5877002 3', mRNA sequence.
ACCESSION BQ020473
VERSION BQ020473.1 GI:19755751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 690)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
```

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source

Location/Qualifiers
1..690
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5877002"
/tissue_type="Fibrosarcoma"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Fsl"
/note="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Fsl is
a cDNA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1080 (ATCC number CCL-121). The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTTCTACGAG.
TAG_TISSUE=fibrosarcoma
TAG_LIB=UI-H-DPO
TAG_SEQ=GTCTTACGAG"

ORIGIN

Query Match 78.0%; Score 623.9; DB 12; Length 690;
Best Local Similarity 97.4%; Pred. No. 1.2e-158;
Matches 634; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```
QY 150 AGGAAACAGGAGCAGGACGCTTATTGAGGCTCTGCCATGTCCAAAGAAAGAG 209
DB 690 AGGAAACAGGAGCAGGACGCTTATTGAGGCTCTGCCATGTCCAAAGAAAGAG 631
QY 210 CTTATCAGCAGCATCTATTCCACCCGCAATTGGATTCTCAGATTGATGACTTCACT 269
DB 630 CTTATCAGCAGCATCTATTCCACCCGCAATTGGATTCTCAGATTGATGACTTCACT 571
QY 270 GGTTCAGCAAGATAGGATGATGCAGAACCTGGTAGCAATGCCCTGTGGGGAAC 329
DB 570 GGTTCAGCAAGATAGGATGATGCAGAACCTGGTAGCAATGCCCTGTGGGGAAT 511
QY 330 GTTACCAGCAGTTTCTCTGGAGATGACCTAGAAATGCAGAGAACAGCCCTCTCTCCCAA 389
DB 510 GTTACCAGCAATTTCTCTGGAGATGACCTAGAAATGCAGAGAACAGCCCTCTCTCCCAA 451
QY 390 AGCCACGCAAAATTAATCTGTATATAAAGCTTAATAGTGAAGAACTCCGATCGCTT 449
DB 450 AGCCACGCAAAATTAATCTGTATATAAAGCTTAATAGTGAAGAACTCCGATCGCTT 391
QY 450 GGAACAAAATATGAAAAATCTTCGAAATGCTTTGAAGGAGTGCAGGACCTACTGCAGTC 509
DB 390 GGAACAAAATATGAAAAATCTTCGAAATGCTTTGAAGGAGTGCAGGACCTACTGCAGTC 331
QY 510 AGAAGGATTTTGAATCCATCATCAGGAGCAGCAGATGATGATGAGCAGACTTT 569
DB 330 AGAAGGATTTTGAATCCATCATCAGGAGCAGCAGATGATGATGAGCAGACTTT 271
QY 570 GTTAAGCACCCTTAAGAGAAATGAAACGATGATTTGAGAACTATTGCTCCCTGGAGGAT 629
DB 270 GTTAAGCACCCTTAAGAGAAATGAAACGATGATTTGAGAACTATTGCTCCCTGGAGGAT 211
```

```
QY 630 TATCACACCCCAATGCATATCTCTGTTAATGTTAGTGAGAGAGAAAGGATCAGATTGCT 689
DB 210 TATCACACCTCAATGCATATCTCTGTTAATGTTAGTGAGAGAGAAAGGATCAGATTGCT 151
QY 690 GTTTTCTTACAATGGAGCAGGATATTGCTGGAAGTCTCTCGCATATGTTACCGAATCAAT 749
DB 150 GTTTTCTTACAATGGAGCAGGATATTGCTGGAAGTCTCTCGCATATGTTACCGAATCACT 91
QY 750 AGCTTCCAGAGCGCTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 800
DB 90 GGCCTTCCAGAGCGCTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 40
```

RESULT 9

BI460396

LOCUS

DEFINITION

BI460396

VERSION

BI460396.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 653)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: Miklos Falkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11675 row: f column: 17

High quality sequence stop: 643.

Location/Qualifiers

1..653

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5267728"

/lab_host="DH10B"

/clone_lib="NIH MGC 97"

/notes="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(grc99); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTVN-3', size-selected for average

insert size 2.2 kb and normalized to 10⁶. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH_MGC Library."

ORIGIN

Query Match 76.6%; Score 613; DB 12; Length 653;

Best Local Similarity 99.8%; Pred. No. 1e-155;

Matches 624; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CTCTCTCCAGCAGGTCAGGACTTCCAGGACTGAAACAATGACCGATAAACAAGAGG 60

DB 29 CTCTCTCCAGCAGGTCAGGACTTCCAGGACTGAAACAATGACCGATAAACAAGAGG 88

QY 61 TGGCTGTAGATCTCTGAAACTGTGTTTAAACGTCCTCCAGGGAATGTGACAGTCCTTCGATC 120

DB 89 TGGCTGTAGATCTCTGAAACTGTGTTTAAACGTCCTCCAGGGAATGTGACAGTCCTTCGATC 148

```
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP DT1"
/notes="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
NCI CGAP DT1 is a normalized cDNA library containing the
following tissue(s): Metastatic Chondrosarcoma in Lung.
The library was constructed according to Bionaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an Ecor I adaptor, digested with Not I, and cloned
directionally into p77T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AACTGTTCGG.
TAG TISSUE=lung metastatic chondrosarcoma
TAG_LIB=UI-H-DT1
TAG_SEQ=AACTGTTCGG"

ORIGIN
Query Match      76.5%; Score 611.8; DB 12; Length 660;
Best Local Similarity 99.5%; Pred. No. 2.1e-155;
Matches 624; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 174 CTTATTGCAGGCTCTGCCATGTCCAAAGAAAGAAAGCTTATGACAGCATGCTATTCCA 233
Db 660 CTTATTGCAGGCTCTGCCATGTCCAAAGAAAGAAAGCTTATGACAGCATGCTATTCCA 601
QY 234 CCCAGCCAAATGGGATTTCTCAGATTGATGACTTCACTGTTTCAGCAAGATAGGATGATG 293
Db 600 CCCAGCCAAATGGGATTTCTCAGATTGATGACTTCACTGTTTCAGCAAGATAGGATGATG 541
QY 294 CAGAAACCTGTAGCAATGACCTGTGGGAGAAAGCTTACCGACAGTCTCTCTGGAGAT 353
Db 540 CAGAAACCTGTAGCAATGACCTGTGGGAGAAAGCTTACCGACAGTCTCTCTGGAGAT 481
QY 354 GACCTAGAAATGCAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGAT 413
Db 480 GACCTAGAAATGCAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGAT 421
QY 414 ATAAACGCTAAATAGTGAAGAACTCCGATGCGTTGGAGCAAAAATATGAAAAATCTTC 473
Db 420 ATAAACGCTAAATAGTGAAGAACTCCGATGCGTTGGAGCAAAAATATGAAAAATCTTC 361
QY 474 GAAATGCTTGAAGAGGAGTCAAGGACCTACTGAGTCAGAAAGCGATTTTGAATCCATC 533
Db 360 GAAATGCTTGAAGAGGAGTCAAGGACCTACTGAGTCAGAAAGCGATTTTGAATCCATC 301
QY 534 ATCAAGGAGCAGCAAGATGATGAGAGAGACTTTGTTAAGACCTTTAAGAGAACTG 593
Db 300 ATCAAGGAGCAGCAAGATGATGAGAGAGACTTTGTTAAGACCTTTAAGAGAACTG 241
QY 594 AAACCTGATGATTTGAGATATCTTGTCCCTGGAGGATTTATCACCCCAAAATGCAATCT 653
Db 240 AAACCTGATGATTTGAGATATCTTGTCCCTGGAGGATTTATCACCCCAAAATGCAATCT 181
QY 654 CTTAATGATTCAGAGAGAGAAAGATCAGATGCTGTTTCTTACATGGAGCAGGATAT 713
Db 180 CTTAATGATTCAGAGAGAGAAAGATCAGATGCTGTTTCTTACATGGAGCAGGATAT 121
QY 714 TCGTGAAGTCTCCTGCGATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTT 773
Db 120 TCGTGAAGTCTCCTGCGATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTT 62
QY 774 CTGTTAGTAAAGATGTTCTTTTCC 800
Db 61 CTGTTAGTAAAGATGTTCTTTTCC 35

RESULT 11
BM761296 642 bp mRNA linear EST 04-MAR-2002
LOCUS
```

```
121 AGAAAGGCGAGAGATGGCCCTTTGGCAAGGAAACAGAGAGCAGAGACAGCCTTATTG 180
149 AGAAAGGCGAGAGATGGCCCTTTGGCAAGGAAACAGAGAGCAGAGACAGCCTTATTG 208
181 CAGGCTCTGCATGTCCAAAGAAAGAGCTTATGACAGGACATGCTATTCACCCAGCC 240
209 CAGGCTCTGCATGTCCAAAGAAAGAGCTTATGACAGGACATGCTATTCACCCAGCC 268
241 AATGGAATCTCAGATGATGACTTCACTGTTTCAGCAAGATAGGATGATGCAGAAAC 300
269 AATGGAATCTCAGATGATGACTTCACTGTTTCAGCAAGATAGGATGATGCAGAAAC 328
301 CTGTAGCAATGACCTGTGGAGGAAACGTTACACGAGCTTCTCTGAGAGATGACTAG 360
329 CTGTAGCAATGACCTGTGGAGGAAACGTTACACGAGCTTCTCTGAGAGATGACTAG 388
361 AATGCAAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGATATAAAC 420
389 AATGCAAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGATATAAAC 448
421 GTAATTTAGTGAAGAACTCCGATGCTTGCACAAAATATGAAAAATCTTCGAAATGC 480
449 GTAATTTAGTGAAGAACTCCGATGCTTGCACAAAATATGAAAAATCTTCGAAATGC 508
481 TTGAAGAGTGCAAGGACCTACTGAGTCAGGAGGAGGATTTTGAATCCATCATCAGG 540
509 TTGAAGAGTGCAAGGACCTACTGAGTCAGGAGGAGGATTTTGAATCCATCATCAGG 568
541 AAGCAGCAAGATGATGAGAGGAGCTTGTGAAGCAGCTTAAAGAGAACTGAAACGTA 600
569 AAGCAGCAAGATGATGAGAGGAGCTTGTGAAGCAGCTTAAAGAGAACTGAAACGTA 628
601 TGATTT-GAGAAATCTTGTCCCTGG 624
629 TGATTTGAGAAATCTTGTCCCTGG 653

RESULT 10
BM998183/3
LOCUS
DEFINITION
UI-H-DT1-awc-o-07-0-UI.s1 NCI CGAP DT1 Homo sapiens cDNA clone
IMAGE:5887710 3', mRNA sequence.
ACCESSION
BM998183
VERSION
BM998183.1 GI:19723084
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
Location/Qualifiers
1..660
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5887710"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
```

```

DEFINITION K-EST0042057 S13KMS5 Homo sapiens cDNA clone S13KMS5-2-E10 5', mRNA
sequence.
ACCESSION BM761296
VERSION BM761296.1 GI:19090897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: E column: 10
High quality sequence stop: 642.
FEATURES
Location/Qualifiers
1..642
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-2-E10"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10p"
/clone_lib="S13KMS5"
(note="Vector: PCMS; Site 1: EcoRI; Site 2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoRI site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dT-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10p' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."
ORIGIN
Query Match 76.4%; Score 611.2; DB 12; Length 642;
Best Local Similarity 98.7%; Pred. No. 3.1e-155;
Matches 616; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 16 GTCAGACTTCAGGACTGAAACGATACCGATTAACACAGAGAGGCTGGCTGTAGATCTCTG 75
DB 19 GTCTCTCTCCAGCAAGGAAACATACCGATTAACACAGAGAGGCTGGCTGTAGATCTCTG 78
QY 76 AAACCTGTGTTTAAACCTCCACGGAATGTGACAGTCTCTTCGTATCAGAAAGCCAGAGGA 135
DB 79 AAACCTGTGTTTAAACCTCCACGGAATGTGACAGTCTCTTCGTATCAGAAAGCCAGAGGA 138
QY 136 TGGCCCTCTGTGGCAAGAAACAAAGGACGAGGACGCTTATTCAGGCTCTGCCATGT 195
DB 139 TGGCCCTCTGTGGCAAGAAACAAAGGACGAGGACGCTTATTCAGGCTCTGCCATGT 198
QY 196 CCAAGAAAGAAAGCTTATGACAGGACATGCTATTCCACCCAGCAATTTGGATTCTTCAGA 255
DB 199 CCAAGAAAGAAAGCTTATGACAGGACATGCTATTCCACCCAGCAATTTGGATTCTTCAGA 258
QY 256 TTGATGACTTCACTGGTTTCAGCAAGATAGATGATGACAGAAACCTGTAGCAATGCAC 315

```

```

DB 259 TTGATGACTTCACTGGTTTCAGCAAGATAGATGATGACAGAAACCTGTAGCAATGCAC 318
QY 316 CTGTGGAGGAAACGTTACCAAGCTTTCTCTGGAGATGACCTAGATGTCAGAGAAACAG 375
DB 319 CTGTGGAGGAAACGTTACCAAGCTTTCTCTGGAGATGACCTAGATGTCAGAGAAACAG 378
QY 376 CCTCTCTCTCCAAAGCCCAACGAGAAATTAATGCTGATATAAAAGCTAAATTAGTGAAGG 435
DB 379 CCTCTCTCTCCAAAGCCCAACGAGAAATTAATGCTGATATAAAAGCTAAATTAGTGAAGG 438
QY 436 AACTCCGATCGCTTGACCAAAAATATGAAAAAATCTTCGAAATGCTTGAAGGAGTGCAAG 495
DB 439 AACTCCGATCGCTTGACCAAAAATATGAAAAAATCTTCGAAATGCTTGAAGGAGTGCAAG 498
QY 496 GACCTACTGAGTCAGAGGAGGATTTTTCATCCATCATCAGGAAGCAGCAAGATGTA 555
DB 499 GACCTACTGAGTCAGAGGAGGATTTTTCATCCATCATCAGGAAGCAGCAAGATGTA 558
QY 556 TGAGACGAGACTTTGTTAAGCACCTTTAAGCAAACTGAAGAACTGAACGATGATTTGAGATACT 615
DB 559 TGAGACGAGACTTTGTTAAGCACCTTTAAGCAAACTGAAGAACTGAACGATGATTTGAGATACT 618
QY 616 TGTCCCTCGAGGATTCACACC 639
DB 619 TGTCCCTCGAGGATTCACACC 642

```

```

RESULT 12
LOCUS AV700754 696 bp mRNA linear EST 16-JAN-2002
DEFINITION AV700754 GKC Homo sapiens cDNA clone GKCRA02 3', mRNA sequence.
ACCESSION AV700754
VERSION AV700754.1 GI:10302725
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
Location/Qualifiers
1..696
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCRA02"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
XhoI"

```

```

ORIGIN
Query Match 75.7%; Score 605.4; DB 9; Length 696;

```

```
Best Local Similarity 97.4%; Pred. No. 1.2e-153;
Matches 667; Conservative 0; Mismatches 13; Indels 5; Gaps 5;

Qy 120 CAGAAAGGAGGAGGAT-GGCCCTGTGGCAGAGAAACAAGAGCA-GGAGACAGCCTTA 177
Db 695 CAGAAAGGAGGAGGATGGGCTTGTGGCAAGNACCAAGAGGAGGAGGAGGCTTA 636
Qy 178 TTGCAGGCTCTGCCATGTCCAAAGAAAGAGCTTATGACAGGACATGCTATTCCACCC- 236
Db 635 TGCAAGGCTCTGCCATGTCCAAAC-AAAGAGCTTATGACAGGACATGCTATTCCACCCA 577
Qy 237 AGCCAAATGGATTTCTAGATGATGATTC-ACGTGTTTCCAGAAAGATAGGATGATGA 295
Db 576 AGCCATTTGGATTTCTAGATGATGATTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 517
Qy 296 GAAACCTGTGTAGCAATCCACTGTGGGAGGAAAGCTTATGACAGGACATGCTATTCCAGATGA 355
Db 516 GAAACCTGTGTAGCAATCCACTGTGGGAGGAAAGCTTATGACAGGACATGCTATTCCAGATGA 457
Qy 356 CTTAGATGACAGAAACAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 415
Db 456 CTTAGATGACAGAAACAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 397
Qy 416 AAAACGTAATTTAGTGAAGAACTCCGATGCTGTGGACAAAATATGAAAAATCTTCGA 475
Db 396 AAAACGTAATTTAGTGAAGAACTCCGATGCTGTGGACAAAATATGAAAAATCTTCGA 337
Qy 476 AATCCTTTGAAGAGTCAAGACCTACTGACGACAGAAAGCGATTTTGAATCCATCAT 535
Db 336 AATCCTTTGAAGAGTCAAGACCTACTGACGACAGAAAGCGATTTTGAATCCATCAT 277
Qy 536 CAAGGAAGCAGCAGATGATGACAGCAGACTTGTGTAAGCCTTAAAGAAAGAACTGAA 595
Db 276 CAAGGAAGCAGCAGATGATGACAGCAGACTTGTGTAAGCCTTAAAGAAAGAACTGAA 217
Qy 596 ACGTATGATTGAAATCTTGTGCTCCGAGGATTAATCAACCCCAATGCAATTAATCTCG 655
Db 216 ACGTATGATTGAAATCTTGTGCTCCGAGGATTAATCAACCCCAATGCAATTAATCTCG 157
Qy 656 TTAATGATTGAGGAGAGAAAGATGATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 715
Db 156 TTAATGATTGAGGAGAGAAAGATGATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 97
Qy 716 CTGAAGTCTCTGTCATATGTTACCGAATCAATAGCCTTCCAGAGCTTAAGAAATTTCT 775
Db 96 CTGAAGTCTCTGTCATATGTTACCGAATCAATAGCCTTCCAGAGCTTAAGAAATTTCT 37
Qy 776 GTTAGTAAAGATGTTCTTTTCCC 800
Db 36 GTTAGTAAAGATGTTCTTTTCCC 12

RESULT 13
LOCUS BU940543
DEFINITION AGENCOURT 10580391 NIH_MGC_128 Homo sapiens cDNA clone
IMAGE:6710386 5', mRNA sequence.
ACCESSION BU940543
VERSION BU940543.1 GI:24129362
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

```
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM3015 row: m column: 10
High quality sequence stop: 465.
Location/Qualifiers
source
1..832
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6710386"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_128"
/notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-RAGCAGTGTATCAACGACAGTGCATACGCGCGG-3' and
5'-ATTCTAGAGCGCGGCGGCGGACATG-3' Full-length
Creator SMART kit and size-selected using the Clontech
size fraction (other fractions present in NIH_MGC_128 and
NIH_MGC_127). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."
```

ORIGIN

```
Query Match 75.0%; Score 599.6; DB 13; Length 832;
Best Local Similarity 95.9%; Pred. No. 4.6e-152;
Matches 637; Conservative 0; Mismatches 24; Indels 3; Gaps 2;

Qy 16 GTCAGGACTTCAGACCTGAAACAATGACCGATAAAACAGAGAGGTGGCTGTAGATCTG 75
Db 28 GTCTCTCTCCAGCAGGAACAATGACCGATAAAACAGAGAGGTGGCTGTAGATCTG 87
Qy 76 AAATGTGTTTAAACGTCCTCCAGGGAATGTGACGTCTCTGATATCAGAAAGGAGAGGA 135
Db 88 AAATGTGTTTAAACGTCCTCCAGGGAATGTGACGTCTCTGATATCAGAAAGGAGAGGA 147
Qy 136 TGGCCCTCTTCCAGAGGAACAAGCAGCAGCAGCAGCTTATTGCAAGGCTCTCCCATGT 195
Db 148 TGGCCCTCTTCCAGAGGAACAAGCAGCAGCAGCAGCTTATTGCAAGGCTCTCCCATGT 207
Qy 196 CCAAGAAAGAAAGCTTATGACAGGACATGCTATTCCACCAGCAATTTGATTTCTCAGA 255
Db 208 CCAAGAAAGAAAGCTTATGACAGGACATGCTATTCCACCAGCAATTTGATTTCTCAGA 267
Qy 256 TTGATGACTTCACCTGTTTCAGCAAGATAGGATGATGCAAGAACCTGGTAGCAATGCAC 315
Db 268 TTGATGACTTCACCTGTTTCAGCAAGATAGGATGATGCAAGAACCTGGTAGCAATGCAC 327
Qy 316 CTGTGGAGGAAACGTTTACCAGCAGTCTTCTCTGGAGATGACCTAGAAATGCAAGAGAAACAG 375
Db 328 CTGTGGAGGAAACGTTTACCAGCAGTCTTCTCTGGAGATGACCTAGAAATGCAAGAGAAACAG 387
Qy 376 CCTCTCTCTCCAAAGCCCAACGAGAAATTAATGCTGATATATAACGTAATTAATGTAAGG 435
Db 388 CCTCTCTCTCCAAAGCCCAACGAGAAATTAATGCTGATATATAACGTAATTAATGTAAGG 447
Qy 436 AACTCCGATGCTTGGACAAAATATGAAAAATCTTCGAAATCTTTGAAAGAGTGAAG 495
Db 448 AACTCCGATGCTTGGACAAAATATGAAAAATCTTCGAAATCTTTGAAAGAGTGAAG 507
Qy 496 GACCTACTGCACTGAGGAGCGATTTTGTGATCCATCATCAGGAGGAGCAGAGATGA 555
Db 508 GACCTACTGCACTGAGGAGCGATTTTGTGATCCATCATCAGGAGGAGCAGAGATGA 567
```

```

QY 556 TGAGACGAGACTTTGTTAAGCACC-TTAAGAAGAAACTGAAACGATGATGATTGAGATAC 614
|||||
DB 568 TGAGACGAGACTTTGTTAAGCACC-TTAAGAAGAAACTGAAACGATGATGATTGAGATAC 627
|||||
QY 615 TTGT--CCCTGGAGGATTAATCACACCCCAAAATGCATAATCTCGTTAATGATTGAGGAG 672
|||||
DB 628 TTGTCCCCGGGAGGATTAATCACACCCCAAAATGCATAATCTCGTTAATGAAATTGAGGAG 687
|||||
QY 673 AAAA 676
|||||
DB 688 AAAA 691
|||||

RESULT 14
BI552760
LOCUS
DEFINITION
603193727F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5265006 5',
mRNA sequence.
ACCESSION
BI552760
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 946)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11668 row: e column: 07
High quality sequence stop: 863.

FEATURES
source
1..946
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5265006"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN
Query Match 73.4%; Score 587.2; DB 12; Length 946;
Best Local Similarity 92.8%; Pred. No. 1.1e-148;
Matches 661; Conservative 0; Mismatches 43; Indels 8; Gaps 4;

QY 16 GTCAGGACTTCAGGACTGAACAATGACCGATAAAACAGAGAAGTGCGTGTAGATCTCTG 75
|||||
DB 228 GTCTCTCTCCAGCAAGGAACAATGACCAATAAAACAGAGAAGTGCGTGTAGATCTCTG 287
|||||
QY 76 AAACCTGTTTAAACCTCCAGGATGTGACAGTCTTCGTATCAGAAAGGCGAGGA 135
|||||

```

```

DB 288 AAACCTGTTTAAACCTCCAGGATGTGACAGTCTTCGTATCAGAAAGGCGAGGA 347
QY 136 TGGCCCTGTTGGCAAGGAAACAAGGAGCAGGACAGCCCTTATTGCAAGGCTCTGCCATGT 195
|||||
DB 348 TGGCCCTGTTGGCAAGGAAACAAGGAGCAGGACAGCCCTTATTGCAAGGCTCTGCCATGT 407
|||||
QY 196 CCAAGAAGAAGAGCTTATGACAGGACATGCTATTCCACCAGCCCAATTGGATTCTCAGA 255
|||||
DB 408 CCAAGCAAGAAGAGCTTATGACAGGACATGCTATTCCACCAGCCCAATTGGATTCTCAGA 467
|||||
QY 256 TTGATGACTTTCACCTGGTTTCAGCAAAAGATAGGATGATGACAGAAACCTGGTAGCAATGCAC 315
|||||
DB 468 TTGATGACTTTCACCTGGTTTCAGCAAAAGATAGGATGATGACAGAAACCTGGTAGCAATGCAC 527
|||||
QY 316 CTGTGGGAGAAAGCTTACCAGCAGTTTCTCTGGAGATGACCTAGATAATGACAGAAACAG 375
|||||
DB 528 CTGTGGGAGAAAGCTTACCAGCAGTTTCTCTGGAGATGACCTAGATAATGACAGAAACAG 587
|||||
QY 376 CCTCCTCTCCAAAAGCAACGAGAAATTAATGCTGATATATAAAACGTAATAATTAAGTGAAG 435
|||||
DB 588 CCTCCTCTCCAAAAGCAACGAGAAATTAATGCTGATATATAAAACGTAATAATTAAGTGAAG 647
|||||
QY 436 AACTCCGATGCGTTGGACAAAATAATGAAAAATCTTCGAAATGCTTGAAGAGTGCAG 495
|||||
DB 648 AACTCCGATGCGTTGGACAAAATAATGAAAAATCTTCGAAATGCTTGAAGAGTGCAG 707
|||||
QY 496 GACCTACTGCACTCAGGAGCGATTTTTCGATATATAAAACGTAATAATTAAGTGAAG 555
|||||
DB 708 GACCTACTGCACTCAGGAGCGATTTTTCGATATATAAAACGTAATAATTAAGTGAAG 767
|||||
QY 556 TGAGACGAGA---CTTTGTTAAGCACCTTAAGAAGAAACTGAAACCGTAT-GATTTGAGAA 611
|||||
DB 768 ATGAGACGAGAGACCTTTGTTAAGCACCTTAAGAAGAAACTGAAACCGTATGATTTCAGAA 827
|||||
QY 612 TACTTGTCCCTCGAGGATTAATCACACCCCAAAATGCAATACTCGTAAATGATTGAGG--A 669
|||||
DB 828 TTTGTGTCCTCGAGGATTAATCACACCCCAAAATGCAATACTCGTAAATGATTGAGGAG 887
|||||
QY 670 GAGAAAAGGATCAGATTGC--TGTTTTCTACAATGGAGCAGGATATTGCTGA 719
|||||
DB 888 CGCACAGGCTCCGATTGCGTGTTCCTCAATGGAGCAGAGATTGCTGA 939
|||||

RESULT 15
CA419457 614 bp mRNA linear EST 07-NOV-2002
LOCUS
DEFINITION
UT-H-FHO-bci-m-22-0-UI.s1 NCI CGAP FHO Homo sapiens cDNA clone
UT-H-FHO-bci-m-22-0-UI 3', mRNA sequence.
ACCESSION
CA419457
VERSION
CA419457.1 GI:24782112
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 614)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..614
/organism="Homo sapiens"

```


Search completed: April 26, 2004, 01:59:02
Job time : 1457.53 secs

```
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="UI-H-FHO-bci-m-22-0-UI"  
/tissue_type="Human Chondrosarcoma Cell Line"  
/dev_stage="Adult"  
/lab_host="DH10B (Life Technologies)"  
/clone_lib="NCI CGAP_FHO"  
/notes="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP_FHO is a cDNA library containing the following  
tissue(s): Human Grade 1 Chondrosarcoma Cell Line. The  
library was constructed according to Bonaldo, Lennon and  
Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into pT7T3-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dT)18 tail. The sequence tag for this  
library is AGAATCCGGC. The cell line was provided by Dr  
James Martin from University of Iowa  
TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
Chondrosarcoma  
TAG_LIB=UI-H-FHO  
TAG_SEQ=AGAATCCGGC"
```

ORIGIN

```
Query Match      72.0%; Score 576; DB 14; Length 614;  
Best Local Similarity 99.0%; Pred. No. 1.1e-145;  
Matches 590; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
  
QY 206 GAAGCTTATGACAGGACGCTATTCCCA-CCAGCCAAATGGATCTCAGATTGATGACT 264  
DB 614 GAAGCTTATGACAGGACGCTATTCCACCCAGCCAAATGGATCTCAGATTGATGACT 555  
  
QY 265 TCACTGGTTTCAGCAAGATAGGATGATGACAGAAACCTGGTAGCAATGCACCTGTGGGAG 324  
DB 554 TCACTGGTTTCAGCAAGATAGGATGATGACAGAAACCTGGTAGCAATGCACCTGTGGGAG 495  
  
QY 325 GAACCTTACACAGCTTTCTCTGGAGATGACCTAGAAATGCAGAGNAAACAGCCTCTCTC 384  
DB 494 GAACCTTACACAGCTTTCTCTGGAGATGACCTAGAAATGCAGAGNAAACAGCCTCTCTC 435  
  
QY 385 CCAAAAGCCCAACGAGAAATTAATGCTGATATAAAACGTAAATAGTGAAGGAACCTCCGAT 444  
DB 434 CCAAAAGCCCAACGAGAAATTAATGCTGATATAAAACGTAAATAGTGAAGGAACCTCCGAT 375  
  
QY 445 GCGTTGACAAAATATGAAAAATCTTGGAAATGCTTGAAGAGTGCAGGACCTACTG 504  
DB 374 GCGTTGACAAAATATGAAAAATCTTGGAAATGCTTGAAGAGTGCAGGACCTACTG 315  
  
QY 505 CAGTCAGGAAGCGATTTTGTGAATCCATCATCAAGGAAGCAGCAAGATGTATGAGACGAG 564  
DB 314 CAGTCAGGAAGCGATTTTGTGAATCCATCATCAAGGAAGCAGCAAGATGTATGAGACGAG 255  
  
QY 565 ACTTTGTTAAGCACTTAAGAGAAACCTGAAACGTATGATTTGAGAATACTTGTCCCTGG 624  
DB 254 ACTTTGTTAAGCACTTAAGAGAAACCTGAAACGTATGATTTGAGAATACTTGTCCCTGG 195  
  
QY 625 AGGATTATCACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAAAAGGATCAGA 684  
DB 194 AGGATTATCACCCCAATGCAATATCTCATTTAATGATTGAGGAGAGAAAAGGATCAGA 135  
  
QY 685 TTGCTGTTTTCTCAATGGAGCAGGATATTGCTGAAGTCTCTCTGGCATATGTTACCGAAT 744  
DB 134 TTGCTGTTTTCTCAATGGAGCAGGATATTGCTGAAGTCTCTCTGGCATATGTTACCGAAT 75  
  
QY 745 CAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 800  
DB 74 CAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 19
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 07:15:18 ; Search time 39.687 Seconds
(without alignments)
1186.557 Million cell updates/sec

Title: US-10-051-835-12
Perfect score: 800
Sequence: 1 ctctctccagcaaggtcag.....taaaagatgtctttttccc 800

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	223.6	27.9	3812	4	US-09-784-316-1
2	70.6	8.8	65042	4	US-09-784-316-3
3	52	6.5	7218	1	US-08-232-463-14
4	37.2	4.7	6008	1	US-07-789-915A-5
5	37.2	4.7	6008	1	US-08-005-002C-5
6	37.2	4.7	6008	1	US-08-487-203A-5
7	36.8	4.6	656	4	US-08-936-165A-87
8	35.8	4.5	4084	3	US-08-866-340-1
9	35.8	4.5	4460	3	US-09-103-875-4
10	34.2	4.3	5829	4	US-08-809-254A-4
11	34.2	4.3	9828	4	US-08-961-527-41
12	34	4.2	981	4	US-09-543-681A-3279
13	32.6	4.1	505	4	US-09-621-976-15639
14	32.6	4.1	87350	3	US-08-781-881-79
15	32.6	4.1	87350	4	US-09-618-166-79
16	32.6	4.1	87543	4	US-09-791-211-3
17	32.4	4.0	561	4	US-09-328-352-3577
18	32	4.0	2718	4	US-09-134-000C-1015
19	31.8	4.0	1329	4	US-09-134-001C-196
20	31.6	4.0	1914	4	US-09-543-681A-1697
21	31.6	4.0	2169	4	US-09-434-408-3
22	31.4	3.9	1101	4	US-09-891-641-67
23	31.4	3.9	2013	4	US-09-543-681A-1807
24	31.4	3.9	4034	4	US-09-883-134-5
25	31.2	3.9	1272	4	US-09-134-001C-2358
26	31	3.9	366	4	US-09-134-001C-997
27	31	3.9	481	4	US-09-621-976-211

C 28	31	3.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
C 29	31	3.9	1237	4	US-09-620-312D-419	Sequence 419, App
C 30	31	3.9	1311	4	US-09-833-381-872	Sequence 872, App
C 31	31	3.9	3429	4	US-09-936-989A-1	Sequence 1, Appli
C 32	31	3.9	4342	3	US-09-338-907-107	Sequence 107, App
C 33	31	3.9	4342	4	US-09-218-207-107	Sequence 118, App
C 34	31	3.9	4582	3	US-09-338-907-118	Sequence 117, App
C 35	31	3.9	4582	4	US-09-218-207-118	Sequence 117, App
C 36	31	3.9	4686	3	US-09-338-907-117	Sequence 117, App
C 37	31	3.9	4686	4	US-09-218-207-117	Sequence 114, App
C 38	31	3.9	4875	3	US-09-218-207-114	Sequence 114, App
C 39	31	3.9	4875	4	US-09-338-907-116	Sequence 116, App
C 40	31	3.9	4958	3	US-09-218-207-116	Sequence 116, App
C 41	31	3.9	4958	4	US-09-338-907-121	Sequence 121, App
C 42	31	3.9	4986	3	US-09-218-207-121	Sequence 120, App
C 43	31	3.9	4986	4	US-09-338-907-120	Sequence 120, App
C 44	31	3.9	5020	3	US-09-218-207-120	Sequence 120, App
C 45	31	3.9	5020	4	US-09-338-907-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-09-784-316-1
; Sequence 1, Application US/09784316
; Patent No. 6461843
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01139
; CURRENT APPLICATION NUMBER: US/09/784,316
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3812
; TYPE: DNA
; ORGANISM: Human
; US-09-784-316-1

Query Match 27.9%; Score 223.6; DB 4; Length 3812;
Best Local Similarity 64.6%; Pred. No. 6.9e-60;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;

Qy	212	TATGACGAGCATGCTATTTCACCCAGCCCAATGGATTCTCAGATTGATGACTTCACTCG	271
Db	2429	TATGACGAGGATCTTTATGCCACCCCAACCAAGTGGATTCTCTGTGACGACTTCAAG	2488
Qy	272	TTTCAGCAAGATAGGATGATGACAGAACTGCTAGCAATGCACCTGTGGAGGAAACCT	331
Db	2489	TCTCAGCAAGATGGCTGATTCAAAAACCTGTAGTACGCAATTTGTAGGAGGCCAA	2548
Qy	332	TACACAGTTTCTCTGGAGATGACCTAGAAATGCAGAGAAAAGAGCCTC	379
Db	2549	AAACTGCAGTCTCTCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGCTAT	2608
Qy	380	-----CTCTCCCAAAAGCCCAAGAGAAATTAATGCTGATATAAAGC	421
Db	2609	GCCAAATACATTACAATCACTCTGCTATGSCACNAGGAATCAATGCTGATATAAACA	2668
Qy	422	TAAATTAGTGAAGGAATCCGATGGCTGGACAAAATATGAAAAAATCTTGAATGCT	481
Db	2669	TCAATTAATGAAGGAAGTTTGAAGAGTTTGTGCGAAAATATGAAGAAATTTTCATTT	2728
Qy	482	TGAAGGATGCAAGGACCTACTGCACTAGGAGGAGGATTTTGTGATCCATCATCAAG	541
Db	2729	TGAAGGATGCAAGGACCTCTTGAGATGAAGAAACAGTTTGTGATTTCCATCAAG	2788
Qy	542	AGCAGCAAGATGTATGAGACGAGACTTTGTTAAGCACCTTAAGAGAAACTGAACGTA	601

Db	2789	AGCCGCAAGGGTAAAGACGAGCTCTTAATTCAGTACCTTTGAGAAAGGTACTGAAAAAAT	2848
QY	602	GATTTGAGAAATCTGTCTCCCTGGAGGATTATCACGCCCAAAATGCAATAATCTCGTTAAATG	661
Db	2849	AAATTTCCCAACCTTTCACAAACAACATTAGTCACATCAACAGCAGATCATCATGTTTAGTG	2908
QY	662	-----ATTGAGGAGAGAAAGGATCAGATTGCTGTTTTCTACAATGGACGAGATATTG	715
Db	2909	CAAAGACCAGTGAGAAAAAATGACAAGTTTTCTGTGCTAGATGGAACAGGATATTG	2968
QY	716	CTGAAGTCTCTGGCATATGTTACCGNATCAAAATAGCCTTCCAGAGCTTAAGAA	769
Db	2969	TTCAAGCTCTCGGAATGTTTGAGTCAAGGGAATTGTTTTCCAGATGCTAAGAA	3022

RESULT 2

```

US-09-784-316-3
/ Sequence 3, Application US/09784316
/ Patent No. 6461843
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: CL001139
/ CURRENT APPLICATION NUMBER: US/09/784,316
/ CURRENT FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 65042
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(65042)
/ OTHER INFORMATION: n = A,T,C or G
US-09-784-316-3

```

	Query Match	8.8%	Score 70.6;	DB 4;	Length 65042;
	Best Local Similarity	59.6%;	Pred. No. 3.4e-11;		
	Matches 140;	Conservative	0;	Mismatches 89;	Indels 6; Gaps 1;
QY	549	AGATGTATGAGACGAGACTTTGTTAAGCACCCTTAAGAGAAACTGGAACGTTATGATTTGA	608		
Db	62066	AGGTTTAAAGACGAGCTCTTAATTCAGTACCTTGAGAAGGTACTAGAAAAATTAATTC	62125		
QY	609	GAATACTTGTCCCTGGAGGATTATCACACCCAAATGCAATAATCTGTTTAATGA	662		
Db	62126	CACCACCTTCACAAACAATTAGTTCATCAACAGCAGATCATCATGTTAGTGCAAAGAC	62185		
QY	663	TTGAGGAGAGAAAAGGATCAGATTGCTGTTTTCTCAATGGAGCAGGATATTGCTGAAGT	722		
Db	62186	CAGTGAGAAAAAATGACAAAGTTTCTGTGCTGTAGGATGGACACAGATATTGTTGAAGC	62245		
QY	723	CTCTGTCATATGTTTACCGAAATCAAAATAGCCTTCCAGAGCGCTAAGAAAAATTCCTGT	777		
Db	62246	CTCTGCGAATGTTTGAGTCAAGGGAATGCTTTCTCAGATGCTTAAGACGACGAGT	62300		

RESISTANCE

RESULT 3
 US-08-232-463-14/c
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 2213-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 839149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ19pt-Fls
US-08-232-463-14

[illegible]

RESULT 5
US-08-005-002C-5/c
; Sequence 5, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshevsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.

```

RESULT 6
US-08-487-203A-5/c
Sequence 5, Application US/08487203A
Patent No. 5683904
GENERAL INFORMATION:
APPLICANT: Baker, Rohan T.
APPLICANT: Tobias, John W.
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: Maine
COUNTRY: U.S.A.
ZIP: 03911
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,203A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,002
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-5091A32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207-363-0558
TELEFAX: 207-363-0528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 983..4774
US-08-487-203A-5

Query Match 4.7%; Score 37.2; DB 1; Length 6008;
Best Local Similarity 50.6%; Pred. No. 0.29;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 565 ACTTTGTTAAGCAGCTTAAAGAGAACTGAAAGCTATGATTGAGAACTACTTGTCCTCGG 624
Db 2413 AATATTTTCAGGATCCAAAGAGACAAAGATTCTGATTCTATATCTATCTATCGGT 2354
QY 625 AGAATTATCACCCCAAAATGCAATATCTCGTTAAATGATTGAGAGAGAAAAGGATCAGA 684
Db 2353 ATAATAATGCGAAACGGAAGATTAAATAAATGAGGTTCTCGCTCCAAAGGAGAATGAGT 2294
QY 685 TTGCTGTTTCTACATGAGGAGGAGATATTGCTGAAGTCTCCGCGATATGTTACCGGA 742
Db 2293 TTGCTCATTTGMAATTTAATAGATCTTGTCTCTGGATTCTCCCAATAATGGAAACCA 2236

RESULT 7
US-08-936-165A-87
Sequence 87, Application US/08936165A
Patent No. 6348582
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 656 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-936-165A-87

Query Match 4.6%; Score 36.8; DB 4; Length 656;
Best Local Similarity 52.6%; Pred. No. 0.12;
Matches 80; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 392 CCAACGAGAAATTAATCTGTATATAAAGCGTAATTAATGTAAGAACTCCGATCGTTGG 451
Db 423 CCCAGGTGACGATCTACCTGTAATCGCTGTTAGCATTAAAGCTTTAGAGCGCGATGC 482
QY 452 ACAAATATGAAAAATCTTCGAAATGCTTGAAGGAGTGCAGAGACCTACTGCGTCCAG 511
Db 483 TCATACGAGAAAAATCTTAGAATTAATGGAAGCTGTAGATACCTTACATTCCACTCCA 542
QY 512 GAAGCGATTTTGAATCCATCATCAAGGAAG 543
Db 543 GACGTGATCCTGACAAAACCATCAAGATGCCAG 574

RESULT 8
US-08-866-340-1/c
Sequence 1, Application US/08866340
Patent No. 6020318
GENERAL INFORMATION:
APPLICANT: Szvf, Moshe
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani, Shyam
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,340
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 106.101.187
TELECOMMUNICATION INFORMATION:

```
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4084 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-866-340-1

Query Match      4.5%; Score 35.8; DB 3; Length 4084;
Best Local Similarity 51.6%; Pred. No. 0.65; 77; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 319 TGGGAGAAACGTTACCAAGAGTCTTCTCGAGATGACCTAGAAATGCAGAGAAACAGCCT 378
DB 2865 TGGGTGACAGAGTGAGACTCTGCTCAAAAAACAAAAACAAACAAAAACACCCAC 2806
QY 379 CCTCTCCCAAGCCACGAGAAATTAATGCTGATATAAAACGTAATTAATGTAAGGAAC 438
DB 2805 CACCACCACTATTAGCAGCAAAATAGTCTGACATTAACAGAAATATCCAAATTATC 2746
QY 439 TCCGATGGCTTGGCAAAAAATATGAAAAATCTTCGAAA 477
DB 2745 TTGAACTCCATCGGAAAAATGCAAAATCCATTAAA 2707

RESULT 9
US-09-103-875-4/c
; Sequence 4, Application US/09103875A
; Patent No. 6221849
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: 106101.194
; CURRENT APPLICATION NUMBER: US/09/103,875A
; CURRENT FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/069,865
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 08/866,340
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 4460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-103-875-4

Query Match      4.5%; Score 35.8; DB 3; Length 4460;
Best Local Similarity 51.6%; Pred. No. 0.68; 77; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 319 TGGGAGAAACGTTACCAAGAGTCTTCTCGAGATGACCTAGAAATGCAGAGAAACAGCCT 378
DB 2863 TGGGTGACAGAGTGAGACTCTGCTCAAAAAACAAAAACAAACAAAAACACCCAC 2804
QY 379 CCTCTCCCAAGCCACGAGAAATTAATGCTGATATAAAACGTAATTAATGTAAGGAAC 438
DB 2803 CACCACCACTATTAGCAGCAAAATAGTCTGACATTAACAGAAATATCCAAATTATC 2744
QY 439 TCCGATGGCTTGGCAAAAAATATGAAAAATCTTCGAAA 477
DB 2743 TTGAACTCCATCGGAAAAATGCAAAATCCATTAAA 2705

RESULT 10
```

```
US-08-809-254A-4/c
; Sequence 4, Application US/08809254A
; Patent No. 6660852
; GENERAL INFORMATION:
; APPLICANT: KESHI ET AL
; TITLE OF INVENTION: PROBE FOR DIAGNOSING INFECTIOUS DISEASES
; FILE REFERENCE: 19036/33767
; CURRENT APPLICATION NUMBER: US/08/809,254A
; CURRENT FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: PCT/JP95/02036
; PRIOR FILING DATE: 1995-10-02
; PRIOR APPLICATION NUMBER: JP 236348
; PRIOR FILING DATE: 1994-09-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 5829
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic probe
US-08-809-254A-4

Query Match      4.3%; Score 34.2; DB 4; Length 5829;
Best Local Similarity 71.4%; Pred. No. 2.5; 18; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 385 CCAAAAGCCCAACGAGAAATTAATGCTGATATAAAACGTAATTAATGTAAGGAACCTCCGAT 444
DB 3392 CAAAAGCAACTAGAAAGTTATGCTCAAAATAAAATCTAAATTTGACAATGTAACCCGAG 3333
QY 445 GCG 447
DB 3332 TCG 3330

RESULT 11
US-08-961-527-41
; Sequence 41, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9828 base pairs
```


; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-41

Query Match 4.3%; Score 34.2; DB 4; Length 9828;
Best Local Similarity 71.4%; Pred. No. 3.3;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 385 CCAAGCCACGAGAAATTAAGCTGATATAAAGCTAAATAGTGAAGGAACCTCGAT 444
Db 4164 CAAAGCAAACTAGAAAGTATGCTCAATAAATCTAAATTTGACAAATGTAACCGAG 4223

QY 445 GCG 447
Db 4224 TCG 4226

RESULT 12
US-09-543-681A-3279
; Sequence 3279, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3279
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3279

Query Match 4.2%; Score 34; DB 4; Length 981;
Best Local Similarity 66.2%; Pred. No. 1.1;
Matches 49; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 414 ATAAAGCTAAATAGTGAAGGAACCTCGATGGCTGGACAAATAATGAAAAATCTTC 473
Db 253 ATAAATAAATATTAATAAGAGTTCGCTCTATTGCTCTGAAATGTAATAATATC 312

QY 474 GAAATGCTGAAG 487
Db 313 CAAATCGCAAGG 326

RESULT 13
US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 8639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054P2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match 4.1%; Score 32.6; DB 4; Length 505;
Best Local Similarity 12.3%; Pred. No. 2.1;

Matches 35; Conservative 123; Mismatches 127; Indels 0; Gaps 0;

QY 123 AAAAGGCAGAGATGGCCCTGTTGGCAAGAAACAAGAGCAGAGACAGCCTTATTGCA 182
Db 401 AAMRGWRGRCARGTGSGWKGKGYRMGRGMAAKRMAAAGSYCGMITSYTSKRWIG 342

QY 183 GGCTCTGCATGTCCTCAAGAAAGAAAGCTTATGACAGACATGCTATTCCACCCAGCAA 242
Db 341 RKGWTKKRWMTYSGMWTSYKCTKTKYTGKSKKTWTCTSWKYMMSGCGWARS 282

QY 243 TTGATTTCTCAGATGATGATCTCACTGGTTTCAGCAAGATAGGATGATGAGAAACCT 302
Db 281 MKSWARSWYSWACWCMWSASAYRARSMTYGARRSMWRAGAGWWRARRGKRARGKSSMM 222

QY 303 GGTAGCAATGCACCTGTGGGAGGAAAGCTTACACGACAGTTCTCTGAGATGACCTAGAA 362
Db 221 RSKMSSWMSAGKARMCRRWMSCRMYSYSCMSKSCRGTCXKRWRYARYAKRYASSM 162

QY 363 TGCAGAGAAACAGCCTCTCTCCCAAAAGCAAGCAAGAAATTAAT 407
Db 161 GKYMGRWCYAKCARMYGYRRSRSTGSRGMKRYRRKMYMMK 117

RESULT 14
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-79

Query Match 4.1%; Score 32.6; DB 3; Length 87350;
Best Local Similarity 49.7%; Pred. No. 34;
Matches 83; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 450 GGACAAAAATATGAAAAATCTTCGAAATCTTGAAGAGCTGCAAGGACCTACTGCAATC 509

Search completed: April 26, 2004, 02:10:47
Job time : 41.687 secs

Db 49651 GAAGAAAAAATTTAAGAGAAATGAAGAAATAAAGAAATGCAATGAAAAAGTGAATAA 49592
QY 510 AGGAAGCGATTTTTGTATCCATCATCAAGGAGCAGCAAGATGTATGAGACGAGACTTT 569
Db 49591 TTGAAGCTGGGTAAATGAAGATCCCAACATACATGTATAGCAGAGTCTCTGAAGAAGAAAT 49532
QY 570 GTTAAAGCACTTAAAGAGAAATGAAGAGTATGATTTGAGATACTT 616
Db 49531 ATGAAGTAATGGAATAAAACACTAAAGATATGATTTAAGAAAAACTT 49485

RESULT 15

US-09-618-166-79/c

; Sequence 79, Application US/09618166

; Patent No. 6583112

; GENERAL INFORMATION:

; APPLICANT: Fu, Ying-Hui

; Yu, Chang-En

; Oshima, Junko

; Mulligan, John T.

; Schellenberg, Gerald D.

; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO

; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed Intellectual Property Law Group

; STREET: 701 Fifth Avenue, Suite 6300

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/618,166

; FILING DATE: 17-Jul-2000

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: McMasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 240052.419C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 79:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 87350 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 79:

US-09-618-166-79

Query Match 4.1%; Score 32.6; DB 4; Length 87350;

Best Local Similarity 49.7%; Pred. No. 34;

Matches 83; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 450 GGACAAAAATGAAAAAATCTTCGAAATGCTTGAAGAGTGCAAGGACCTACTGCGATC 509

Db 49651 GAAGAAAAAATTTAAGAGAAATGAAGAAATAAAGAAATGCAATGAAAAAGTGAATAA 49592

QY 510 AGGAGCGATTTTGAATCCATCATCAAGGAGCAGCAAGATGTATGAGACGAGACTTT 569

Db 49591 TTGAAGCTGGGTAAATGAAGATCCCAACATACATGTATAGCAGAGTTCTCTGAAGAAGAAAT 49532

QY 570 GTTAAAGCACTTAAAGAGAAATGAAGAGTATGATTTGAGATACTT 616

Db 49531 ATGAAGTAATGGAATAAAACACTAAAGATATGATTTAAGAAAAACTT 49485

Aa139862 DNA codin
Aa39661 Nucleic a
Aa26608 Tumor s
Aa23207 Human sdp
Aa32307 Human sdp
Aa11227 Prokaryot
Aa29200 Prokaryot
Aa19138 Rine gene
Aa14289 Ubiquitin
Aa39347 DNA encod
Aa33387 DNA encod
Continuation (2 of
Aa31370 Human cDN
Aa13461 Human per
Aa46684 Human pol
Aa40716 Human cDN
Aa31210 Human cDN
Aa46653 Human pol
Aa40156 Human cDN
AaBn5744 Novel hum
AaQ32524 Oligonuel
AaQ32525 Oligonuel

ALIGNMENTS

RESULT 1	
ABX77562	
IID	ABX77562 standard; cDNA; 800 BP.
XX	
XX	
AC	ABX77562;
XX	
XX	
DT	09-APR-2003 (first entry)
XX	
XX	
DP	Differentially expressed breast cancer associated cDNA #57.

xx
Breast cancer; differential gene expression; BC-cDNA;
Breast cancer diagnosis; breast cancer monitoring;
Breast cancer treatment; breast cancer staging; gene;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	800	100.0	800	7	ABX77562 Different
2	800	100.0	800	8	ACD42209 Human put
3	768	96.0	1121	7	ABX76277 Lung canc
4	760	95.0	1121	7	ABX76278 Lung canc
5	748	93.5	1120	7	ABX76281 Lung canc
6	746.4	93.3	1120	7	ABX76279 Lung canc
7	716	89.5	1117	7	ABX76280 Lung canc
8	419	52.4	533	5	ABX76597 DNA encod
9	223.6	27.9	3812	7	ABX55710 cDNA enco
10	223.6	27.9	3812	8	ACA63028 Human cDN
11	187.6	23.4	2021	2	ABZ32204 Human sdp
12	186	23.2	3045	7	ABZ18334 Group III
13	178.4	22.3	1914	6	ABX56938 cDNA enco
14	166	20.8	1222	6	ABZ70855 Human cys
15	157.6	19.7	3092	9	ADO66992 Novel cod
16	130	16.2	551	6	ABL83301 Human ova
17	127.4	15.9	366	5	ABX64431 DNA encod
18	99.6	12.4	1030	4	AA161041 Human pol
19	99.6	12.4	1085	4	AA159255 Human pol
20	98.8	12.3	497	5	ABX76576 DNA encod
21	70.6	8.8	65042	7	ABX55711 DNA encod
22	70.6	8.8	65042	8	ACA63029 Human gen
23	69.8	8.7	2718	4	AAK94793 Human ful

Claim 1: SEQ ID NO 69: 30pp: English:

The invention describes a combination of cDNAs (designated BC-cDNAs), which are differentially expressed in breast cancer. The combination includes 152 cDNA sequences, or their complements. The protein encoded by any of these BC-cDNAs is useful for screening several molecules or compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or purifying antibodies from a sample. The antibodies, which specifically bind the protein differentially expressed in breast cancer is useful for detecting the expression of a protein in a sample. The BC-cDNAs are also useful for diagnosing, monitoring the treatment of, or staging, breast

CC cancer. This sequence represents a differentially expressed breast cancer
CC associated cDNA. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=20020156263
XX

SQ Sequence 800 BP; 265 A; 157 C; 188 G; 190 T; 0 U; 0 Other;

Query Match 100.0%; Score 800; DB 7; Length 800;

Best Local Similarity 100.0%; Pred. No. 4.2e-238; Indels 0; Gaps 0;

Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTCTCCAGCAAGTCCAGGACTTCAGGACTGGAACAAATGACCGATAAAACAGAGAAGG 60

DB 1 CTCTCTCCAGCAAGTCCAGGACTTCAGGACTGGAACAAATGACCGATAAAACAGAGAAGG 60

QY 61 TGGCTGTAGATCTGAACTGTGTTTAAACGTCCTCCAGGGAATGTGACAGTCTTCCTGATC 120

DB 61 TGGCTGTAGATCTGAACTGTGTTTAAACGTCCTCCAGGGAATGTGACAGTCTTCCTGATC 120

QY 121 AGAAAGGCGAGGATGGCCCTGTTGGCAAGGAACAAAGGAGGAGACAGCCCTTATTG 180

DB 121 AGAAAGGCGAGGATGGCCCTGTTGGCAAGGAACAAAGGAGGAGACAGCCCTTATTG 180

QY 181 CAGGCTCTGCAATGTCCTCAAGAAAGCAAGCTTATGACAGGACATGCTATCCACCCAGCC 240

DB 181 CAGGCTCTGCAATGTCCTCAAGAAAGCAAGCTTATGACAGGACATGCTATCCACCCAGCC 240

QY 241 AATTGGATTCTCAGATTGATGACTTCACCTGGTTTCAGCAAAAGATGATGATGCAAGAAC 300

DB 241 AATTGGATTCTCAGATTGATGACTTCACCTGGTTTCAGCAAAAGATGATGATGCAAGAAC 300

QY 301 CTGGTAGCAATGCACTGTGGGAGGAACGTTTACAGGAGCTTCTCTGAGATGACCTAG 360

DB 301 CTGGTAGCAATGCACTGTGGGAGGAACGTTTACAGGAGCTTCTCTGAGATGACCTAG 360

QY 361 AATGCGAGAAACAGGCTCTCTCCAAAGCCAGGAAATTAATGCTGATATAAAAC 420

DB 361 AATGCGAGAAACAGGCTCTCTCCAAAGCCAGGAAATTAATGCTGATATAAAAC 420

QY 421 GTAAATTAGTGAAGAACTCCGATGCGTTGGACAAAATATGAAAATCTTCGAAATGC 480

DB 421 GTAAATTAGTGAAGAACTCCGATGCGTTGGACAAAATATGAAAATCTTCGAAATGC 480

QY 481 TTGAAGGAGTCCAGGAGCACTTCTGCACTCAGGAGGCGATTTTGAATCCATCATCAAGG 540

DB 481 TTGAAGGAGTCCAGGAGCACTTCTGCACTCAGGAGGCGATTTTGAATCCATCATCAAGG 540

QY 541 AAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACCTTAAGAGAACTGAAACGTA 600

DB 541 AAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACCTTAAGAGAACTGAAACGTA 600

QY 601 TGATTTGAGAAATCTTCTCTGAGGATTAATCAACCCCAATGCAATATCTCGTTAAT 660

DB 601 TGATTTGAGAAATCTTCTCTGAGGATTAATCAACCCCAATGCAATATCTCGTTAAT 660

QY 661 GATTGAGAGAGAAAGGATCAGATTCCTGTTTCTAATAGGAGAGGATATGCTGAA 720

DB 661 GATTGAGAGAGAAAGGATCAGATTCCTGTTTCTAATAGGAGAGGATATGCTGAA 720

QY 721 GTCTCTGGCATATGTTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAG 780

DB 721 GTCTCTGGCATATGTTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAG 780

QY 781 TAAAGATGTTCTTTTCCC 800

DB 781 TAAAGATGTTCTTTTCCC 800

RESULT 2

ACD42209

ID ACD42209 standard; cDNA; 800 BP.

XX

AC ACD42209;

XX 05-SEP-2003 (first entry)

XX Human putative tumour antigen cDNA Incyte 347492.1.

XX Human; ss; DNA methylation; cancer; colon cancer.

XX Homo sapiens.

XX US2003013099-A1.

XX 16-JAN-2003.

XX 07-MAR-2002; 2002US-00093766.

XX 19-MAR-2001; 2001US-0277380P.

XX (LASEK/) LASEK A K W.

XX (JONE/) JONES D A.

XX (KARF/) KARF A R.

XX Lasek AKW, Jones DA, Karpf AR;

XX WPI; 2003-503249/47.

XX New combination comprising cDNAs that are expressed in a disorder or
XX process associated with DNA methylation, useful for diagnosing, staging,
XX treating or monitoring treatment of cancer, e.g. colon cancer.

XX Claim 2; Page 26-27; 66pp; English.

XX The invention relates to a combination comprising cDNAs which are
XX expressed in a disorder or process associated with DNA methylation. The
XX combination and cDNAs are useful for diagnosing, staging, treating or
XX monitoring treatment of cancer, e.g. colon cancer and for detecting or
XX changes in expression of genes encoding proteins that are associated with
XX DNA methylation. The protein is useful for screening molecules or
XX compounds to identify at least one ligand that binds to the protein and
XX for producing an antibody. The present sequence represents a cDNA
XX expressed in a disorder or process associated with DNA methylation

XX Sequence 800 BP; 265 A; 157 C; 188 G; 190 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 800; DB 8; Length 800;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-238;
XX Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTCTCCAGCAAGTCCAGGACTTCAGGACTGGAACAAATGACCGATAAAACAGAGAAGG 60

DB 1 CTCTCTCCAGCAAGTCCAGGACTTCAGGACTGGAACAAATGACCGATAAAACAGAGAAGG 60

QY 61 TGGCTGTAGATCTGAAACTGTGTTTAAACGTCCTCCAGGGAATGTGACAGTCTTCGTTATC 120

DB 61 TGGCTGTAGATCTGAAACTGTGTTTAAACGTCCTCCAGGGAATGTGACAGTCTTCGTTATC 120

QY 121 AGAAAGGCGAGGATGGCCCTGTTGGCAAGGAACAAAGGAGGAGACAGCCCTTATTG 180

DB 121 AGAAAGGCGAGGATGGCCCTGTTGGCAAGGAACAAAGGAGGAGACAGCCCTTATTG 180

QY 181 CAGGCTCTGCCATGTCCTCAAGAAAGGCTTATGACAGGACATGCTATTCACCCAGCC 240

DB 181 CAGGCTCTGCCATGTCCTCAAGAAAGGCTTATGACAGGACATGCTATTCACCCAGCC 240

QY 241 AATTGGATTCTCAGATTGATGACTTCACCTGGTTTCAGCAAAAGATGATGATGCAAGAAC 300

DB 241 AATTGGATTCTCAGATTGATGACTTCACCTGGTTTCAGCAAAAGATGATGATGCAAGAAC 300

QY 301 CTGGTAGCAATGCACTGTGGAGGAAACGTTTACAGCAGTTCCTGAGAGATGACCTAG 360

DB 301 CTGGTAGCAATGCACTGTGGAGGAAACGTTTACAGCAGTTCCTGAGAGATGACCTAG 360

QY 361 AATGCGAGAAACAGGCTCTCTCCAAAGCCAGGAAATTAATGCTGATATAAAAC 420

Db	361	ANTGCAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGATATAAAAC	420
Qy	421	GTAATTTAGTGAAGGAATCCGATGCGTTGGACAAAATATGAAAAATCTTCGAAATGC	480
Db	421	GTAATTTAGTGAAGGAATCCGATGCGTTGGACAAAATATGAAAAATCTTCGAAATGC	480
Qy	481	TTGAGGAGTGCAGAGACTACTGCGAGTCAGGACGAGAGCGATTTTGAATCCATCATCAAGG	540
Db	481	TTGAGGAGTGCAGAGACTACTGCGAGTCAGGAGCGATTTTGAATCCATCATCAAGG	540
Qy	541	AAGCAGCAAGATGTATGAGACGAGACTTTGTTAAGCACCTTAAGAGAGAACTGAAACGTA	600
Db	541	AAGCAGCAAGATGTATGAGACGAGACTTTGTTAAGCACCTTAAGAGAGAACTGAAACGTA	600
Qy	601	TGATTTGACAATACCTTTGTCCTCGAGGAGTATACACCCCAATGCAATATCTCGTTAAT	660
Db	601	TGATTTGACAATACCTTTGTCCTCGAGGAGTATACACCCCAATGCAATATCTCGTTAAT	660
Qy	661	GATTGAGGAGAGAAAGGATCAGATTGCTGTTTTCTACAATGAGCAGGATATTGCTGAA	720
Db	661	GATTGAGGAGAGAGAAAGGATCAGATTGCTGTTTTCTACAATGAGCAGGATATTGCTGAA	720
Qy	721	GTCCTCTGGCATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAG	780
Db	721	GTCCTCTGGCATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAG	780
Qy	781	TAAAGATGTTCTTTTCCC 800	
Db	781	TAAAGATGTTCTTTTCCC 800	
RESULT 3			
ABX76277			
ID	ABX76277 standard; DNA; 1121 BP.		
XX	ABX76277;		
DT	02-APR-2003 (first entry)		
DE	Lung cancer-associated polynucleotide #142.		
XX	Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;		
KW	antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;		
KW	small cell lung cancer; benign lesion; precancerous lesion; bronchitis;		
KW	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;		
KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.		
XX	Unidentified.		
OS	Unidentified.		
XX	W0200286443-A2.		
FN	31-OCT-2002.		
PD	18-APR-2002; 2002WO-US012476.		
PF	18-APR-2001; 2001US-0284770P.		
XX	10-MAY-2001; 2001US-0290492P.		
PR	09-NOV-2001; 2001US-0339245P.		
PR	13-NOV-2001; 2001US-0350665P.		
PR	29-NOV-2001; 2001US-0334370P.		
PR	12-APR-2002; 2002US-0372246P.		
XX	(EOSB-) EOS BIOTECHNOLOGY INC.		
PA	Aziz N, Murray R;		
XX	WPI; 2003-093161/08.		
DR	P-PSDB; ABUS65649.		
XX			

expression in lung cancer.

Claim 22; Page 297; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention

XX Sequence 1121 BP; 329 A; 243 C; 269 G; 280 T; 0 U; 0 Other;

Query Match 96.0%; Score 768; DB 7; Length 1121;
 Best Local Similarity 100.0%; Pred. No. 4.5e-228;
 Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 33 GAAACAATGACCGATATAAACACAGAGAAGTGCGCTGTAGATCCTTGAAACTGTGTTTAAACGT 92
 DB 241 GAAACAATGACCGATATAAACACAGAGAAGTGCGCTGTAGATCCTTGAAACTGTGTTTAAACGT 300

QY 93 CCCAGGGAATGTGACATGCTCTTGGTATCAGAAAGCAGAGGATGCCCTGTGGCAAG 152
 DB 301 CCCAGGGAATGTGACATGCTCTTGGTATCAGAAAGCAGAGGATGCCCTGTGGCAAG 360

QY 153 AAACAAGGACGAGGACAGCAGCTTATTGCAAGCTCTGCCATGTCCAAAGAAAGAACGTT 212
 DB 361 AAACAAGGACGAGGACAGCAGCTTATTGCAAGCTCTGCCATGTCCAAAGAAAGAACGTT 420

QY 213 ATGACAGGACATGTAATTCACCCAGCCAAATGGATCTTCAGATTGATGACATTCCTACTGT 272
 DB 421 ATGACAGGACATGTAATTCACCCAGCCAAATGGATCTTCAGATTGATGACATTCCTACTGT 480

QY 273 TTTCAGCAAGATAGGATGATGTCAGAAACCTGGTAGCAATGCACCTGTGGAGGAAACGTT 332
 DB 481 TTTCAGCAAGATAGGATGATGTCAGAAACCTGGTAGCAATGCACCTGTGGAGGAAACGTT 540

QY 333 ACCAGCAGTTCTCTGGAGATGACCTAGATGCAGAGAAACAGCCCTCTCCCAAAGC 392
 DB 541 ACCAGCAGTTCTCTGGAGATGACCTAGATGCAGAGAAACAGCCCTCTCTCCCAAAGC 600

QY 393 CAACAGAGAAATTAATGCTGATATAAAACGTAATATTAGTGAAGAACTCCGATGCGTTGGA 452
 DB 601 CAACAGAGAAATTAATGCTGATATAAAACGTAATATTAGTGAAGAACTCCGATGCGTTGGA 660

QY 453 CAATAATATGAAAAATCTTCGAAATGCTTGAAGGAGTGCAGAGACCTACTGCAGTCAGG 512
 DB 661 CAATAATATGAAAAATCTTCGAAATGCTTGAAGGAGTGCAGAGACCTACTGCAGTCAGG 720

QY 513 AAGCGATTTTTTGAATCCATCATCAAGAGAACGACAGATGTAATGAGACGAGACTTTGTT 572
 DB 721 AAGCGATTTTTTGAATCCATCATCAAGAGAACGACAGATGTAATGAGACGAGACTTTGTT 780

QY 573 AAGCACCTTAAAGAGAAACTGAAACGTAATGATTTGAAATACCTTGTCCCTGGAGGATAT 632
 DB 781 AAGCACCTTAAAGAGAAACTGAAACGTAATGATTTGAAATACCTTGTCCCTGGAGGATAT 840

QY 633 CACACCCCAATATGCAATATCTCGTTAAATGATTCAGAGAGAGAAAGGATCAGATTCGTGT 692
 DB 841 CACACCCCAATATGCAATATCTCGTTAAATGATTCAGAGAGAGAAAGGATCAGATTCGTGT 900

QY 693 TTCTACATGGAGCAGGATATTGCTGAAGTCTCTGGCATATGTTACCGAATCAAAATAGC 752
Db |||||
901 TTCTACATGGAGCAGGATATTGCTGAAGTCTCTGGCATATGTTACCGAATCAAAATAGC 960
QY 753 CTTCCAGAGCGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 800
Db |||||
961 CTTCCAGAGCGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 1008

RESULT 4

ID ABX76278 standard; DNA; 1121 BP.
XX
AC ABX76278;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #143.
XX
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR P-PSDB; ABUS6550.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.

Claim 22; Page 297; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the

CC invention

XX
SQ Sequence 1121 BP; 329 A; 244 C; 268 G; 280 T; 0 U; 0 Other;
Query Match 95.0%; Score 760; DB 7; Length 1121;
Best Local Similarity 99.3%; Pred. No. 1.4e-225;
Matches 763; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 33 GAAACAATGACCGATATAAAACAGAGAAAGGTGGCTGTAGATCCTGAAACTGTGTTAAACGT 92
Db |||||
241 GAAACAATGACCGATATAAAACAGAGAAAGGTGGCTGTAGATCCTGAAACTGTGTTAAACGT 300
QY 93 CCCAGGGAATGTGACAGTCTCTCGTATCAGAAAAGGCAGAGATGCCCTGTGTCGAAG 152
Db |||||
301 CCCAGGGAATGTGACAGTCTCTCGTATCAGAAAAGGCAGAGATGCCCTGTGTCGAAG 360
QY 153 AAACAAGGACGAGACAGACGCTTATTGAGGGCTCTGCCATGTCACAAAGAAAAGAGCTT 212
Db |||||
361 AAACAAGGACGAGACAGACGCTTATTGAGGGCTCTGCCATGTCACAAAGAAAAGAGCTT 420
QY 213 ATGACAGGACATCTATTCCACCCAGCCCAATTGCTGATTTCTCAGATTGATGACTTCACTGGT 272
Db |||||
421 ATGACAGGACATCTATTCCACCCAGCCCAATTGCTGATTTCTCAGATTGATGACTTCACTGGT 480
QY 273 TTCAGCAAAAGATAGGATGATGCAAGAAACCTGGTAGCAATGCACCTGTGGAGGAAACGTT 332
Db |||||
481 TTCAGCAAAAGATAGGATGATGCAAGAAACCTGGTAGCAATGCACCTGTGGAGGAAACGTT 540
QY 333 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCTCTCTCCCAAAAGC 392
Db |||||
541 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCTCTCTCCCAAAAGC 600
QY 393 CAACGAGAAATTAATGCTGATATATAAAACGTTAAATTAGTGAAGAACTCCGATCGTTGGA 452
Db |||||
601 CAACGAGAAATTAATGCTGATATATAAAACGTTAAATTAGTGAAGAACTCCGATCGTTGGA 660
QY 453 CAAAAATATGAAAAAATCTTCGAAATGCTTGAAGGAGTGAAGGACCTACTGCAATCAGG 512
Db |||||
661 CAAAAATATGAAAAAATCTTCGAAATGCTTGAAGGAGTGAAGGACCTACTGCAATCAGG 720
QY 513 AAGCGATTTTTTGAATCCATCATCAAGGAGCAGCAGAGATGATAGACGAGACTTTGTT 572
Db |||||
721 AAGCGATTTTTTGAATCCATCATCAAGGAGCAGCAGAGATGATAGACGAGACTTTGTT 780
QY 573 AAGCACCCTTAAGAGAAACTGAAACGTTATGATTTGGAATACCTTGTCCCTGGAGGATTAT 632
Db |||||
781 AAGCACCCTTAAGAGAAACTGAAACGTTATGATTTGGAATACCTTGTCCCTGGAGGATTAT 840
QY 633 CACACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAAAAGGATCAGATTGCTGTT 692
Db |||||
841 CACACCCCAATGCAATATCTCATTATGATTGAGGAGAGAAAAGGATCAGATTGCTGTT 900
QY 693 TTCTACAAATGAGCAGGATATTGCTGAAGTCTCTCGCATATGTTACCGAATCAAAATAGC 752
Db |||||
901 TTCTACAAATGAGCAGGATATTGCTGAAGTCTCTCGCATATGTTACCGAATCAAAATAGC 960
QY 753 CTTCCAGAGCGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 800
Db |||||
961 CTTCCAGAGCGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 1008

RESULT 5

ABX76281
ID ABX76281 standard; DNA; 1120 BP.
XX
AC ABX76281;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #146.
XX
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 OS
 PN WO200286443-A2.
 PD
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOSE-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX
 DR WPI: 2003-093161/08.
 DR P-PSDB; ABUS6553.
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX
 PS Claim 22; Page 298; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
 CC invention
 XX
 SQ Sequence 1120 BP; 329 A; 243 C; 266 G; 282 T; 0 U; 0 Other;
 Query Match 93.5%; Score 748; DB 7; Length 1120;
 Best local Similarity 99.2%; Pred. No. 7.4e-222;
 Matches 762; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 33 GAAACATGACCCGATGAAACAGAGAGGCTGCTAGATCCTGAAACTGTGTTAAACCT 92
 DB 241 GAAACATGACCCGATGAAACAGAGAGGCTGCTAGATCCTGAAACTGTGTTAAACCT 300
 QY 93 CCCAGGGAATGTGACAGTCTCTTCATCAGAAAAGGAGGAGGATGCCCTGTGGCAAGG 152
 DB 301 CCCAGGGAATGTGACAGTCTCTTCATCAGAAAAGGAGGAGGATGCCCTGTGGCAAGG 360
 QY 153 AAACAGGAGCAGGAGACGCTTATGAGGCTCTGCCATGTCCTCAAGAAAGAGAGCTT 212
 DB 361 AAACAGGAGCAGGAGACGCTTATGAGGCTCTGCCATGTCCTCAAGAAAG-AGCTT 419
 QY 213 ATGACAGGACATGCTATTCCAGCCAGCCAAATTGATTTCTCAGATTGATGACTTCACTGTT 272

DB 420 ATGACAGGACATGCTATTCCACCAGCAATTTGGATTCTCAGATTGATGATTCACCTGGT 479
 QY 273 TTGAGCAAAAGATAGGATGATGAGAAAACCTGGTAGCAATGCACTCTGTGGAGGAAACGTT 332
 DB 480 TTGAGCAAAAGATAGGATGATGAGAAAACCTGGTAGCAATGCACTCTGTGGAGGAAACGTT 539
 QY 333 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCCTCTCTCCAAAAGC 392
 DB 540 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCCTCTCTCCAAAAGC 599
 QY 393 CAACGAGAAATTAATGCTGATATATAAACGTAATTAATAGTGAAGAACTCCGATGCGTTGGA 452
 DB 600 CAACGAGAAATTAATGCTGATATATAAACGTAATTAATAGTGAAGAACTCCGATGCGTTGGA 659
 QY 453 CAAAATATCAAAAATATCTTCGAAATCTTGAAGAGTGAAGAGCACTACTGAGTCAAGG 512
 DB 660 CAAAATATCAAAAATATCTTCGAAATCTTGAAGAGTGAAGAGCACTACTGAGTCAAGG 719
 QY 513 AAGCGATTTTGAATCCATCATCAAGGAAGCAGCAAGATGATGAGACGAGACTTTGTT 572
 DB 720 AAGCGATTTTGAATCCATCATCAAGGAAGCAGCAAGATGATGAGACGAGACTTTGTT 779
 QY 573 AAGCACCTTAAGAGAAACTGAAACGATGATGATTTGAGAACTACTTGCTCCCTGGAGGATAT 632
 DB 780 AAGCACCTTAAGAGAAACTGAAACGATGATGATTTGAGAACTACTTGCTCCCTGGAGGATAT 839
 QY 633 CACACCCCAATGCAATATCTCGTGAATGATGAGGAGAGAAAGGATCAGATTGCTGTT 692
 DB 840 CACACCCCAATGCAATATCTCGTGAATGATGAGGAGAGAAAGGATCAGATTGCTGTT 899
 QY 693 TTCTACAAATGGAGCAGGATATGCTGAAGTCTCCTGGCATATGTTACCGAATCAAAATAGC 752
 DB 900 TTCTACAAATGGAGCAGGATATGCTGAAGTCTCCTGGCATATGTTACCGAATCAAAATAGC 959
 QY 753 CTTCCAGAGCTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 800
 DB 960 CTTCCAGAGCTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 1007
 RESULT 6
 ABX76279
 ID ABX76279 standard; DNA; 1120 BP.
 AC
 XX ABX76279;
 DT 02-APR-2003 (first entry)
 XX Lung cancer-associated polynucleotide #144.
 DE Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 PN WO200286443-A2.
 XX
 PD 31-OCT-2002.
 PF 18-APR-2002; 2002WO-US012476.
 XX
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOSE-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;

XX WPI; 2003-093161/08.
DR P-PSDB; ABUS6551.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 297-298; 453pp; English.
PS
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention
XX
SQ Sequence 1120 BP; 327 A; 245 C; 268 G; 280 T; 0 U; 0 Other;
Query Match 93.3%; Score 746.4; DB 7; Length 1120;
Best Local Similarity 99.1%; Pred. No. 2.3e-221;
Matches 761; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
33 GAAACATGACCGATGACAGTAAACAGAGAGAGGTCGTGTAGATCCTGAAACTGTTTAAACGT 92
241 GAAACATGACCGATGACAGTAAACAGAGAGAGGTCGTGTAGATCCTGAAACTGTTTAAACGT 300
93 CCACAGGAGATGTGACAGTCTTGTATCAGAAAGGAGAGGATGCCCTGTTGGCAAGG 152
301 CCACAGGAGATGTGACAGTCTTGTATCAGAAAGGAGAGGATGCCCTGTTGGCAAGG 360
153 AAACAGAGGAGAGAGAGAGGATGTGAGGCTGTGCCATGTCCAAAGAAAGAGCTT 212
361 AAACAGAGGAGAGAGAGAGGATGTGAGGCTGTGCCATGTCCAAAGCAAG-AGCTT 419
213 ATGACAGGAGATGCTATTTCCACCCAGCAATTTGATTTCTCAGATTTGATGACTTCACTGT 272
420 ATGACAGGAGATGCTATTTCCACCCAGCAATTTGATTTCTCAGATTTGATGACTTCACTGT 479
273 TTCAGCAAGATAGGATGATGCAAGAACCTGGTAGCAATGCACTGTGGAGAGAAACGTT 332
480 TTCAGCAAGATAGGATGATGCAAGAACCTGGTAGCAATGCACTGTGGAGAGAAACGTT 539
333 ACCAGCAGTTTCTCTGAGATGACCTAGATGACAGACACAGCCTCTCCCAAAGC 392
540 ACCAGCAGTTTCTCTGAGATGACCTAGATGACAGACACAGCCTCTCCCAAAGC 599
393 CAACAGAGAAATTAATGCTGATATATAAAGCTAAATAGTGAAGAACTCCGATCGTTGGA 452
600 CAACAGAGAAATTAATGCTGATATATAAAGCTAAATAGTGAAGAACTCCGATCGTTGGA 659
453 CAACAGATGAGAAATTAATGCTGATGAGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAGG 512
660 CAACAGATGAGAAATTAATGCTGATGAGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAGG 719
513 AAGCGATTTTGTGATTCATCATCAAGAGAGAGAGAGATGATGAGACGAGACTTTGTT 572
720 AAGCGATTTTGTGATTCATCATCAAGAGAGAGAGAGATGATGAGACGAGACTTTGTT 779

QY 573 AAGCACCTTAAGAGAGAACTGAAACGATGATGATTTGAGATACTTGTCCCTGGAGGATTAT 632
DB 780 AAGCACCTTAAGAGAGAACTGAAACGATGATGATTTGAGATACTTGTCCCTGGAGGATTAT 839
QY 633 CACACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
DB 840 CACACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 899
QY 693 TTCTACAAATGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
DB 900 TTCTACAAATGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
QY 753 CTTCCAGAGGCTAAGAAATTTCTTTAGTAAAGATGTTCTTTTCCC 800
DB 960 CTTCCAGAGGCTAAGAAATTTCTTTAGTAAAGATGTTCTTTTCCC 1007
RESULT 7
ABX76280
ID ABX76280 standard; DNA; 1117 BP.
XX AC ABX76280;
XX 02-APR-2003 (first entry)
XX Lung cancer-associated polynucleotide #145.
XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX Unidentified.
OS WO200286443-A2.
XX
XX
XX
XX 31-OCT-2002.
XX
XX 18-APR-2002; 2002WO-US012476.
XX
XX 18-APR-2001; 2001US-0284770P.
XX 10-MAY-2001; 2001US-0290492P.
XX 09-NOV-2001; 2001US-0339245P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
XX P-PSDB; ABUS6552.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX
XX Claim 22; Page 298; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell

QY 562 GAGACTTTGTTAAGCACTTAAGAGAACTGAACGTAATGATTGAGAAATCTTGTCCC 621
DB 353 GAGACTTTGTTAAGCACTTAAGAGAACTGAACGTAATGATTGAGAAATCTTGTCCC 294
QY 622 TGGAGGATTATCACACCCCAATGCTAATCTGTTAATGATTGAGGAGAGAAAAGGATC 681
DB 293 TGGAGGATTATCACACCCCAATGCTAATCTGTTAATGATTGAGGAGAGAAAAGGATC 234
QY 682 AGATTGCTGTTTCTACATGAGAGAGAGATGCTGAAAGTCTCTCGGCATATGTTACCG 741
DB 233 AGATTGCTGTTTCTACATGAGAGAGAGATGCTGAAAGTCTCTCGGCATATGTTACCG 174
QY 742 AATCAATAGCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 800
DB 173 AATCAATAGCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 115

RESULT 9
ABS55710
ID ABS55710 standard; cDNA; 3812 BP.
XX
AC ABS55710;
XX
DT 17-JAN-2003 (first entry)
XX
XX cDNA encoding novel human deleted in cancer 1 (DICE1) like protein.
XX Human; deleted in cancer 1; DICE1; helicase family; carcinoma;
XX transgenic animal; ribozyme design; drug screening; gene therapy;
XX tumour suppressor; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 321..2906
XX /tag= a
XX /product= "DICE1"
XX /notes= "Deleted in cancer 1 like protein"

XX US2002128188-A1.
XX
XX 12-SEP-2002.
XX
XX 16-FEB-2001; 2001US-00784316.
XX
XX 16-FEB-2001; 2001US-00784316.
XX
XX (WEIM/) WEI M.
XX (YEJ/) YE J.
XX (KTC/) KETCHUM K A.
XX (DFR/) DI FRANCESCO V.
XX (BEAS/) BEASLEY E M.
XX
XX Wei M, Ye J, Ketchum KA, Di Francesco V, Beasley EM;
XX
XX WPI; 2003-039599/03.
XX P-PSDB; ABG71111.
XX
XX Novel human enzyme protein, related to helicase subfamily, useful as
XX model for developing human therapeutic targets and serves as target for
XX human therapeutics.
XX
XX Claim 22; Fig 1; 86pp; English.

XX
XX The invention describes an isolated human enzyme peptide (I) that is
XX related to the helicase family. (I), its allelic variant, orthologue or
XX fragment is useful for identifying a modulator of a human enzyme peptide.
XX The method optionally involves contacting a cell expressing the peptide
XX with an agent and determining if the agent has modulated the expression
XX of the peptide. (I) and the polynucleotide encoding it (iii) can be used
XX as models for the development of human therapeutic targets, aid in the
XX identification of therapeutic proteins and serve as targets for the
XX development of human therapeutic agents that modulate enzyme activity in

CC cells and tissue that express the enzyme. The proteins can also be used
CC in screening assays to screen a compound for its ability to stimulate or
CC inhibit interaction between enzyme protein and a molecule that normally
CC interacts with the enzyme protein. The proteins also provide a target for
CC diagnosing a disease or predisposition to disease mediated by the
CC peptide, and in pharmacogenomic analysis. The peptides are also useful
CC for treating a disorder characterised by altered expression of the
CC protein e.g. carcinoma. Anti-(I) antibodies are also useful for assessing
CC normal and aberrant subcellular localisation of cells in various tissues
CC in an organism, in pharmacogenomic analysis, for tissue typing and for
CC inhibiting protein function. The nucleic acid molecules are useful for
CC constructing recombinant vectors, host cells and transgenic animals, and
CC for designing ribozymes. The nucleic acids are also useful in drug
CC screening assays and as a target for treatment by the compounds
CC identified through drug screening. The nucleic acid molecules are also
CC useful in diagnostic assays for qualitative changes in expression of
CC nucleic acid encoding enzyme and particularly in qualitative changes that
CC lead to pathology. Detection of mutated form of gene encoding enzyme
CC associated with a dysfunction provides a diagnostic tool for a active
CC disease or susceptibility to disease which results from altered
CC expression of enzyme protein. (iii) also provides vectors for gene
CC therapy in patients with aberrant expression of gene encoding enzyme.
CC This sequence encodes the novel human protein deleted in cancer 1 (DICE1)
XX like protein, a candidate tumour suppressor gene
SQ Sequence 3812 BP; 1169 A; 796 C; 840 G; 1007 T; 0 U; 0 Other;

Query Match 27.9%; Score 223.6; DB 7; Length 3812;
Best Local Similarity 64.6%; Pred. No. 1.9e-58;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;
QY 212 TATGACAGGACATGCTATTCACCCAGCCCAATGGATTTCTCAGATTGATGACTTCTACTGG 271
DB 2429 TATGACAGGAGATCTTATGCGCCCAACCAAGTGGATTTCTCTGCTGACGACTTCAAG 2488
QY 272 TTTTCAGCAAGATAGGATGATGAGAAACCTGCTAGCAATGCACCTGTGGAGGAAACGT 331
DB 2489 TCTCAGCAAGATAGGCTGATTCAGAAACCTGCTAGTACGCTTTGTAGGAGAGCCAA 2548
QY 332 TACCAGCAGTTTCTCTGGAGATGACCTAGAAATGCAGAGAAACAGCCTC----- 379
DB 2549 AAACCTGCAGTCTCTCCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGGCTAT 2608
QY 380 -----CTCTCCAAAGCCACGAGAAATTAATGCTGATATAAAACG 421
DB 2609 GCCAAATACATTAATCAATCACTCTGCTATGCGACAGGATCAATGCTGATATAAACA 2668
QY 422 TAAATTAGTGAAGAACTCCGATGCGTTGGCAAAAATATGAAAAAATCTTCGAAATGCT 481
DB 2669 TCAATTAATGAAGGAGTTCCGAAAGTTTGGTCCGAAATATGAAAGAAATTTTCATTTTGTCT 2728
QY 482 TGRAGGAGTGCAGGACCTACTGCAGTCAGGAAGCGATTTTTTGAATCCATCATCAAGGA 541
DB 2729 TGAAGAGTGCAGGACCTCTGGAGATGAAGAAACAGTTTGTGTAATTTACCATCAAGGA 2788
QY 542 AGCAGCAAGATGTTATGAGACGAGACCTTTGTTAAGCACCTTTAAGAGAAACTGAAACGCTAT 601
DB 2789 AGCCGCAAGGTTTAAAGAGACGAGTCTCTAATTCAGTACCTTGAAGAGGTACTAGAAAAAT 2848
QY 602 GATTGTGAGATCTGTCCTCGGAGGATATACACCCCAATGCATATCTCGTTAATG 661
DB 2849 AAATTCGCCACCTTCCAGCAACCAATAGTCATCAACAGCAGATCATCTGTTAGTG 2908
QY 662 -----ATTGAGGAGAGAAAAAGGATCAGATTGCTGTTTTTCTACAATGGAGCAGGATATTG 715
DB 2909 CAAAGACCAGTGAGAAAAAATGACAAAGTTTCTGTGCTCTAGGATGGAACAGGATATTG 2968
QY 716 CTGAAGTCTCTGTCATATGTTACCGGATCAATAGCTTCCAGAGGCTTAAGAA 769
DB 2969 TTGAAGGCTCTGGAATGTTTGTAGTCAAGGAAATGCTTTCCAGATGCTTAAGAA 3022

RESULT 10

ACA63028
ID ACA63028 standard; cDNA; 3812 BP.
AC
AC ACA63028;
XX
DT 25-AUG-2003 (first entry)
XX
XX Human cDNA encoding a DICE-1-like RNA helicase.
DE
XX Human; ss; gene; RNA helicase; DICE-1; deleted in cancer 1;
KW tumour suppressor gene; chromosome X; gene therapy; cytostatic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..320
FT 5'UTR *tag= a
FT CDS 321..2906
FT /*tag= b
FT /product= "DICE-1-like protein"
FT 2907..3812
FT 3'UTR /*tag= c
XX
XX US2003013158-A1.
XX
XX 16-JAN-2003.
XX
XX 28-AUG-2002; 2002US-00229124.
XX
XX 16-FEB-2001; 2001US-00784316.
XX
XX (APPL-) APPLERA CORP.
XX
XX Wei M, Ye J, Ketchum KA, Di Francesco V, Beasley EM;
XX
XX WPI: 2003-491970/46.
XX
XX P-PSDB; AB061992.

XX New isolated human enzyme proteins, useful as models for developing human
XX therapeutic targets, aid in identifying therapeutic proteins, or for
XX diagnosing, treating or preventing enzyme protein-related conditions,
XX e.g. carcinomas.

XX Claim 4; Fig 1; 90pp; English.

XX The invention relates to a new protein, human DICE1-like RNA helicase
XX (deleted in cancer 1, a tumour suppressor gene). The protein may be an
XX allelic variant or orthologue encoded by a nucleic acid molecule that
XX hybridises under stringent conditions to the cDNA and gene appearing as
XX ACA63028 and ACA63029, or a fragment of the protein of at least 10 amino
XX acids. Also included are an antibody selectively binding to the helicase,
XX a gene chip comprising nucleic acids, a transgenic non-human animal
XX comprising the nucleic acid molecule, a nucleic acid vector comprising
XX the nucleic acid molecule, a host cell containing the vector, identifying
XX the protein or nucleic acids in a sample, identifying agents that bind to
XX and/or modulate the activity of the protein (or expression of the nucleic
XX acids), treating a disease or condition mediated by a human enzyme
XX protein, an isolated human enzyme peptide having an amino sequence that
XX shares at least 70% homology with the helicase and an isolated nucleic
XX acid molecule encoding a human enzyme peptide, where the nucleic acid
XX molecule shares at least 80% homology with the cDNA or gene. The methods
XX are useful for detecting the presence of any of the claimed peptides, a
XX nucleic acid molecule, a modulator of a peptide, an agent that binds to
XX any of the peptides, and for identifying a modulator of expression of a
XX peptide. The methods are also useful for treating a disease or condition
XX mediated by a human enzyme protein. The human enzyme peptides and nucleic
XX acid molecules are useful as models for developing human therapeutic
XX targets, aid in the identification of therapeutic proteins, or as targets
XX for the development of human therapeutic agents that modulate enzyme
XX activity in cells and tissue that express the enzyme. They are useful in
XX the diagnosis, prevention and treatment of enzyme protein-related
XX conditions or disorders associated with the absence of, inappropriate, or
XX unwanted expression of the protein, e.g. carcinomas. The peptides or

CC proteins may be used in drug screening assays, in assays to determine the
CC biological activity of the protein, to raise antibodies or to elicit
CC another immune response, as a reagent in assays designed to
CC quantitatively determine levels of the protein in biological fluids, or
CC as markers for tissues in which the corresponding protein is
CC preferentially expressed. The nucleic acid molecules are useful as
CC probes, primers, chemical intermediates, or in biological assays. The
CC gene for the helicase is located on chromosome X. The present sequence is
CC the cDNA encoding the DICE-1-like helicase

XX Sequence 3812 BP; 1169 A; 796 C; 840 G; 1007 T; 0 U; 0 Other;

Query Match 27.9%; Score 223.6; DB 8; Length 3812;
Best Local Similarity 64.6%; Pred. NO. 1.9e-58;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;

QY	212	TATGACAGGACATGCTATTCCACCCAGCAATTCAGATTTCAGATTGACTTCACTGG	271
DB	2429	TATGACAGGAGATCTTATGCCACCAACCAAGTGGATTCTCTGTGACGATTCACAAG	2488
QY	272	TTTCAGCAAGATAGGATGATGCGAGAACTGTGTAGCAATGCACCTGTGGGAGGAACGT	331
DB	2489	TCTCAGCAAGATGGGCTGATTCCAAAACCTGGTAGACGCAATTTGTAGGAGGACCAA	2548
QY	332	TACCAGCAGTTTCTCTGGGAGATGACCTAGAAATGCAGAGAAACAGCCCTC	379
DB	2549	AAACTGCAGTCTCTCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGGAGCTAT	2608
QY	380	-----CTCTCCAAAAGCCAAACGAGAAATTAATGCTGATATAAACG	421
DB	2609	GCCAAATACATTACAAATCACTCTCTATGGCACAAGGAATCAATGCTGATATAAACG	2668
QY	422	TAAATTAGTGAAGCACTCCGATGCGTTGGACAAAATATGAAAAATCTTCGAAATGCT	481
DB	2669	TCAATTAATGAAGAGTTCGAAAGTTTGTGCAAAATATGAAGAATTTTCATTTTGTCT	2728
QY	482	TGAAGGAGTCCAAAGGACCTACTCCAGTCAGGAGCGAATTTTTTGAATCCATCATCAAGGA	541
DB	2729	TGAAGAGTGCAGGACCTCTGGAGATGAAGAACAGTTTGTGTAATTTACCATCAAGGA	2788
QY	542	AGCAGCAGATGATGAGCAGAGACTTTGTTAGCACCTTTAAGAAGAACTGGAACCTAT	601
DB	2789	AGCCGCAAGGGTTAAAGACGAGTCTTAATTCAGTACCTTCAGAGAGTACTAGAAAAAT	2848
QY	602	GATTTGAGAAATCTTGTCCCTGGAGGATTATCACCCCCAAATGCATAATCTCGTTAATG	661
DB	2849	AAATTCCCAACCTTCAACAACCAATAGTCATCAATCAACAGCAGATCATCATGTTAGTG	2908
QY	662	-----ATTGAGGAGAGAAAGGATCAGATTGCTGTTTCTACAAATGGAGCAGGATATG	715
DB	2909	CAAAAGCCAGTGAGAAAAAATGCAAGTTTCTGCTGTAGATGGAAACAGGATATG	2968
QY	716	CTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCTTCCAGAGGCTAAGAA	769
DB	2969	TTGAAGCTCTGGAATGTTTGTAGTCAAGGAATGCTTTCCAGATGCTAAGAA	3022

RESULT 11

AAZ32204
ID AAZ32204 standard; cDNA; 2021 BP.

XX AAZ32204;

AC AAZ32204;
XX 14-JAN-2000 (first entry)

DE Human sdph3.10 (SAGE) encoding cDNA.

XX Human; sdph3.10; SAGE; sdph3.8; HAGE; sdph3.5; TRAP; sarcoma;
KW tumour rejection antigen precursor; tumour associated nucleic acid;
KW carcinoma; cancer; immune response; diagnosis; ss.

OS Homo sapiens.

XX

Key Location/Qualifiers
CDS 119..1834
/*tag= a
/product= "sdph3.10 (SAGE)"

W09953061-A2.
21-OCT-1999.
14-APR-1999; 99WO-US008163.
15-APR-1998; 98US-00060706.
27-JUL-1998; 98US-00122989.
30-OCT-1998; 98US-00183706.
30-OCT-1998; 98US-00183789.
(LUDW-) LUDWIG INST CANCER RES.
Martelange V, De Smet C, Boon-Falleur T;
WPI; 1999-620430/53.
P-PSDB; AAY49634.

New nucleic acid encoding sarcoma-associated gene products, useful for diagnosing, e.g. treating and preventing cancer.

Claim 1; Page 79-81; 93pp; English.

The present sequence encodes human sdph3.10 (SAGE), a sarcoma-associated gene product (I). Agents, specifically sarcoma associated nucleic acids (II) or their expression products that are tumour rejection antigens (TRA), that selectively increase formation of HLA (human leucocyte antigen)/(II) complexes are used for treating cancer, especially sarcoma and carcinoma, in humans and other animals. Compositions containing autologous cytolytic T cells (CTL), specific for the HLA/(II) complex, are similarly useful, also transformed cells that stimulate such CTL in vivo. (II) are also used: (i) as source of therapeutic antisense sequences that reduce expression of (iii); (ii) for recombinant production of (i); (iii) particularly its fragments, as primers and probes in usual hybridisation and amplification assays, for diagnosis, prognosis and monitoring of tumours; (iv) for measuring binding specificity of HLA molecules or CTL clones; (iv) to identify related sequences; and (v) for generating transgenic animals, e.g. for studying cancer and immune responses to it. (I) are used to raise specific antibodies (Ab) and therapeutically. Ab are used to diagnose tumours in immunoassays, also for delivering drugs, toxins, imaging agents etc. to (i)-expressing cells

Sequence 2021 BP; 559 A; 436 C; 429 G; 497 T; 0 U; 0 Other;

Query Match 23.4%; Score 187.6; DB 2; Length 2021;
Best Local Similarity 60.2%; Pred. No. 2.2e-47;
Matches 365; Conservative 0; Mismatches 209; Indels 32; Gaps 2;

195 TCACAGAGAAAGAGCTTATGACAGGACATGCTATTCACCCAGCCAAATGGATTCTCAG 254
1349 TCACAGAGCTGATAAATATATGACAGGACATGCTATTCACCCAAATGGATTCTTC 1408
255 ATTGATGACTTCACTGGTTTCAGCAAGATAGGATGATGACAGAACTGTAGCAATGCA 314
1409 TCTCAGACTTCAAGTCTCAGCAAGATAGGATGCTGTTTACAACTGATATGAA 1468
315 CCTGTGGAGAAACGTTTACCAGCAGTTCTCTGGAGATGACCTAGATGTCAGAGAAACA 374
1469 TTTGCGGTAGCACCAAAAACCTACAGTGTCTCTGAGGTGACCCAGTTACAGTAATG 1528
375 GCCTC-----CTCTCCCAAGCCACAGAAAT 404
1529 TCTTCGGTGAACCTGTGCCAATACACCAATAATCTCTGCTCCATGGCAAAAAAAT 1588
405 AATGCTGATATAAACGTAATTAAGTGAAGAACTCCGATGCGTTGACAAAAATATGAA 464
1589 AATGATGATATAAATATCAATTAATGAAGAGCTTCGAAGGTTTGGGCAAAATATGAA 1648

465 AAAATCTTCGAAATGCTTGAAGGAGTGCAAGGACCTACTACTCAGTCAGAGACGATTTTT 524
1649 AGAATTTTCATTTTGTGTTGAAGAGGTACAAGGATCTATGAAAGTCAAGAGCAATTTGTT 1708
525 GAATCCATCATCAAGGAGGAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACTTAAG 584
1709 GAATTTACCATCAAGGAGGAGCAGCAAGGTTTAAAAAGTTGCTTAATTCAGCACTGAG 1768
585 AAGAACTGAAACGATGATGTTGAGAAATCTGTCTCGCTGGAGGATTTATCATCACCCCAAT 644
1769 AAGGCGCTTAAAGAAATAGATTCCCACTGCCATCTCAGAAAAGTTAAGCACATGAGAAA 1828
645 GCATAATCTCGTTAATGATGTTGAGAAATCTGTCTCGCTGGAGGATTTATCATCACCCCAAT 704
1829 AGATAATGTTGTTAGTG--CAAGACCAAGGAGGAGGAGGACATATGCTGTAGGATGGA 1886
705 GCAGGATATTGCTCAAGTCTCTCGGCAATATGTTTACCGAATCAATAGCCCTTCAGAGGCT 764
1887 ACAGGTTATTGCTCAAGTCTCTGATAATCTGAAATGAGAGAAATCCCTTCCAGAGCT 1946
765 AAGAAA 770
1947 ACGAAA 1952

RESULT 12
ABZ18334
ID ABZ18334 standard; cDNA; 3045 BP.
XX
AC ABZ18334;
XX
DT 23-JAN-2003 (first entry)
XX
DE Group III cDNA cancer related clone SEQ ID NO:760.
XX
KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
KW immune response; virology; immunology; microbiology; molecular biology;
KW recombinant DNA technology; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200278516-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US010421.
XX
PR 30-MAR-2001; 2001US-0280255P.
PR 28-AUG-2001; 2001US-0315563P.
PR 09-JAN-2002; 2002US-0347313P.
PR (CORI-) CORIYA CORP.
PI Wang T, Wang S, Bangur CS, Gaiger A;
PI WPI; 2003-058387/05.
DR
PT New immunogenic polynucleotides or polypeptides useful for diagnosing,
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in
PT virology, immunology, microbiology, molecular biology and recombinant DNA
PT techniques.
PS
PS Claim 1; SEQ ID NO 760; 207pp; English.
CC
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP5446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytostatic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses CT or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques. N.B. The sequence data for this patent did not form part of

XX DE Human cysteine protease 10.89-encoding cDNA.
 XX KW Human; cysteine protease 10.89; recombinant production; gene therapy;
 XX KW neuropathy; tumor; cancer; developmental disorder;
 XX KW embryonic development disorder; immune disorder; inflammatory condition;
 XX KW cytosolic; antiinflammatory; immunomodulator; gene; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 20..319
 XX FT /*tag= a
 XX FT /product= "Human cysteine protease 10.89"
 XX CN1361276-A.
 XX PD 31-JUL-2002.
 XX PF 26-DEC-2000; 2000CN-00135907.
 XX PR 26-DEC-2000; 2000CN-00135907.
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX PI Mao Y, Xie Y;
 XX DR WPI; 2002-751607/82.
 XX DR P-PSDB; ABP58982.
 XX KW Human cysteine proteinase 10.89 polypeptides and polynucleotides encoding
 XX PT it.
 XX PS Claim 6; Page 25-26 (Disclosure); 32pp; Chinese.
 XX CC The invention relates to human cysteine protease 10.89 (ABP58982) and
 XX CC nucleic acids encoding it (ABZ70855). The protein has a molecular weight
 XX CC of 10.89 kD. The invention also relates to a method for the recombinant
 XX CC production of the protein, an antagonist of the protein, and the use of
 XX CC the protein, gene and antagonist in therapeutic applications. Cysteine
 XX CC protease 10.89 can be used in the treatment of a variety of diseases such
 XX CC as neuropathy, tumor, cancer, developmental disorders (particularly embryonic
 XX CC development disorders), immune disorders and inflammatory conditions. The
 XX CC present sequence represents cDNA encoding human cysteine protease 10.89
 XX CC
 XX SQ Sequence 1222 BP; 392 A; 210 C; 254 G; 366 T; 0 U; 0 Other;
 Query Match 20.8%; Score 166; DB 6; Length 1222;
 Best Local Similarity 65.7%; Pred. No. 9.2e-41;
 Matches 260; Conservative 0; Mismatches 130; Indels 6; Gaps 1;
 QY 380 CTCTCCMAAGCCACGAGAAATTAATGCTGATATAAAACGTAATTAAGTGAAGAACT 439
 DB 40 CATCTCTGCTATGCGACAGGATCAATGCTGATATAAAACATCAATTAATGAGGAGT 99
 QY 440 CGATGCTTGGACAAATAATGAAATAATCTTCGAAATGCTTGAAGGAGTGCAGGACC 499
 DB 100 TCGAAAGTTTGGTTCGAAATATGAAAGAAATTTTCATTTTGGTTCGAAAGTGCAGGACC 159
 QY 500 TACTGCAGTCAGGAGCGATTTTTCGATCCATCATCAAGGAGCAGCAAGATGATGAG 559
 DB 160 TCTGGAGATGAGAAACAGTTTGTGATTTTACCATCAAGGAGCGCGAAGTTTAAAG 219
 QY 560 ACAGAGCTTTGTTAAGCACCTTAAGAGAAACCTGAAACGATGATGATGAGATCTTGTTC 619
 DB 220 ACAGTCTCTAATTCAGTACCTTGAAGGAGTACTAGAAAAAATAAATCCACCACTTCA 279
 QY 620 CCTGGAGGATTCACACCCCAATATGCAATATCTCGTTAATG-----ATTGAGGAGA 673
 DB 280 CAACACATTAGTCAATCATCAACAGGAGATCATCTGTTAGTCAAGACCAAGTGAAGAA 339
 QY 674 AAAGGATCAGATTCTGTTTTCATCAATGAGCAGGATATTCGTAAGTCTCTCGCATAT 733

DB 340 AAATGACAAAGTTTCTGCTGTAGGATGGAACAGGATATTGTTGAAGCTCTCTGAATG 399
 QY 734 TGTACCGATCAATAGAGCTTCCAGAGGCTAAGAA 769
 DB 400 TTTGAGTCAAGGAATGCTTTCCAGATGCTAAGAA 435
 RESULT 15
 ADE06992
 ID ADE06992 standard; DNA; 3092 BP.
 XX AC ADE06992;
 XX DT 29-JAN-2004 (first entry)
 XX DE Novel coding sequence (useful for identifying genetic disorders) #58.
 XX KW novel gene; novel protein; tissue marker; molecular weight marker;
 XX KW chromosome marker; genetic disorder; gene; ds.
 XX OS Unidentified.
 XX FN WO2003054152-A2.
 XX PD 03-JUL-2003.
 XX PF 10-DEC-2002; 2002WO-US039555.
 XX PR 10-DEC-2001; 2001US-0339739P.
 XX PR 11-DEC-2001; 2001US-0339453P.
 XX PR 14-MAR-2002; 2002US-0365091P.
 XX PR 12-APR-2002; 2002US-0372381P.
 XX PR 12-APR-2002; 2002US-0372615P.
 XX PR 22-APR-2002; 2002US-00128558.
 XX PR 24-APR-2002; 2002US-0376045P.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 XX PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 XX PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX DR WPI; 2003-569235/53.
 XX DR P-PSDB; ADE07903.
 XX PT New polynucleotides, useful for expressing recombinant proteins for
 XX PT analysis, characterization of therapeutic use, or as markers for tissues
 XX PT in which the corresponding protein is preferentially expressed.
 XX PS Claim 1; SEQ ID NO 58; 1177pp; English.
 XX CC The invention comprises the amino acid and coding sequences of novel
 XX CC proteins. The DNA and protein sequences of the invention are useful as:
 XX CC markers for tissues in which the corresponding protein is preferentially
 XX CC expressed; as molecular weight markers on gels; as chromosome markers or
 XX CC tags; to identify chromosomal or to map related gene positions; and to
 XX CC compare with endogenous DNA sequences in patients to identify potential
 XX CC genetic disorders. The present DNA sequence represents a gene of the
 XX CC invention.
 XX SQ Sequence 3092 BP; 894 A; 722 C; 726 G; 750 T; 0 U; 0 Other;
 Query Match 19.7%; Score 157.6; DB 9; Length 3092;
 Best Local Similarity 67.8%; Pred. No. 5.9e-38;
 Matches 251; Conservative 0; Mismatches 89; Indels 30; Gaps 1;
 QY 212 TATCAGGAGATCTTATTCACCCAGCCCAATTCGATTCCTCAGATTGATCTTCACTGG 271
 DB 2687 TATCAGGAGATCTTATTCACCCAGCCCAATTCGATTCCTCCTGACCTTCACAG 2746
 QY 272 TTTCAGCAAGATAGGATGATGCGAAGAACTGTTAGCAATGACCTGTGGGAGAACTG 331

Db	2747	TCTCAGCAAGATGGGCTGATTCAAAAACCTGGTAGTAACGCATTTGTAGGAGGAGCCAA	2806
Qy	332	TACCAGCAGTTTCTCTGGAGATGACCTAGATGCGAGAGAAACAGCCTC-----	379
Db	2807	AAACTGCAGTCTCTCCGTAGATGACCAAAAGAGCCAGTAGCATCTACTTTGGGAGCTAT	2866
Qy	380	-----CTCTCCAAAGCCAAAGAGAAATTAATGCTGATATAAAAG	421
Db	2867	GCCAAATACATTACAAATCACTCCTGCTATGGCAAGGAATCAATGCTGATATAAAACA	2926
Qy	422	TAAATTAGTGAAGGAACCTCCGATGGTTGGACAAAAATATGAAAAATCTTCGAAATGCT	481
Db	2927	TCATTATAGAGGAGTTCGAAAGTTTGGTCGAAATATGAAAGAAATTTTCATTGCT	2986
Qy	482	TGAAGGAGTGAAGGACCTACTGCAAGTCAGGAGGATTTTGAATCCATCATCAAGGA	541
Db	2987	TGAAGAGTGAAGGACCTCTGGAGATGAAGAAACAGTTTGTGAATTTACCATCAAGGA	3046
Qy	542	AGCAGCAAGA	551
Db	3047	AGCCGCAAGA	3056

Search completed: April 25, 2004, 08:45:45
Job time : 217.564 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:54:27 ; Search time 2106.57 Seconds
(without alignments)
16460.143 Million cell updates/sec

Title: US-10-051-835-12

Perfect score: 800

Sequence: 1 ctctctccagcaggttcag.....taaaagatgtttttttccc 800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pin:*

35: em_htg_rnd:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sv:*

39: em_higo_hum:*

40: em_higo_mus:*

41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	769	96.1	1048	9	BC028711	BC028711 Homo sapi
2	758.4	94.8	1498	9	AK098689	AK098689 Homo sapi
3	579.2	72.4	177954	9	AC011366	AC011366 Homo sapi
4	579.2	72.4	216067	9	AC008417	AC008417 Homo sapi
5	447.4	55.9	88423	2	AC022624	AC022624 Homo sapi
6	252	31.5	61880	2	AC021135	AC021135 Homo sapi
7	252	31.5	115916	9	AL590618	AL590618 Human DNA
8	252	31.5	115916	9	AL590618	AL590618 Human DNA
9	249.8	31.2	37959	9	BS37333	BS37333 Human DNA
10	248.8	31.1	547	11	HS229C20T	AL032555 H.sapiens
11	248.8	31.1	61880	2	AC021135	AC021135 Homo sapi
12	225.2	28.1	7090	9	HS808260	BS648113 Homo sapi
13	224.8	28.1	69776	9	AL953870	AL953870 Human DNA
14	223.6	27.9	1840	9	AK123209	AK123209 Homo sapi
15	223.6	27.9	3528	6	AX834225	AX834225 Sequence
16	223.6	27.9	3528	9	AK096544	AK096544 Homo sapi
17	223.6	27.9	3812	6	AR235845	AR235845 Sequence
18	223.6	27.9	3812	6	AX702086	AX702086 Sequence
19	223.6	27.9	6823	9	HS804632	AL833319 Homo sapi
20	187.6	23.4	2021	6	BD205409	BD205409 Tumor-ass
21	187.6	23.4	3069	9	HS278111	AJ728111 Homo sapi
22	178.4	22.3	3075	9	AK126202	AK126202 Homo sapi
23	152	19.0	476	11	HS22882T	AL032554 H.sapiens
24	126.6	15.8	1281	10	BC019773	BC019773 Mus muscu
25	99.6	12.4	144896	9	AL391380	AL391380 Human DNA
26	96.6	12.4	168431	2	AC040972	AC040972 Homo sapi
27	96.6	12.1	161	9	HSU11738	U11738 Homo sapien
28	84.2	10.5	144896	9	AL391380	AL391380 Human DNA
29	82	10.2	69776	9	AL953870	AL953870 Human DNA
30	81.2	10.2	209211	10	AC048362	AC048362 Mus muscu
31	70.6	8.8	65042	6	AR235846	AR235846 Sequence
32	70.6	8.8	65042	6	AX702088	AX702088 Sequence
33	69.8	8.7	1738	9	HS801162	AL117626 Homo sapi
34	69.8	8.7	2110	9	AF141326	AF141326 Homo sapi
35	69.8	8.7	2718	6	BD127822	BD127822 Primer fo
36	69.8	8.7	2718	9	AK074946	AK074946 Homo sapi
37	69.8	8.7	2984	9	BC040581	BC040581 Homo sapi
38	69.8	8.7	3398	9	HS804837	AL833524 Homo sapi
39	69.8	8.7	3690	6	AX467719	AX467719 Sequence
40	69.8	8.7	3690	9	AF097645	AF097645 Homo sapi
41	69.8	8.7	3691	6	A94608	A94608 Sequence 1
42	69.8	8.7	3691	6	E37827	E37827 Novel carci
43	69.8	8.7	3691	6	AX019045	AX019045 Sequence
44	69.8	8.7	3692	9	BC039829	BC039829 Homo sapi
45	69.8	8.7	3970	9	AK128795	AK128795 Homo sapi

ALIGNMENTS

RESULT 1
BC028711
LOCUS
DEFINITION Homo sapiens hypothetical protein MGC27005, mRNA (cDNA clone
1048 bp mRNA linear PRI 21-OCT-2003
MGC:27005 IMAGE:4828274), complete cds.
ACCESSION BC028711
VERSION BC028711.2 GI:34192071
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1048)
Srausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,
Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,

Altschul, S.F., Ziesberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shewchenko, Y., Bouffard, G.G., Blackesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalins, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1048)

Strausberg, R.

Direct Submission

Submitted (29-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

On Aug 25, 2003 this sequence version replaced gi:20381102.

Contact: MGC help desk

Email: cgaps-x@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

Contact: amadansystemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettner, Amuratha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 34 Row: d Column: 10

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22749202.

FEATURES

Location/Qualifiers

1..1048

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:27005 IMAGE:4828274"

/tissue_type="Testis"

/clone_lib="NIH MGC 97"

/lab_host="DH10B"

/note="Vector: pBluescript"

1..1048

/gene="MGC27005"

/db_xref="LocusID:158852"

246..815

/codon_start=1

/product="hypothetical protein MGC27005"

/protein_id="AAH28711.1"

/db_xref="GI:20381103"

/db_xref="LocusID:158852"

/translations="MTDKTEKVAVDPETVFKPRECDSPSYQKRMALLARKQAGD SLIAGLAMSKEKMLTGCHAI PPSQLDSQIDDTFGSKRMQKPGSNAPVGNVTSF SGDDLCRETPASSPKQRIINADIKRLVKELRCVQKYEKIFEMLEGVQGPVAVRKR FFSIIKEAARCMWRDFVXHLKKLKRMI"

gene

CDS

96.13; Score 769; DB 9; Length 1048;

ORIGIN

Query Match

Best Local Similarity 98.7%; Pred. No. 6.7e-201; Matches 775; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 16 GTCAGGACTTTCAGGACTGAAACCAATGACCGATGAAACAGAGAGGCTGTAGATCCTG 75

DB 223 GTCTCTCTCCAGCAAGGAAACCAATGCCGATTAACAGAGAGGCTGTAGATCCTG 282

QY 76 AAATGCTGTTTAAACGTCGCCAGGAATGTGACAGTCTCTGATCAGAAAAGCAGAGGA 135

DB 283 AAATGCTGTTTAAACGTCGCCAGGAATGTGACAGTCTCTGATCAGAAAAGCAGAGGA 342

QY 136 TGGCCCTGTTGGCAAGGAAACAGGAGCAGGAGACAGCCTTATTGCAAGGCTCTGCCATGT 195

DB 343 TGGCCCTGTTGGCAAGGAAACAGGAGCAGGAGACAGCCTTATTGCAAGGCTCTGCCATGT 402

QY 196 CCAAGAAAAAGAGCTTATGACAGGACATGCTATTCCACCCAGCCAAATTGGATTCTCAGA 255

DB 403 CCAAGAAAAAGAGCTTATGACAGGACATGCTATTCCACCCAGCCAAATTGGATTCTCAGA 462

QY 256 TTGATGACTTCACTGCTTTCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGCGAC 315

DB 463 TTGATGACTTCACTGCTTTCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGCGAC 522

QY 316 CTGTGGAGGAAACGTTTACAGCAGGTTTCTCTGGAGATGACCTAGATGACAGAGAACAG 375

DB 523 CTGTGGAGGAAACGTTTACAGCAGGTTTCTCTGGAGATGACCTAGATGACAGAGAACAG 582

QY 376 CCTCTCTCCCAAGCCACGAGAAATTAATCTGATATAAAACCTGTAATTAAGTGAAGG 435

DB 583 CCTCTCTCCCAAGCCACGAGAAATTAATCTGATATAAAACCTGTAATTAAGTGAAGG 642

QY 436 AACTCCGATCGTTGGCAAAAATATGAAAAATCTTCGAAATGCTTGAAGGATGCGAAG 495

DB 643 AACTCCGATCGTTGGCAAAAATATGAAAAATCTTCGAAATGCTTGAAGGATGCGAAG 702

QY 496 GACCTACTGAGTCAGGAGGAGGATTTTGAATCCATCATCAAGGAGCAGCAGATGTA 555

DB 703 GACCTACTGAGTCAGGAGGAGGATTTTGAATCCATCATCAAGGAGCAGCAGATGTA 762

QY 556 TGAGACGAGACTTTGTTAAGCACCCTTAAGAGAAACCTGAAACCTGATGATTGAGATACT 615

DB 763 TGAGACGAGACTTTGTTAAGCACCCTTAAGAGAAACCTGAAACCTGATGATTGAGATACT 822

QY 516 TGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAATGATTGAGAGAGAGAAA 675

DB 823 TGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAATGATTGAGAGAGAGAAA 882

QY 676 AGGATCAGATTGCTGTTTCTTACAATGGAGCAGGATATTGCTCAAGTCTCTGGCATATG 735

DB 883 AGGATCAGATTGCTGTTTCTTACAATGGAGCAGGATATTGCTCAAGTCTCTGGCATATG 942

QY 736 TTACGGAATCAATAGCGCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAGATGTTCTTT 795

DB 943 TTACGGAATCAATAGCGCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAGATGTTCTTT 1002

QY 796 TTCCC 800

DB 1003 TTCCC 1007

RESULT 2

AK098689

LOCUS

AK098689 1498 bp mRNA linear PRI 12-SEP-2003

DEFINITION Homo sapiens cDNA FLJ25823 fis, clone TST07974.

ACCESSION AK098689

VERSION AK098689.1 GI:21758775

KEYWORDS cllgo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,

Arata, M., Mushino, K., Yuuki, H., Hara, H., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 1498)
 Sugano, S. and Suzuki, Y.
 Direct Submission
 Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan
 (E-mail: fldcna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
 Location/Qualifiers
 1. .1498
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TST07974"
 /tissue="testis"
 /clone_lib="TST"
 /note="cloning vector: pME18SFL3"
 91. .660
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="BAC05380.1"
 /db_xref="GI:21758776"
 /translation="MTKTKVAVDPETVFRPRECDSVQKRWALLARKQAGD
 SLIAGRSKAKLMTGHALPPSOLDSQIDDFGFKDRMKQKGNVPGNVTSPF
 SGDLRETRASSPSQENADIRKLVRCVGOKYKIFEMLEGVQGPVAVKR
 FFSIIKEARFCMERDFVKKLKKLKKMI"

ORIGIN

Query Match 94.8%; Score 758.4; DB 9; Length 1498;
 Best Local Similarity 99.2%; Pred. No. 5.5e-198;
 Matches 762; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 33 GAAACAATGACCGATAAACAAGAGAGGTGGCTGTAGATCTGAACTGTGTTTAAACGT 92
 85 GAAACAATGACCGATAAACAAGAGAGGTGGCTGTAGATCTGAACTGTGTTTAAACGT 144
 93 CCCAGGAATGTGACGTCTTCGTATCAGAAAGGAGAGATGGCCCTGTGGCAAGG 152
 145 CCCAGGAATGTGACGTCTTCGTATCAGAAAGGAGAGATGGCCCTGTGGCAAGG 204
 153 AAACAAGGAGGAGAGAGAGAGCTTATTCAGGCTTCGCTGCTCCAAAGAAAGAGCTT 212
 205 AAACAAGGAGGAGAGAGAGAGCTTATTCAGGCTTCGCTGCTCCAAAGAAAGAGCTT 264
 213 ATGACAGGACATGCTATTTCACCCAGCAATGGATTCCTAGATTCACCTGCTT 272
 265 ATGACAGGACATGCTATTTCACCCAGCAATGGATTCCTAGATTCACCTGCTT 324
 273 TTCCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGACCTGTGGGAGGAAAGCTT 332
 325 TTCCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGACCTGTGGGAGGAAAGCTT 384
 333 ACCAGAGTTTCTTGGAGATGACCTAGATGACAGAAACAGAGCTCTCTCCCAAGC 392
 385 ACCAGAGTTTCTTGGAGATGACCTAGATGACAGAAACAGAGCTCTCTCCCAAGC 444
 393 CAACAGAGAAATTAAGCTGATATAAAAGCTAAATAGTGAAGAACTCCGATGCGTTGGA 452
 445 CAACAGAGAAATTAAGCTGATATAAAAGCTAAATAGTGAAGAACTCCGATGCGTTGGA 504

453 CAAAATATGAAAAATCTTCGAATCTTGAAGAGTGCAGGAGCTACTGCACTCAGG 512
 505 CAAAATATGAAAAATCTTCGAATCTTGAAGAGTGCAGGAGCTACTGCACTCAGG 564
 513 AAGCGATTTTGAATCCATCATCAAGAGAGCAGCAAGATGTATGAGACGAGACTTGT 572
 565 AAACGATTTTGAATCCATCATCAAGAGAGCAGCAAGATGTATGAGACGAGACTTGT 624
 573 AAGCACCTTGAAGAGAACTGAAACGTATGATTGAGATACCTTGTCTGAGGAGATTAT 632
 635 AAGCACCTTGAAGAGAACTGAAACGTATGATTGAGATACCTTGTCTGAGGAGATTAT 684
 633 CACACCCCAATGCAATATCTCGTTAATGATGAGGAGAGAGAAAGATCAGATTCGTGT 692
 685 CACACCCCAATGCAATATCTCAATTAATGATGAGGAGAGAGAAAGATCAGATTCGTGT 744
 693 TTCTACATGAGCAGGATATGCTGAGTCTCTGCAATATGTTACCGAATCAAAATAGC 752
 745 TTCTACATGAGCAGGATATGCTGAGTCTCTGCAATATGTTACCGAATCAAAATAGC 804
 753 CTTCCAGAGGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 800
 805 CTTCCAGAGGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 852

AC011366 177954 bp DNA linear PRI 27-FEB-2002
 Homo sapiens chromosome 5 clone CTC-568L21, complete sequence.

AC011366
 AC011366
 AC011366.6 GI:18958631
 HTG.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 177954)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 Direct Submission
 Unpublished
 2 (bases 1 to 177954)
 DOE Joint Genome Institute.
 Direct Submission
 Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 177954)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 Direct Submission
 Submitted (27-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Feb 27, 2002 this sequence version replaced gi:7711494.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99.9% of Sequence;
 Estimated Total Number of Errors is 0.8.

Location/Qualifiers
 1. .177954
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTC-568L21"

FEATURES
 source

Query Match 72.4%; Score 579.2; DB 9; Length 177954;
 Best Local Similarity 86.2%; Pred. No. 1.1e-148;
 Matches 652; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

33 GAAACAATGACCGATAAACAAGAGAGGTGGCTGTAGATTCCTGAACTGTGTTTAAACGT 92
 158859 GAAACAATGACCGATAAACAAGAGAGAGGTGGCTGTAGATTCCTGAACTGTGTTTAAACGT 158918

ORIGIN
 Query Match 72.4%; Score 579.2; DB 9; Length 177954;
 Best Local Similarity 86.2%; Pred. No. 1.1e-148;
 Matches 652; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

33 GAAACAATGACCGATAAACAAGAGAGGTGGCTGTAGATTCCTGAACTGTGTTTAAACGT 92
 158859 GAAACAATGACCGATAAACAAGAGAGAGGTGGCTGTAGATTCCTGAACTGTGTTTAAACGT 158918


```

QY 93 CCCGGGAATGTGACAGTCCCTTGGTATCAGAAAAGGACAGAGATGGCCCTGTTGGCAAGG 152
Db 158919 CCCAGGGAATCTGAGACTCCCTTCATCTCAGAAAGGACAGAGATGGCCCTGTTGTAAGG 158978
QY 153 AAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
Db 158979 AAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159038
QY 213 ATGACAGAGACATGCTATTCCACCAAGCAATTTGGATTCTCAGATTGATGACTTCACTGGT 272
Db 159039 ATGCGCAGAGATGGTATTCCCAAGCAAGCAATTTGGATTCTCGTTGATGACTTCACTGGT 159098
QY 273 TTACGCAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 332
Db 159099 TGCAGCAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 159158
QY 333 ACCAGCAGTTTCTCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 392
Db 159159 ACCAGCAATTTCTCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 159218
QY 393 CAACGAGAAATTAATGCTGATATAAAAGCTAAATTAATTAATTAATTAATTAATTAATTAAT 452
Db 159219 CAAGAAGAAATTAATGCTGATATAAAAGCTAAATTAATTAATTAATTAATTAATTAATTAAT 159278
QY 453 CAATATATCAAAATCTTCGAAATGCTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 512
Db 159279 CGAAATATGAAATCTTCGAAATGCTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 159338
QY 513 AAGCGATTTTGAATPCCATCATCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 572
Db 159339 AAGTGAATTTTGAATPCCATCATCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159398
QY 573 AAGCACCCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 632
Db 159399 AAGCACCCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159458
QY 633 CACACCCCAATGTCATTAATCTGTTAATGATGAGGA-CAGAAAAGGATGAGATGCTGT 691
Db 159459 CTCACCGCAATGTCATTAATCTGTTAATGATGAGGA-CAGAAAAGGATGAGATGCTGT 159518
QY 692 TTCTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
Db 159519 TTCTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159578
QY 752 CCTTCAGAGGCTAAGAAATTTCTGTTAGTAAAGA 787
Db 159579 CCTTCAGAGGCTAAGAAATTTCTGTTAGTAAAGA 159614

RESULT 4
AC008417/c 216067 bp DNA linear PRI 18-APR-2000
LOCUS Homo sapiens chromosome 5 clone CTC-28708, complete sequence.
DEFINITION AC008417
ACCESSION AC008417
VERSION AC008417.3 GI:6730695
KEYWORDS FIG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 216067)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 216067)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 216067)
AUTHORS DOE Joint Genome Center and Stanford Human Genome Center.
TITLE Direct Submission

```

Submitted (22-JAN-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

4 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (01-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

5 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (02-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

6 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (15-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

7 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jan 22, 2000 this sequence version replaced gi:6165190.

Draft Sequence Produced by DOE Joint Genome Institute

www.tgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.6% of Sequence;

Estimated total Number of Errors is 0.7.

Location/Qualifiers

1. 216067

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="CTC-28708"

Query Match 72.4%; Score 579.2; DB 9; Length 216067;

Best Local Similarity 86.2%; Pred. No. 1.1e-148;

Matches 652; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

QY 33 GAACATATGACCATTAACACAG 92

Db 191217 GAACATATGACCATTAACACAG 191158

QY 93 CCCAGGAATGTGACAGTCCCTTCGATCAGAAAAGGACAGAGATGGCCCTGTTGGCAAGG 152

Db 191157 CCCAGGAATGTGACAGTCCCTTCGATCAGAAAAGGACAGAGATGGCCCTGTTGGTAAGG 191098

QY 153 AAACAGGACGAG 212

Db 191097 AAACAGGACGAG 191038

QY 213 ATGACAGAGATGCTATTTCACCCAGCCAAATTCGATTTCTCAGATTGATGACTTCACTGGT 272

Db 191037 ATGACAGAGATGCTATTTCACCCAGCCAAATTCGATTTCTCAGATTGATGACTTCACTGGT 190978

QY 273 TTACGCAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 332

Db 190977 TTACGCAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 190918

QY 333 ACCAGCAGTTTCTCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 392

Db 190917 ACCAGCAGTTTCTCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 190858

QY 393 CAACGAGAAATTAATGCTGATATAAAAGCTAAATTAATTAATTAATTAATTAATTAATTAAT 452

Db 190857 CAACGAGAAATTAATGCTGATATAAAAGCTAAATTAATTAATTAATTAATTAATTAATTAAT 190798

QY 453 CAATATATGAAATCTTCGAAATGCTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 512

Db 190797 CAATATATGAAATCTTCGAAATGCTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 190738

QY 513 AAGCGATTTTGAATCCATCATCAAGAGCAGCAAGATGATGACGAGACTTTGTT 572
Db 190737 AAATGATTTTGAATCCATCATCAAGAGCAGCAAGATGATGACGAGACTTTAAT 190678
QY 573 AAGCACCTTAAAGAGAACTCAAGACGATGATTTGAGAACTACTTGTCCCTGGAGGATTA 632
Db 190677 CAGCACCTTGAAGAGAACTCGACAAATGATTTCTGGCTACTTGTTCAGAGAGGATCAT 190618
QY 633 CACACCCCAATGATTAATTCGTTAATGATGAGGA-GAGAAAGGATGAGATTCGTGT 691
Db 190617 CTCACCGCAATGATTAATTCGTTAATGATGAGGAGGAGGAGGAGGATCAAAATTCGTGT 190558
QY 692 TTTCTACAAATGAGCAGGATATTCGTAAGTCTCTGCGATATCTTACCGAATCAAAATAG 751
Db 190557 TTTCTAGAAATGAGCAGGATATTCGTAAGTCTCTGAGGCTCTAGCATGTTAGTGAATAAATGG 190498
QY 752 CTTCCAGAGGCTAAGAAATTCGTTAGTAAAGA 787
Db 190497 CTTCCAGAGGCTAAGACATTCGTTAAAAA 190462

RESULT 5
AC022624/c
LOCUS
DEFINITION Homo sapiens clone RP11-24B6, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC022624
VERSION AC022624.2 GI:9129767
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 88423)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-24B6
Unpublished

2. (bases 1 to 88423)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lander, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, F., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Zimmer, A. and Zody, M.
Direct Submission

TITLE
JOURNAL
COMMENT
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6910695.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4425
Center clone name: 24_B_6

* NOTE: This record contains 89 individual
* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 944: contig of 944 bp in length
* 945 1044: gap of 100 bp
* 1045 1949: contig of 905 bp in length
* 1950 2049: gap of 100 bp
* 2050 2954: contig of 905 bp in length
* 2955 3054: gap of 100 bp
* 3055 3944: contig of 890 bp in length
* 3945 4044: gap of 100 bp
* 4045 4933: contig of 889 bp in length
* 4934 5034: gap of 100 bp
* 5034 5921: contig of 888 bp in length
* 5921 6021: gap of 100 bp
* 6022 6920: contig of 899 bp in length
* 6921 7020: gap of 100 bp
* 7021 7897: contig of 877 bp in length
* 7898 7997: gap of 100 bp
* 7998 8903: contig of 906 bp in length
* 8904 9003: gap of 100 bp
* 9004 9915: contig of 912 bp in length
* 9916 10015: gap of 100 bp
* 10016 10881: contig of 866 bp in length
* 10882 10981: gap of 100 bp
* 10982 11886: contig of 905 bp in length
* 11887 11886: gap of 100 bp
* 11887 12876: contig of 890 bp in length
* 12877 12976: gap of 100 bp
* 12977 13851: contig of 875 bp in length
* 13852 13951: gap of 100 bp
* 13952 14856: contig of 905 bp in length
* 14857 14956: gap of 100 bp
* 14957 15847: contig of 891 bp in length
* 15848 15947: gap of 100 bp
* 15948 16860: contig of 913 bp in length
* 16861 16960: gap of 100 bp
* 16961 17906: contig of 946 bp in length
* 17907 18006: gap of 100 bp
* 18007 18894: contig of 888 bp in length
* 18895 18994: gap of 100 bp
* 18995 19913: contig of 919 bp in length
* 19914 20013: gap of 100 bp
* 20014 20920: contig of 907 bp in length
* 20921 21883: contig of 863 bp in length
* 21884 21983: gap of 100 bp
* 21984 22890: contig of 907 bp in length
* 22891 22990: gap of 100 bp
* 22991 23912: contig of 922 bp in length
* 23913 24012: gap of 100 bp
* 24013 24990: contig of 878 bp in length
* 24991 24990: gap of 100 bp
* 24991 25869: contig of 879 bp in length
* 25870 25969: gap of 100 bp
* 25970 26835: contig of 866 bp in length
* 26836 26935: gap of 100 bp
* 26936 27836: contig of 901 bp in length
* 27837 27936: gap of 100 bp
* 27937 28785: contig of 849 bp in length
* 28786 28885: gap of 100 bp
* 28886 29801: contig of 916 bp in length
* 29802 29901: gap of 100 bp
* 29902 30798: contig of 897 bp in length
* 30799 30898: gap of 100 bp
* 30899 31808: contig of 910 bp in length
* 31809 31908: gap of 100 bp

COMMENT

On Jun 16, 2000 this sequence version replaced ga:7109601.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----
 Center project name: H.NH0405U13

----- Summary Statistics -----

Sequencing vector: M13; 94%

Chemistry: Dye-terminator ET; 94% of reads

Chemistry: Dye-terminator Big Dye; 6% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 56291 bases at least Q40

Consensus quality: 57906 bases at least Q30

Consensus quality: 58786 bases at least Q20

Insert size: 222000; agarose-fp

Quality coverage: 5.00 in Q20 bases; agarose-fp

Quality coverage: 5.67 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 14 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 2127: contig of 2127 bp in length
 * 2128 2227: gap of unknown length
 * 2228 3313: contig of 1086 bp in length
 * 3314 3413: gap of unknown length
 * 3414 4919: contig of 1506 bp in length
 * 4920 5013: gap of unknown length
 * 5020 6500: contig of 1481 bp in length
 * 6501 6601: gap of unknown length
 * 6601 7629: contig of 1029 bp in length
 * 7630 7729: gap of unknown length
 * 7730 10811: contig of 3082 bp in length
 * 10812 10911: gap of unknown length
 * 10912 14705: contig of 3794 bp in length
 * 14706 14805: gap of unknown length
 * 14806 18987: contig of 4182 bp in length
 * 18988 19087: gap of unknown length
 * 19088 23840: contig of 4753 bp in length
 * 23841 23940: gap of unknown length
 * 23941 26787: contig of 2847 bp in length
 * 26788 26887: gap of unknown length
 * 26888 31613: contig of 4726 bp in length
 * 31614 31713: gap of unknown length
 * 31714 38659: contig of 6946 bp in length
 * 38660 38759: gap of unknown length
 * 38760 50631: contig of 11872 bp in length
 * 50632 50731: gap of unknown length
 * 50732 61880: contig of 11149 bp in length.

FEATURES

source

1. 61880
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="X"
 /clone="RP11-405U13"

ORIGIN

Query Match 31.5%; Score 252; DB 2; Length 61880;
 Best Local Similarity 100.0%; Pred. No. 1.9e-58;
 Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 AGATGTATGACGAGACTTGTATACCACTTAAGAGAACTGAACGATGATTGA 608
 |||||
 DB 51098 AGATGTATGACGAGACTTGTATACCACTTAAGAGAACTGAACGATGATTGA 51157

QY 609 GAATACCTGCTCCTGGAGGATTATCACACCCCAATGATAATCTCGTTAATGATTGAGG 668
 |||||
 DB 51158 GAATACCTGCTCCTGGAGGATTATCACACCCCAATGATAATCTCGTTAATGATTGAGG 51217
 |||||
 QY 669 AGAGAAAAGGATCAGATTGCTGTTTCTACATGAGCAGGATATTGCTGAAGTCTCCTG 728
 |||||
 DB 51218 AGAGAAAAGGATCAGATTGCTGTTTCTACATGAGCAGGATATTGCTGAAGTCTCCTG 51277
 |||||
 QY 729 GCATATGTTACCAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTAGTAAAGAT 788
 |||||
 DB 51278 GCATATGTTACCAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTAGTAAAGAT 51337
 |||||
 QY 789 GTTCTTTTCCC 800
 |||||
 DB 51338 GTTCTTTTCCC 51349
 |||||

RESULT 7

AL590618

LOCUS

DEFINITION

Human DNA sequence from clone RP13-36C9 on chromosome X, complete

sequence.

ACCESSION

AL590618

VERSION

AL590618.18 GI:32131111

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 115916)

Whitehead,S.

Direct Submission

Submitted (20-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 20, 2003 this sequence version replaced gi:18121499.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Emi, EMBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information

on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome X, constructed by the Sanger Centre Chromosome X Mapping

Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>

RP13-36C9 is from the library RPCL-13.1 constructed by the group of

Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest, except on the rare

occasion of the clone being a YAC.

FEATURES

source

Location/Qualifiers

1. 115916

/organism="Homo sapiens"

```
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chrmosome="X"
/clone="RP13-36C9"
/clone_lib="RPCI-13.1"

ORIGIN
Query Match      31.5%; Score 252; DB 9; Length 115916;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 AGATGATGAGACGAGACACTTTGTTAGCACCCTTAAGAGAAACTGAACGTTATGATTGA 608
Db 29193 AGATGATGAGACGAGACACTTTGTTAGCACCCTTAAGAGAAACTGAACGTTATGATTGA 29252
QY 609 GAATACCTTGTCCCTGGAGGATTATCACACCCCAAAATGCAATCTCGTTAAATGATTGAGG 668
Db 29253 GAATACCTTGTCCCTGGAGGATTATCACACCCCAAAATGCAATCTCGTTAAATGATTGAGG 29312
QY 669 AGAGAAAGGATCAGATTGCTGTTTCTACATGAGGAGGATATGCTGGAAGTCTCCTG 728
Db 29313 AGAGAAAGGATCAGATTGCTGTTTCTACATGAGGAGGATATGCTGGAAGTCTCCTG 29372
QY 729 GCATATGTTACCGAAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGAT 788
Db 29373 GCATATGTTACCGAAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGAT 29432
QY 789 GTTCTTTTTCCT 800
Db 29433 GTTCTTTTTCCT 29444

RESULT 8
AL590618/c      115916 bp      DNA      linear      PRI 20-JUN-2003
LOCUS           Human DNA sequence from clone Rpl3-36C9 on chromosome X, complete
DEFINITION
ACCESSION       AL590618
VERSION         AL590618.18 GI:32131111
KEYWORDS        HTG.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
REFERENCE       Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE           1 (bases 1 to 115916)
JOURNAL         Whitehead,S.
COMMENT         Direct Submission
Submitted (20-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 20, 2003 this sequence version replaced gi:18121499.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RP13-36C9 is from the library RPCI-13.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC

Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
Location/Qualifiers
1. 115916
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chrmosome="X"
/clone="RP13-36C9"
/clone_lib="RPCI-13.1"

FEATURES
source
ORIGIN
Query Match      31.5%; Score 252; DB 9; Length 115916;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 AGATGATGAGACGAGACACTTTGTTAGCACCCTTAAGAGAAACTGAACGTTATGATTGA 608
Db 66875 AGATGATGAGACGAGACACTTTGTTAGCACCCTTAAGAGAAACTGAACGTTATGATTGA 66816
QY 609 GAATACCTTGTCCCTGGAGGATTATCACACCCCAAAATGCAATCTCGTTAAATGATTGAGG 668
Db 66815 GAATACCTTGTCCCTGGAGGATTATCACACCCCAAAATGCAATCTCGTTAAATGATTGAGG 66756
QY 669 AGAGAAAGGATCAGATTGCTGTTTCTACATGAGGAGGATATGCTGGAAGTCTCCTG 728
Db 66755 AGAGAAAGGATCAGATTGCTGTTTCTACATGAGGAGGATATGCTGGAAGTCTCCTG 66696
QY 729 GCATATGTTACCGAAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGAT 788
Db 66695 GCATATGTTACCGAAATCAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTTAGTAAAGAT 66636
QY 789 GTTCTTTTTCCT 800
Db 66635 GTTCTTTTTCCT 66624

RESULT 9
BX537333        37959 bp      DNA      linear      PRI 24-JUN-2003
LOCUS           Human DNA sequence from clone XX-86277B6 on chromosome X, complete
DEFINITION
ACCESSION       BX537333
VERSION         BX537333.1 GI:31746321
KEYWORDS        HTG.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
REFERENCE       Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE           1 (bases 1 to 37959)
JOURNAL         Whitehead,S.
COMMENT         Direct Submission
Submitted (21-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
```

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX> XX-88277B6 is from a Whitehead human fosmid library VECTOR: pEpiFos-5.

FEATURES

```

source
1. 37959
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="XX-88277B6"
/clone_lib="Whitehead_fosmid"

ORIGIN
Query Match 31.2%; Score 249.8; DB 9; Length 37959;
Best Local Similarity 97.3%; Pred. No. 7.7e-58;
Matches 254; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 208 AGCTTATGACAGGACATGCTATTCCACCAGCCCAATTCGATTCAGATTCGATTCCTCA 267
DB 28675 AGCTTATGACAGGACATGCTATTCCACCAGCCCAATTCGATTCAGATTCGATTCCTCA 28734

QY 268 CTGGTTTCAGCAAGATGATGATGCGAGAAACCTGGTAGCATGCACTGCGAGGAA 327
DB 28735 CTGGTTTCAGCAAGATGATGATGCGAGAAACCTGGTAGCATGCACTGCGAGGAA 28794

QY 328 AGCTTACAGCAGGTTCTCTGAGATGACCTAGATGACAGAGAAACAGCCCTCTCCCA 387
DB 28795 AGCTTACAGCAGGTTCTCTGAGATGACCTAGATGACAGAGAAACAGCCCTCTCCCA 28854

QY 388 AAAGCCACGAGAAATTAATGCTGATATATAAAGCGTAATTAATGTAAGAACTCCGATCG 447
DB 28855 AAAGCCACGAGAAATTAATGCTGATATATAAAGCGTAATTAATGTAAGAACTCCGATCG 28914

QY 448 TTGGACAAAAATGAAAAA 468
DB 28915 TTGGACAAAGTAAGTAATATA 28935

RESULT 10
HS229C20T 547 bp DNA linear STS 29-OCT-1998
LOCUS H.sapiens STS from genomic clone 229C20, sequence tagged site.
DEFINITION AL032555
ACCESSION AL032555.1 GI:3810773
VERSION STS; single read.
KEYWORDS STS; single read.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
AUTHORS Ross, M., Dunham, A., Huckle, E., Taylor, R. and Hunt, S.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) E-mail contact: humquery@sanger.ac.uk
COMMENT Marker stsG55155 (Primer A : ACCCCAAATGCATATCTCG; Primer B :
```

CTTTCAATAAAGCGTTGGG; amplicon size : 184 bp) is from sequence generated from the T7 end of PAC 229C20. 229C20 is part of the bacterial clone contigs constructed by the Chromosome X Mapping Group. (<http://www.sanger.ac.uk/HGP/ChrX/>) 229C20 is from the library constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see <http://bacpac.med.buffalo.edu/>.

Location/Qualifiers

FEATURES

```

source
1. 547
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="229C20"

ORIGIN
Query Match 31.1%; Score 248.8; DB 11; Length 547;
Best Local Similarity 99.2%; Pred. No. 1.8e-57;
Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 549 AGATGATGAGAGAGACTTTGTTAAGCACCTTAAGAGAAACTGAACGTATGATTGA 608
DB 262 AGATGATGAGAGAGACTTTGTTAAGCACCTTAAGAGAAACTGAACGTATGATTGA 321

QY 609 GAATACCTTGTCCTGGAGGATATACACCCAAATGCATATCTCGTTAATGATTGAG 668
DB 322 GAATACCTTGTCCTGGAGGATATACACCCAAATGCATATCTCGTTAATGATTGAG 381

QY 669 AGAGAAAGAGATCAGATTCCTGTTTCTACAATGGAGCAGGATATTCGTAAGTCCTCG 728
DB 382 AGAGAAAGAGATCAGATTCCTGTTTCTACAATGGAGCAGGATATTCGTAAGTCCTCG 441

QY 729 GCATATGTTACCAATCAATAGCCCTTCAGAGGCTTAAGAAATTCCTGTTAGTAAAGAT 788
DB 442 GCATATGTTACCAATCAATAGCCCTTCAGAGGCTTAAGAAATTCCTGTTAGTAAAGAT 501

QY 789 GTTCTTTTTCCTCC 800
DB 502 GTTCTTTTTCCTCC 513
```

RESULT 11

```

AC021135/c 61880 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome X clone RP11-405J13, WORKING DRAFT
DEFINITION SEQUENCE, 14 unordered pieces.
ACCESSION AC021135.4 GI:8568570
VERSION AC021135
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 61880)
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 61880)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2000) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 16, 2000 this sequence version replaced gi:7109601.
```

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0405J13
----- Summary Statistics -----
Sequencing vector: M13; 94%
```



```
Sequencing vector: plasmid; 6%
Chemistry: Dye-primer ET; 94% of reads
Assembly: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 56291 bases at least Q40
Consensus quality: 57906 bases at least Q30
Consensus quality: 58786 bases at least Q20
Insert size: 222000; agarose-fp
Insert size: 60580; sum-of-contigs
Quality coverage: 5.00 in Q20 bases; agarose-fp
Quality coverage: 5.67 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1
2127: contig of 2127 bp in length
2128: gap of unknown length
2228: contig of 1086 bp in length
3313: contig of unknown length
3314: gap of unknown length
3413: contig of 1506 bp in length
4919: contig of unknown length
5019: gap of unknown length
6000: contig of 1481 bp in length
6600: gap of unknown length
7629: contig of 1029 bp in length
7729: gap of unknown length
7730: contig of 3082 bp in length
10811: contig of 3082 bp in length
10911: gap of unknown length
14705: contig of 3794 bp in length
14805: gap of unknown length
18987: contig of 4182 bp in length
19088: gap of unknown length
23840: contig of 4753 bp in length
23841: gap of unknown length
26787: contig of 2847 bp in length
26788: gap of unknown length
31613: contig of 4726 bp in length
31713: gap of unknown length
38659: contig of 6946 bp in length
38660: gap of unknown length
50631: contig of 11872 bp in length
50632: gap of unknown length
50731: gap of unknown length
50732: contig of 11149 bp in length.
-----
FEATURES
    source
    1. 61880
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /chromosome="X"
        /clone="RP11-405J13"
    Location/Qualifiers
    1. 61880
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /chromosome="X"
        /clone="RP11-405J13"
    Query Match
    Best Local Similarity 31.1%; Score 248.8; DB 2; Length 61880;
    Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
    ORIGIN
    QY 549 AGATGATGAGAGAGAGACTTTGTTAGACCTTAAGAGAACTGAACGTTATGATTGA 608
    DB 41284 AGATGATGAGAGAGAGACTTTGTTAGACCTTAAGAGAACTGAACGTTATGATTGA 41225
    QY 609 GAATACTGTGCTGGAGGATTATCACACCCCAATGCATAATCTCGTTTAATGATTGAGG 668
    DB 41224 GAATACTGTGCTGGAGGATTATCACACCCCAATGCATAATCTCGTTTAATGATTGAGG 41165
    QY 669 AGAGAAAAGATCAGATTGCTGTTTCTACAAATGGAGAGGATATGCTGAAGTCTCCCTG 728
    DB 41164 AGAGAAAAGATCAGATTGCTGTTTCTACAAATGGAGAGGATATGCTGAAGTCTCCCTG 41105
    QY 729 GCATATGTTACCGAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTAGTAAAGAT 788
    Db 41104 GCATATGTTACCGAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTAGTAAAGAT 41045
    QY 789 GTTCTTTTTCOC 800
    Db 41044 GTTCTTTTTCOC 41033
    RESULT 12
    HSM808260 7090 bp mRNA linear PRI 30-AUG-2003
    LOCUS Homo sapiens mRNA; cDNA DKFZP686E0632 (from clone DKFZP686E0632).
    DEFINITION BX648113
    ACCESSION BX648113.1 GI:34367272
    VERSION
    KEYWORDS Homo sapiens (human)
    SOURCE
    ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    REFERENCE
    1 (bases 1 to 7090)
    AUTHORS Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
    Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
    Wiemann,S.
    CONSRM The German Human cDNA Consortium
    TITLE Direct Submission
    JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
    COMMENT Neuherberg, GERMANY
    Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
    Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
    sequenced by EMBL (European Molecular Biology Laboratories,
    Heidelberg/Germany) within the cDNA sequencing consortium of the
    German Genome Project
    This clone (DKFZP686E0632) is available at the RZPD in Berlin.
    Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
    Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
    information about the clone and the sequencing project is available
    at http://mips.gsf.de/proj/cDNA/.
    FEATURES
    source
    1. 7090
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFZP686E0632"
        /tissue type="human testis"
        /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
        DH10B; sites SfiI + SfiII"
        /dev_stage="adult"
        /polyA_signal
        /polyA_site
        /ORIGIN
        Query Match 28.1%; Score 225.2; DB 9; Length 7090;
        Best Local Similarity 64.8%; Pred. No. 5.1e-51;
        Matches 385; Conservative 0; Mismatches 173; Indels 36; Gaps 2;
    QY 212 TATGACAGGACATGCTATTCCACCCAGCCAAATGGATTCAGATTGATGACTTCCTGG 271
    DB 5731 TATGACAGGACATGCTATTCCACCCACCAAGTGGATTCCTCTGCTGACGACTTCAAG 5790
    QY 272 TTTTCAGCAAGATAGGATGATGACAGAACTGGTAGCAATGCACCTGTGGGAGAACGT 331
    DB 5791 TCTCAGCAAGATGGCTGATTCAGAACTGGTAGTACGATTTGTAGAGAGGCCAA 5850
    QY 332 TACCAGCAGTTTCTCTGGAGATGACCTAGAAATGCAGAGAAACAGCCTC----- 379
    DB 5851 AAACCTGCAGTCTCTCCGTAGATGACCAAAAAGACCCAGTAGCATCTACTTTGGAGGCTAT 5910
    QY 380 -----CTCTCCAAAAGCCACGAGAAATTAATGCTGATATAAAACG 421
    DB 5911 GCCAAATACATCAAAATCACTCTGCTATGGCAGCAAGGAATCAATGCTGATATAAACA 5970
    QY 422 TAAATTAGTGAAGGAATCCCGATCGGTTGGACAAAATATGAAAAATCTTCAAATGCT 481
```

Db 5971 TCATTAATGAGGAAGTTGCGAAGCTTTGGTCGAAATATGAAGAATTTTCATTTTGGT 6030

QY 482 TGAAGGATGCAAGACCTACTGAGTCAGGAGCGATTTTGAATCCATCATCAAGGA 541

Db 6031 TGAAGAATGCAAGACCTCTGGAGATGAAGAAACAGTTTGTGAATTTACCATCAAGGA 6090

QY 542 AGCACAAGATGTATGAGACGAGACTTTGTTAAGCACCTTAAGAGAACTGAAACGCTAT 601

Db 6091 AGCCCAAGGTTTAAAGACGAGTCTTAATTCAGTACCTTTCGAGAGGTACTAGAAAAAT 6150

QY 602 GATTTGAGATACTTGTCTCGGAGATATACACCCCAATATGCAATCTCGTTAATG 661

Db 6151 AAATTTCCACCACTTCAACAACATTAGTCACATCAACAGCAGATCATCATGTAGTG 6210

QY 662 -----ATTGAGCAGAGAAAGCATCAGATTGCTGTTTCTACAAATGAGCAGCATATTG 715

Db 6211 CAAAGACAGTGAAGAAAAATGACAGTTTCTGCTGTAGTATGAAACAGATATTG 6270

QY 716 CTGAAGTCTCTGGCATATGTTACCGAATCAAAATAGCCTTCAGAGGCTAAGAA 769

Db 6271 TTGAAGCCTCTGGAATGTTTTCAGTCAAGGGAATTTGCTTCAGATGCTAAGAA 6324

RESULT 13

AL953870/c

LOCUS

DEFINITION

Human DNA sequence from clone RP11-97N5 on chromosome X, complete sequence.

ACCESSION

AL953870

VERSION

AL953870.2 GI:24527892

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 69776)

Heath, P.

Direct Submission

Submitted (01-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

HumQuery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Nov 3, 2002 this sequence version replaced gi:24410492.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>

RP11-97N5 is from the library RPi-11.1 constructed by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

Location/Qualifiers

1..69776

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="X"

/clone="RP11-97N5"

/clone_lib="RPCI-11.1"

ORIGIN

Query Match 28.1%; Score 224.8; DB 9; Length 69776;

Best Local Similarity 93.3%; Pred. No. 5.8e-51;

Matches 235; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 549 AGATGATGAGACGACACTTTGTTAAGCACCTTAAAGAGAACTGAAACGTTGATTTGA 608

Db 47834 AGATATATGAGCGAGACTTTGTTGAGCTCTTGAAGAGAACTGGAACATGATTTGG 47775

QY 609 GAATACTTGTCTCGGAGGATATACACCCCAATGCAATCTCTGTTAATGATTTGAGG 668

Db 47774 GAGTACTTGTCCATGGAGGATATACACCCCAATGCAATCTCTGTTAATGATTTCAAG 47715

QY 669 AGAGAAAGGATCAGATTGCTGTTTCTACAAATGAGGAGGATATGCTGGAAGTCTCCTG 728

Db 47714 AGAGAAAGGATCAGATTGCTGTTTCTGCAATGAGGAGGATATGCTGGAAGTCTCCTG 47655

QY 729 GCATATGTTACCGAATCAAAATAGCCTTCAGAGGCTTAAGAAATTTCTGTTAGTAAAGAT 788

Db 47654 GCATATGTTACTGAATCAAAATGCGCTTCAGAGGCTTAAGAAATTTCTGTTAGTAAAGAT 47595

QY 789 GTTCTTTTTCCTCC 800

Db 47594 GTTCTTTTTCCTCC 47583

RESULT 14

AK123209

LOCUS

DEFINITION

Homo sapiens cDNA FLJ41215 fis clone BRAL22017359, weakly similar to Homo sapiens RNA helicase HDB/DICE1 mRNA.

ACCESSION

AK123209

VERSION

AK123209.1 GI:34528699

KEYWORDS

oligo capping; fis (full insert sequence).

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Waga, S., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuko, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 1840)

Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-kamakarui, Kisarazu, Chiba 292-0818, Japan

(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers

```
source
1. .1840
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRALZ2017359"
/tissue_type="alzheimer cortex"
/clone_lib="BRALZ2"
/notes="cloning vector: pME189FL3"
47. .973
CDS
/notes="unnamed protein product"
/codon_start=1
/protein_id="BAC85559.1"
/db_xref="GI:34528700"
/translation="MGNVDEYLTASPLREIDROPKELHTFGNPFQDKKGMWIDE
AEFVAPGNKVRFGPEPNSPMSSKRRMSLLLRKQTPPTVTHVGKGFPSRWF
PSYFLIKETLVHIDATIIHDGHEEREMNGITPDGFLSKSPSELINWTDGLMPNQ
VDSLSDDISLQKGLIQEGSNFVGGAKNCSLVDKQDPVASTLGLAMPTLQITP
AMAGINADIKQLMKVEKFKRYERIFILLVEVQGPFLMKKQFVEFTKEAARFKR
RVLIQYLEKVLKINSHLHNNINSHNRSSC"

ORIGIN
Query Match 27.9%; Score 223.6; DB 9; Length 1840;
Best Local Similarity 64.6%; Pred. No. 1.5e-50;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;

QY 212 TATGACAGGACATGCTATTCCACCAGCCAAATGGATTCTCAGATTGATGACTTCACCTGG 271
DB 496 TATGACAGGAGATCTTATGCCACCCCAACCAAGTGGATTCTCTGTCTGACGACTTCACAAG 555
QY 272 TTTTCAGCAAGATAGATGATGACAGAAACCTGTGTAGCAATGCMCTGTGGGAGGAAACGT 331
DB 556 TCTCAGCAAGATGGGCTGATTCANAAACCTGTGTAGTAACGCAATTTGTAGGAGGACAA 615
QY 332 TACCAGCAGTTCTCTGGAGATGACCTAGAAATCAGAGAAACAGCCCTC----- 379
DB 616 AACTGCACTCTCTCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGCTAT 675
QY 380 -----CTCTCCAAAAGCCAAAGCAAAATTAATGCTGTATATAAACG 421
DB 676 GCCAAATACATTACAAATCACTCTGCTATGGCACAAGGAATCAATGCTGTATATAACA 735
QY 422 TAAATTAGTGAAGGAATCCGATGCGTTGGACAAAAATATGAAAAAATCTTCGAAATGCT 481
DB 736 TCAATTAAAGAAGGATTCGAAAGTTGGTCGAAATATGAAGANATTTTCAATTTGCT 795
QY 482 TGAAGAGTCAAGGACCTACTGCAATCAGGAAGCGATTTTGAATCCATCATCAAGGA 541
DB 796 TGAAGAAGTCAAGGACCTCTGGAGATGAAGAAACAGTTTGTGTAATTTACCATCAAGGA 855
QY 542 AGCAGCAAGATGTATGACAGGACATTTGTTAAGCACCTTTAAGAGAAACTGAACGCTAT 601
DB 856 AGCGCAAGGTTTAAAGACGATCTCTAATTCAGTACCTTGAGAGGTAAGTACGAAAAAT 915
QY 602 GATTGAGAAATCTGTCCCTGGAGGATATCAACCCCAATATGCAATATCTCGTTAATG 661
DB 916 AAATTTCCACCACTTCACAAACATTAAGTACATCAACAGCAGATCATATGTTAGTG 975
QY 662 -----ATTGAGGAGAGAAAGGATCAGATTGCTGTTTCTACAAATGGAGCAGGATATTG 715
DB 976 CAAAGACCAATGAGAAAAAATGACAAAGTTTCTGTGCTGTAGATGGACAGGATATTG 1035
QY 716 CTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAA 769
DB 1036 TTGAAGCCTCTGGATGTTTGAATCAAGGGGATTCCTTCCAGATGCTTAAGAA 1089
```

```
RESULT 15
AX834225
LOCUS
DEFINITION
Sequence 1349 from Patent EPI347046.
AX834225
ACCESSION
VERSION
AX834225.1 GI:39920360
KEYWORDS
```

```
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuho, Y.
Full-length cDNA sequences
Patent: EP 1347046-A 1349 24-SEP-2003;
Research Association for Biotechnology (JP)
FEATURES
source
1. .3528
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 27.9%; Score 223.6; DB 6; Length 3528;
Best Local Similarity 64.6%; Pred. No. 1.5e-50;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;

QY 212 TATGACAGGACATGCTATTCCACCAGCCAAATGGATTCTCAGATTGATGACTTCACCTGG 271
DB 2178 TATGACAGGAGATCTTATGCCACCCCAACCAAGTGGATTCTCTGTCTGACGACTTCACAAG 2237
QY 272 TTTTCAGCAAGATAGATGATGACAGAAACCTGTGTAGCAATGCAACCTGTGGGAGGAAACGT 331
DB 2338 TCTCAGCAAGATGGGCTGATTCAAAAACCTGTGTAGTACGCAATTTGTAGGAGGACCAA 2297
QY 332 TACCAGCAGTTCTCTGGAGATGACCTAGAAATCAGAGAAACAGCCCTC----- 379
DB 2298 AAACCTGCACTCTCTCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGCTAT 2357
QY 380 -----CTCTCCAAAAGCCAAAGCAAAATTAATGCTGTATATAAACG 421
DB 2358 GCCAAATACATTACAAATCACTCTGCTATGGCACAAGGAATCAATGCTGTATATAACA 2417
QY 422 TAAATTAGTGAAGGAATCCGATGCGTTGGACAAAAATATGAAAAAATCTTCGAAATGCT 481
DB 2418 TCAATTAAAGAAGGATTCGAAAGTTGGTCGAAATATGAAGAAATTTTCATTTTGTCT 2477
QY 482 TGAAGGATGCAAGGACCTACTGCAATCAGGAAGCGATTTTGAATCCATCATCAAGGA 541
DB 2478 TGAAGAAGTCAAGGACCTCTGGAGATGAAGAAACAGTTTGTGTAATTTACCATCAAGGA 2537
QY 542 AGCAGCAAGATGTATGACAGGACATTTGTTAAGCACCTTTAAGAGAAACTGAACGCTAT 601
DB 2538 AGCGCAAGGTTTAAAGACGAGTCTCTAATTCAGTACCTTTGAGAAGGTAAGTACGAAAAAT 2597
QY 502 GATTGAGAAATCTGTCCCTGGAGGATATCAACCCCAATATGCAATATCTCGTTAATG 661
DB 2598 AAATTTCCACCACTTCACAAACATTAAGTACATCAACAGCAGATCATCATGTTAGTG 2657
QY 662 -----ATTGAGGAGAGAAAGGATCAGATTGCTGTTTCTACAAATGGAGCAGGATATTG 715
DB 2658 CAAAGACCAATGAGAAAAAATGACAAAGTTTCTGTGCTGTAGATGGACAGGATATTG 2717
QY 716 CTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAA 769
DB 2718 TTGAAGCCTCTGGATGTTTGAATCAAGGGAAATTCCTTCCAGATGCTTAAGAA 2771

Search completed: April 25, 2004, 18:57:33
Job time : 2112.57 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 07:00:48 ; Search time 923.538 Seconds
(without alignments)
16458.288 Million cell updates/sec

Title: US-10-051-835-11

Perfect score: 509

Sequence: 1 gactgtgagggtgtgagg.....agttttctccaaaaaaa 509

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:**

2: em_esthum:**

3: em_estin:**

4: em_estmu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_estc:**

9: gb_est1:**

10: gb_est2:**

11: gb_est3:**

12: gb_est4:**

13: gb_est5:**

14: gb_est6:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pln:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_phg:**

27: em_gss_vrl:**

28: gb_gss1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509	100.0	570	14	CB994958
2	507.4	99.7	570	14	CB992682
3	502.4	98.7	524	11	AF318372
4	499	98.0	499	12	BG354572

5	499	98.0	547	14	N40147	N40147 yw73812.r1
6	481.2	94.5	849	12	BG436305	BG436305 602508742
7	469.4	92.2	520	14	CB961487	CB961487 AGENCOURT
8	432.8	85.0	1176	14	CK230556	CK230556 ILLUMIGEN
9	431.4	84.8	503	9	A1742551	A1742551 wg55c11.x
10	425.8	83.7	429	9	A1189067	A1189067 qd18a09.x
11	419.8	82.5	534	12	BG436468	BG436468 602509139
12	413.8	81.3	430	14	N27023	N27023 yw73812.r1
13	387	76.0	1157	14	CK230595	CK230595 ILLUMIGEN
14	380.4	74.7	394	14	D59091	D59091 HOM521C10B
15	371	72.9	382	13	BX283272	BX283272 BX283272
16	337.4	66.3	756	10	BE903565	BE903565 601677770
17	337.4	66.3	780	10	BZ734431	BZ734431 601566206
18	335.4	65.9	673	14	CB995986	CB995986 AGENCOURT
19	334	65.6	569	12	BG435916	BG435916 602508269
20	333.6	65.5	453	9	A1189715	A1189715 qd28608.x
21	333.6	65.5	468	9	A1128458	A1128458 qc39a12.x
22	331.6	65.1	496	9	A1188535	A1188535 qd09e11.x
23	331.2	65.1	571	14	N32547	N32547 yw86a06.s1
24	330.6	65.0	468	9	AA039331	AA039331 zk39e06.s
25	329.4	64.7	908	12	BG336433	BG336433 602405375
26	329	64.6	483	9	A1149003	A1149003 qc75a02.x
27	327.6	64.4	496	9	AA993399	AA993399 ct93c08.s
28	326.6	64.2	387	14	T84951	T84951 yd55d10.r1
29	325.4	63.9	592	10	AW972530	AW972530 EST384621
30	322.6	63.4	543	14	N30289	N30289 yw69f02.s1
31	320	62.9	706	10	BE281431	BE281431 601154945
32	318.6	62.6	445	10	BE302172	BE302172 bb92d02.x
33	317.4	62.4	532	9	AA737311	AA737311 nw51g04.s
34	317	62.3	533	14	T87105	T87105 yd88a11.s1
35	316.6	62.2	422	9	AA505794	AA505794 mh98c05.s
36	313	61.5	782	12	BG336384	BG336384 602405325
37	309.8	60.9	437	9	A1740470	A1740470 wg15g08.x
38	309.4	60.8	652	12	BG623213	BG623213 602648125
39	305.4	60.0	982	10	BE900651	BE900651 601673578
40	304.6	59.8	421	9	AA722699	AA722699 zg82c03.s
41	302.4	58.4	588	10	BE733225	BE733225 601568462
42	300	58.9	429	9	A1200158	A1200158 qf97d02.x
43	288.4	56.7	512	14	W93043	W93043 zd93f02.s1
44	280.2	55.0	404	14	H95793	H95793 yv18604.s1
45	273.8	53.8	349	9	A1186558	A1186558 qd21a09.x

ALIGNMENTS

RESULT 1	CB994958	570 bp	mRNA	linear	EST 01-MAY-2003
LOCUS	AGENCOURT_13643389	NIH_MGC_148	Homo sapiens	cdna clone	
DEFINITION	IMAGE:30335086.5	5'	mRNA sequence.		
ACCESSION	CB994958				
VERSION	CB994958.1	GI:30289478			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 570)				
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Dr. Stefan Hansson CDNA library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Fiero Carninci (RIKEN) CDNA library Arrayed by: The I.M.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM356 row: f column: 23				


```
Db 463 AAGCTGAACACACAAACAGTCTTTTATCTAAGATATTTGACTTAAAAATATCAACA 522
QY 481 AACTTTTCAGCTTTCTCCAAAAA 509
Db 523 AACTTTTCAGCTTTCTCCAAAAA 551

RESULT 3
LOCUS AF318372 524 bp mRNA linear HTC 01-JAN-2002
DEFINITION Homo sapiens pp9012 mRNA, complete cds.
ACCESSION AF318372
VERSION AF318372.1 GI:18027835
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 524)
AUTHORS Zhou,X.M., Zhang,P.P., Jiang,H.Q., Huang,Y., Qin,W.X., Zhao,X.T.,
Wan,D.F. and Gu,J.R.
TITLE Novel human cDNA clones with function of inhibiting cancer cell
growth
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 524)
AUTHORS Zhou,X.M., Zhang,P.P., Jiang,H.Q., Huang,Y., Qin,W.X., Zhao,X.T.,
Wan,D.F. and Gu,J.R.
DIRECT SUBMISSION
JOURNAL Direct Submission
TITLE Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai
200032, P. R. China
FEATURES
source 1..524
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..524
/gene="pp9012"
73..408
/gene="pp9012"
/codon_start=1
/product="unknown"
/protein_id="AAL55879.1"
/db_xref="GI:18027836"
/translation="MIWRGRSTYRHRPRRSVPPPELIGPMLPEGDPEPQEEPTESR
DPAQGEEDQGAETQVPLEADLQELSQSKTGBCGNGPDDQGLPKSEQKXP
EGSDRQPV"

ORIGIN
Query Match 98.7%; Score 502.4; DB 11; Length 524;
Best Local Similarity 99.8%; Pred. No. 4.3e-112;
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTGAGGGTGTAGGGTTCGGTTCCTGCTGTGGACTTTTCTGCCACTGAGACGCAG 65
Db 2 GTGAGGGTGTAGGGTTCGGTTCCTGCTGTGGACTTTTCTGCCACTGAGACGCAG 61

QY 66 CTGTGTGAATATGATTTGGCGAGGAAGATCAACATATAGCCCTAGGCCGAGGAGAAGTG 125
Db 62 CTGTGTGAATATGATTTGGCGAGGAAGATCAACATATAGCCCTAGGCCGAGGAGAAGTG 121

QY 126 TACCACCTCTGAGCTGATGGCCCTATGCTGGAGCCGGTGATGAGGAGCCTCAGCAAG 185
Db 122 TACCACCTCTGAGCTGATGGCCCTATGCTGGAGCCGGTGATGAGGAGCCTCAGCAAG 181

QY 186 AGGAACCCACCACTGAAAGTCGGGATCCTGCACCTGGTCCAGGAGAGAAGAAGATCAGG 245
Db 182 AGGAACCCACCACTGAAAGTCGGGATCCTGCACCTGGTCCAGGAGAGAAGAAGATCAGG 241

QY 246 GTGAGCTGAGACTCAAGTGCCCTGACCTGGAGCTGATCTCCAGGAGCTGTCTCAGTCAA 305
Db 242 GTGAGCTGAGACTCAAGTGCCCTGACCTGGAGCTGATCTCCAGGAGCTGTCTCAGTCAA 301
```

```
QY 306 AGACTGGGGCTGAATCTGGAATGTCTGTGATGACACAGGGGGAAGATTCTGCCAAATCAG 365
Db 302 AGACTGGGGCTGAATCTGGAATGTCTGTGATGACACAGGGGGAAGATTCTGCCAAATCAG 361
QY 366 AACAAATTAAATGCGCAGAAAGAGGTGACAGGCAACACAGCTTTAAATGAAGACAGCT 425
Db 362 AACAAATTAAATGCGCAGAAAGAGGTGACAGGCAACACAGCTTTAAATGAAGACAGCT 421
QY 426 GAAACAACAACAACCTGTTTTTATCTAAGATATTTGACTTAAAAATATCAAAATAAATT 485
Db 422 GAAACAACAACAACCTGTTTTTATCTAAGATATTTGACTTAAAAATATCAAAATAAATT 481
QY 486 TTGCAGCTTTCTCCAAAAA 509
Db 482 TTGCAGCTTTCTCCAAAAA 505

RESULT 4
LOCUS BG354572 499 bp mRNA linear EST 05-MAR-2001
DEFINITION PLAC6 Human placenta cDNA expression library Homo sapiens cDNA
clone 253708 similar to PLAC6 placenta specific gene 6, mRNA
sequence.
ACCESSION BG354572
VERSION BG354572.1 GI:13198770
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 499)
AUTHORS Wong,S.L. and Walker,M.G.
TITLE Placental genes identified by large-scale expression analysis
JOURNAL Unpublished (2001)
COMMENT Contact: Michael Walker
Incyte Genomics
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 845-5771
Fax: 650 621 8514
Email: mwalker@incyte.com.
FEATURES
source 1..499
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="253708"
/clone_lib="Human placenta cDNA expression library"
/notes="Organ: placenta"

ORIGIN
Query Match 98.0%; Score 499; DB 12; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTGTGAGGGTGTAGGGTTCGGTTCCTGCTGTGTGGACTTTTCTGTCCACTGAGA 60
Db 1 GAGTTGTGAGGGTGTAGGGTTCGGTTCCTGCTGTGTGGACTTTTCTGTCCACTGAGA 60

QY 61 CGCAGCTGTGTGAAATATGATTTGGCGAGGAAGATCAACATATAGCCCTAGGCCGAGGAG 120
Db 61 CGCAGCTGTGTGAAATATGATTTGGCGAGGAAGATCAACATATAGCCCTAGGCCGAGGAG 120

QY 121 AAGTGTACCACTCTCTGAGCTGATTTGGGCTATGTGGAGCCCGGTGATGAGAGCCTCA 180
Db 121 AAGTGTACCACTCTCTGAGCTGATTTGGGCTATGTGGAGCCCGGTGATGAGAGCCTCA 180

QY 181 GCAAGAGGAACCAACCACTGAAAGTCGGGATCCTGCACCTGCTGAGGAGAGAAGAAGA 240
Db 181 GCAAGAGGAACCAACCACTGAAAGTCGGGATCCTGCACCTGCTGAGGAGAGAAGAAGA 240

QY 241 TCAGGGTGTGAGCTGAGACTCAAGTGCCTGACTGAGAGCTGATCTCCAGGAGCTGTCTCA 300
Db 241 TCAGGGTGTGAGCTGAGACTCAAGTGCCTGACTGAGAGCTGATCTCCAGGAGCTGTCTCA 300
```


QY	301	GTCAAAGACTGGGGTGTAATGTGAAATGGTCTGTATGACACGGGGAAGATTCTGCCAAA	360
Db	301	GTCAAAGACTGGGGTGTAATGTGAAATGGTCTGTATGACACGGGGAAGATTCTGCCAAA	360
QY	361	ATCAGAAACAAATTTAAATATGCCAAGGAGGTGACAGCAACACACAGGTTTAAATGAAGAC	420
Db	361	ATCAGAAACAAATTTAAATATGCCAAGGAGGTGACAGCAACACACAGGTTTAAATGAAGAC	420
QY	421	AGCTGAAACAACAACAACTGTTTTTATCTAAGATATTTGACTTAAATAATCAAAATA	480
Db	421	AGCTGAAACAACAACAACTGTTTTTATCTAAGATATTTGACTTAAATAATCAAAATA	480
QY	481	AACTTTTGCAGCTTTCTCC	499
Db	481	AACTTTTGCAGCTTTCTCC	499

RESULT 5	N40147	LOCUS	DEFINITION	N40147	547 bp	mRNA	linear	EST 22-JAN-1996
				yy73e12.r1	Soares	placenta	8c09weeks_2bhp8to9w	Homo sapiens cDNA clone IMAGE:257902 5', mRNA sequence.

N40147
 accession
 version
 keywords
 source
 organism
 N40147.1
 GI:1163692
 EST.
 Homo sapiens
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 547)
 Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, N., Lemon, G., Marra, M.,
 Parsons, J., Rifkin, L., Roelling, T., Soares, M., Tan, F.,
 Trevaske, E., Waterston, R., Williamson, A., Wohlmann, P., and
 Wilson, R.

TITLE
The WashU-Merck EST Project
WILSON, K.

JOURNAL
COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 450

Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7

High quality sequence stop: 450.

FEATURES	
1	Location/Qualifiers
1	547

```
source
1.54 /
/organisms="Homo sapiens"
```

```
/organism="Homo sapiens"
/mol type="mrna"
```

```
/db xref="GDB:3887512"
```

```
/db_xref="taxon:9606"
```

```
/clone="IMAGE:257902"
```

```
/dev_stage="two places
from 8 weeks post conc
```

```
from 9 weeks post conc
/lab host="DH1.08 (ampi
```

```

/Tab_HOVC="DHIVB (ampl
/clone lib="Soares pla

```

```
/note="Organ: placenta
```

modified polylinker; S

strand cDNA was primed

TGTTACCAATCTGAAGTGGGAG

double-stranded cDNA w
adapters (Pharmacia).

adapters (Fluorimacia), the Not I and Eco RI s

and No. 1 and 100 ml (Pharmacia). Library of

M. Fatima Bonaldo."

ORIGIN

[illegible]

Query Match 98.0%; score 493

	Best Local Similarity	98.6%;	Pred: NO. 3e-11l;	Mismatches	0;	Gaps	0;
	Matches	502;	Conservative	0;			
QY	.	1	GAGTTGTGAGGGTGTGAGGGTCGCGTCTCTGCTGTCTGACATTTTTCTGTCCACTGAGA	60			
Db		36	GAGTTGTGAGGGTGTGAGGGTCGCGTCTCTGCTGTCTGACATTTTTCTGTCCACTGAGA	95			
QY		61	CGCAGCTGTGTGAATAATCATATTGGCGAGGAGATCAACATATAGGCCCTAGGCCGAGGAG	120			
Db		96	CGCAGCTGTGTGAATAATCATATTGGCGAGGAGATCAACATATAGGCCCTAGGCCAAGGAG	155			
QY		121	AAGTGTAACCACTCTCTGAGCTGATTTGGGCCTATGCTGGAGCCGCGTGATGAGAGAGCTCA	180			
Db		156	AAGTGTAACCACTCTCTGAGCTGATTTGGSCCTATGCTGGAGCCGCGTGATGAGAGAGCTCA	215			
QY		181	GCAAGAGGAACCAACAACTGAAGAAGTCGGGATCTGTCACTGTGTGAGAGAGAGAAGA	240			
Db		216	GCAAGAGGAACCAACAACTGAAGAAGTCGGGATCTGTCACTGTGTGAGAGAGAGAAGA	275			
QY		241	TCAGGGTGCAGCTGAGACTCAAGTGCTTGACCTGGAAGCTGATCTCCAGGAGCTGTCTCA	300			
Db		276	TCAGGGTGCAGCTGAGACTCAAGTGCTTGACCTGGAAGCTGATCTCCAGGAGCTGTCTCA	335			
QY		301	GTCAAAGACTGGGGGTGAATGTGGAATGGTCTGTATGACCAGGGGAAGATTCGCCCCAAA	360			
Db		336	GTCAAAGACTGGGGGTGAATGTGGAATGGTCTGTATGACCAGGGGAAGATTCGCCCCAAA	395			
QY		361	ATCAGAACATTTTAAATGCCAAGGGGTGACAGGCAACACAGGTTTAAATGAGAC	420			
Db		396	ATCAGAACATTTTAAATGCCAAGGGGTGACAGGCAACACAGGTTTAAATGAGAC	455			
QY		421	AAGCTGAACAACAACAAAACTGTTTTTATCTAAGATATTTGACTTAAAAATATCAAAATA	480			
Db		456	AAGCTGAACAACAACAAAACTGTTTTTATCTAAGATATTTGACTTAAAAATATCGANATT	515			
QY		481	AACTTTGGAGCTTTCTCCAAAAAAAAAAAA	509			
Db		516	AACTTTGGAGCTTTCTCCAAAAAAAAAAAA	544			

RESULT 6	linear	EST 14-MAR-2001
BG436305	849 bp	
LOCUS	mRNA	
DEFINITION	602508742F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:460558 5', mRNA sequence.	

ACCESSION	BG436305	
VERSION	BG436305.1	GI:13342811
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Canidae; Canis
1 (bases 1 to 849)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCMI343 row: d column: 11
High quality sequence stop: 514.

```

FEATURES
source
Location/Qualifiers
1. 849
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:4605658"

```

THE

/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_79"
/note="Organ: placenta; Vector: pNR-LIB (Clontech);
Site 1: SfiI (ggccgctcgcc); Site 2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 94.5%; Score 481.2; DB 12; Length 849;
Best Local Similarity 99.0%; Pred. No. 7.1e-107;
Matches 505; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 GAGTTGTGAGGTTGTGAGGTTGCGGTTCTGCTGTCTGACATTTTCTGCTCCACTGAGA 60
DB 12 GAGTTGTGAGGTTGTGAGGTTGCGGTTCTGCTGTCTGACATTTTCTGCTCCACTGAGA 71
QY 61 CCGACTGTGTCAATATGATTTGGCGGAGATCAATATAGCCCTAGCCGAGGAG 120
DB 72 CCGAGCTGTGTGAATATGATTTGGCGGAGATCAATATAGCCCTAGCCGAGGAG 131
QY 121 AAGTGTACCACTCTCTGAGCTGATTTGGGCTATGCTGGAGCCCGTGTATGAGGACCTCA 180
DB 132 AAGTGTACCACTCTCTGAGCTGATTTGGGCTATGCTGGAGCCCGTGTATGAGGACCTCA 191
QY 181 GCAAGAGAACCAACCACTGAAAGTGGGATCTCTGACCTGTGAGGAGAGAGAGA 240
DB 192 GCAAGAGAACCAACCACTGAAAGTGGGATCTCTGACCTGTGAGGAGAGAGAGA 251
QY 241 TCAGGTTGAGCTGAGACTCAAGTGTGCTGACCTGAAAGTGTATCTCCAGGAGCTGTCTCA 300
DB 252 TCAGGTTGAGCTGAGACTCAAGTGTGCTGACCTGAAAGTGTATCTCCAGGAGCTGTCTCA 311
QY 301 GTCAAAGACTGGGGTGAATGTGAAATGTTGCTGATGACGAGGAGAGATCTGCCAAA 360
DB 312 GTCAAAGACTGGGGTGAATGTGAAATGTTGCTGATGACGAGGAGAGATCTGCCAAA 371
QY 361 ATCAGAACCAATTTAAATCCAGAGAGAGTGCACAGGCAACCAAGTTTAAATCAAGAC 420
DB 372 ATCAGAACCAATTTAAATCCAGAGAGAGTGCACAGGCAACCAAGTTTAAATCAAGAC 431
QY 421 AAGCTGAAACACACAAAAAC-TGTTTTATCTTAAGATATTGACTTTAA-AAATATCAAAA 478
DB 432 AAGCTGAAACACACAAAAACGTTTATCTTAAGATATTGACTTTAAAGAAATATCAAA 491
QY 479 TAACTTTTGCAGCTTTCTCCAAAAAAA 508
DB 492 TAACTTTTGCAGCTTTCTCCAAAAAAA 521

RESULT 7
CB961487
LOCUS
DEFINITION
AGENCOURT 13894159 NIH_MGC_148 Homo sapiens CDNA clone
IMAGE:30348215 5', mRNA sequence.
CB961487
CB961487
EST.
CB961487.1 GI:30217604
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 520)
NIH-MGC http://imgc.ncbi.nih.gov/
AUTHORS
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDM390 row: i column: 24
High quality sequence stop: 520.
Location/Qualifiers

FEATURES
source

1..520
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30348215"
/tissue_type="pre-eclampsic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/notes="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamHI; library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to 80% 5'. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NHGRI, in preparation).
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 92.2%; Score 469.4; DB 14; Length 520;
Best Local Similarity 99.8%; Pred. No. 5e-104; Indels 0; Gaps 0;
Matches 470; Conservative 0; Mismatches 1;

QY 39 GACTTTTCTGTCCTCCACTGAGAGCGAGCTGTGTGAAATATGATTTGGCGAGGAGATCAA 98
DB 27 GACTTTTCTGTCCTCCACTGAGAGCGAGCTGTGTGAAATATGATTTGGCGAGGAGATCAA 86
QY 99 CATATAGCCTAGGCGGAGGAGAGTGTACCACTCTGAGCTGATTTGGCCCTATGCTGG 158
DB 87 CATATAGCCTAGGCGGAGGAGAGTGTACCACTCTGAGCTGATTTGGCCCTATGCTGG 146
QY 159 AGCCCGTGTATGAGGAGCCTCAGCAAGAGAGAACCACTGAAAGTTCGGGATCTCTGCAC 218
DB 147 AGCCCGTGTATGAGGAGCCTCAGCAAGAGAGAACCACTGAAAGTTCGGGATCTCTGCAC 206
QY 219 CTGCTCAGGAGAGAGAGAGATCAGGCTGAGCTGAGACTCAAGTGCCTGACCTGGAAG 278
DB 207 CTGCTCAGGAGAGAGAGAGATCAGGCTGAGCTGAGACTCAAGTGCCTGACCTGGAAG 266
QY 279 CTGATCTCCAGGAGCTGTCTCAGTCAAGAGACTGGGGTGAATGTGAAATGTCCTGATG 338
DB 267 CTGATCTCCAGGAGCTGTCTCAGTCAAGAGACTGGGGTGAATGTGAAATGTCCTGATG 326
QY 339 ACCAGGGAGAGATTCTGCCAAATTCAGAACAAATTTAAATTCAGAGAGAGGTTGACGGC 398
DB 327 ACCAGGGAGAGATTCTGCCAAATTCAGAACAAATTTAAATTCAGAGAGAGGTTGACGGC 386
QY 399 ACCACAGAGTTTAAATGAGACAGCTGGAACACACAAACCTGTTTTATCTTAAGATAT 458
DB 387 ACCACAGAGTTTAAATGAGACAGCTGGAACACACAAACCTGTTTTATCTTAAGATAT 446
QY 459 TTGACTTTAAATATCAAAATAAACTTTTGCAGCTTTCTCCAAAAAAA 509
DB 447 TTGACTTTAAATATCAAAATAAACTTTTGCAGCTTTCTCCAAAAAAA 497

RESULT 8
CK230556
LOCUS
DEFINITION
ILLUMIGEN_MQ9_896 Katze_MWPL2 Macaca mulatta CDNA 5' similar to
1176 bp mRNA linear EST 09-DEC-2003
CK230556


```

Db 392 CACCTCCTGAGCTGATTGGGCGCTATGCTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGG 333
Qy 189 AACCAACCACTGAAAGTCGGGATCCTGCACCTGCTCAGGAGAGAGAAAGATCAGGGTG 248
Db 332 AACCAACCACTGAAAGTCGGGATCCTGCACCTGCTCAGGAGAGAGAAAGATCAGGGTT 273
Qy 249 CAGCTGAGACTCAAGTCCCTGACCTGGAAGCTGATCTCCAGGAGCTCTCTCAGTCAAAGA 308
Db 272 CAGCTAAGACTCAAGTCCCTGACCTGGAAGCTGATCTCCAGGAGCTCTCTCAGTCAAAGA 213
Qy 309 CTGGGGGTGAAATGTGGAATGCTCTGATGACCCAGGGGAAAGATCTCCCAAAATCAGAAC 368
Db 212 CTGGGGGTGAAATGTGGAATGCTCTGATGACCCAGGGGAAAGATCTCCCAAAATCAGAAC 153
Qy 369 AATTTAAANTCCAGAGGAGGTGACAGGCAACCAACAGGTTTAAATCAAGACAGCTGAA 428
Db 152 AATTTAAANTCCAGAGGAGGTGACAGGCAACCAACAGGTTTAAATCAAGACAGCTGAA 93
Qy 429 ACAACACAAAACCTGTTTATCTAAGATATTGACTTAAATAATATCAAAATAAATTTTG 488
Db 92 ACAACCAAAACCTGTTTATTTAAGATATTGACTTAAATAATATCAAAATAAATTTTG 33
Qy 489 CAGCTTCTCCAAAAAATAA 509
Db 32 CAGCTTCTCCAAAAAATAA 12

RESULT 10
A1189067/c
LOCUS
DEFINITION
qdi8a09.x1 Soares placenta 8to9weeks 2NDHPeto9W Homo sapiens cDNA
clone IMAGE:1724056 3', similar to SW:GGSE2_HUMAN Q13066 GAGE-2
PROTEIN. [1] ; mRNA sequence.
A1189067
A1189067.1 GI:3740276
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 602 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 363.
Location/Qualifiers
1..429
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1724056"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares placenta 8to9weeks 2NDHP8to9W"
/note="Organ: placenta; Vector: p7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; site 2: Eco RI; let
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCCCGAGCTTTTATTTTATTTT 3'] ,
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia) , digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia) . Library constructed by Bento Soares and
M. Fatima Bonaldo."
ORIGIN

```

```

Query Match 83.7%; Score 425.8; DB 9; Length 429;
Best Local Similarity 99.5%; Pred. No. 2.2e-93; Indels 0; Gaps 0;
Matches 427; Conservative 0; Mismatches 2;
Qy 77 ATGATTTTGGCGAGGAGATCAACATATAGGCTTAGGCCGAGGAGAGTGTACCACTCTCT 136
Db 429 ATGATTTTGGCGAGGAGATCAACATATAGGCTTAGGCCGAGGAGAGTGTACCACTCTCT 370
Qy 137 GAGCTGATTGGCCCTATGCTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGAACCA 196
Db 369 GAGCTGATTGGCCCTATGCTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGAACCA 310
Qy 197 ACTGAAAGTCGGGATCTCTGCACCTGCTCAGGAGAGAGAGATCAGGGTGCAGTGA 256
Db 309 ACTGAAAGTCGGGATCTCTGCACCTGCTCAGGAGAGAGAGATCAGGGTGCAGTGA 250
Qy 257 ACTCAAGTGCCTGACTGGAAGCTGATCTCCAGGAGCTCTCAGTCAAGAGCTGGGGT 316
Db 249 ACTCAAGTGCCTGACTGGAAGCTGATCTCCAGGAGCTCTCAGTCAAGAGCTGGGGT 190
Qy 317 GAATGTGGAATGCTCTGATGACCCAGGGGAAAGATTTCTCCAAAATCAGAACTTTAAA 376
Db 189 GAATGTGGAATGCTCTGATGACCCAGGGGAAAGATTTCTCCAAAATCAGAACTTTAAA 130
Qy 377 ATGCCAAGAGGAGGTGACAGGCAACCAACAGGTTTAAATGAGACAGCTGAACACACA 436
Db 129 ATGCCAAGAGGAGGTGACAGGCAACCAACAGGTTTAAATGAGACAGCTGAACACACA 70
Qy 437 AAATGTTTTTATCTAAGATATTGACTTAAATAATCAAAATAAATTTTTCAGCTTTC 496
Db 69 AAATGTTTTTATCTAAGATATTGACTTAAATAATCAAAATAAATTTTTCAGCTTTC 10
Qy 497 TCCAAAAA 505
Db 5 TCCAAAAA 1

RESULT 11
BG436468 534 bp mRNA linear EST 14-MAR-2001
602509139F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4619720 5',
mRNA sequence.
BG436468
BG436468.1 GI:13342974
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 534)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM1379 row: n column: 09
High quality sequence stop: 523.
Location/Qualifiers
1..534
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4619720"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech) ;

```